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(21) International Application Number: PCT/US98/04493 (22) International Filing Date: 6 March 1998 (06.03.98) (30) Priority Data: <table border="0"><tr><td>60/040,162</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,333</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/038,621</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,161</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,626</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,334</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,336</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/040,163</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr><tr><td>60/043,580</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr><tr><td>60/043,568</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr></table> <p>(Continued on the following page)</p> (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hills Road, Laytonsville, MD 20882 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield, Place, Centreville, VA 22020 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). BEDNARIK, Daniel, P. [US/US]; 8822 Blue Sea Drive, Columbia, MD 21046 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown,		60/040,162	7 March 1997 (07.03.97)	US	60/040,333	7 March 1997 (07.03.97)	US	60/038,621	7 March 1997 (07.03.97)	US	60/040,161	7 March 1997 (07.03.97)	US	60/040,626	7 March 1997 (07.03.97)	US	60/040,334	7 March 1997 (07.03.97)	US	60/040,336	7 March 1997 (07.03.97)	US	60/040,163	7 March 1997 (07.03.97)	US	60/043,580	11 April 1997 (11.04.97)	US	60/043,568	11 April 1997 (11.04.97)	US	MD 20874 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mount Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment #104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [BU/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US). (74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
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(54) Title: 186 HUMAN SECRETED PROTEINS (57) Abstract <p>The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>																																	

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186 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 12301 Park Lawn Drive, Rockville, Maryland 20852, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA contained within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be
10 single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in testes tumor and to a lesser extent in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly of the testes, and defects of the central nervous system such as seizure and neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly cancer of the testes and central nervous system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, brain and other tissue of the nervous system, and blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of testicular cancer and treatment of central nervous system disorders since this gene is primarily expressed in the testes tumor and developing brain.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in cancer tissues, such as breast cancer and Wilm's tumor, and to a lesser extent in fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and/or tumors, particularly, those found in the breast, and developmental abnormalities or disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and fetal tissue and, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 314 as residues: Pro-11 to Thr-18, Leu-43 to Pro-50, Gly-64 to Leu-72, and Leu-81 to Lys-86.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of cancers and/or tumors, particularly, those found in the breast since expression is mainly in cancer/tumor tissues. May serve as therapeutic proteins for proliferation/differentiation of fetal tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in spleen, chronic lymphocytic leukemia.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or leukemias, diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
- 10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
- 15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders or
- 20 leukemias, diseases of the immune system since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in CD34 depleted buffy coat.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or lymphocytic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 30 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
- 35 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 5**

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous
15 and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 317 as residues:
20 Pro-13 to Lys-21.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 6**

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
30 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., and blood cells, and
35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 318 as residues: Lys-31 to Lys-39.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood diseases since it is expressed in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in pineal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system and brain associated diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders, immune diseases or brain associated diseases (specifically of the pineal gland) since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

The translation product of this gene shares sequence homology with an organic cation transporter which is thought to be important in organic cation uptake in the kidney and liver. (See Accession No. 2343059.) Preferred polypeptide fragments comprise the amino acid sequence ITIAIQMICLVNXELYPTFVRNXGVMVCSSLCDIGGIITP FIVFRLREVWQALPLILFAVLGLLAAGVTL LLPETKGVALPETMKDAENLGRKAKPKENTIY LK VQTSEPSGT (SEQ ID NO: 615) or TMKDAENLGRKAKPKENT (SEQ ID NO: 616) as well as N-terminal and C-terminal deletions of these fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic and renal diseases where drug elimination/cation exchange (organic cation uptake) in the liver and kidney are problematic. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic or renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 320 as residues: Asn-64 to Asn-74, and Gln-81 to Gly-87.

The tissue distribution and homology to organic cation transporter indicate that polynucleotides and polypeptides corresponding to this gene are useful as a polyspecific transporter that is important for drug elimination in the liver (and possibly kidney) since expression is found in the liver.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in eosinophil induced with IL-5 and to a lesser extent in fetal liver and spleen. This gene also maps to chromosome 15, and therefore can be used in linkage analysis as a marker for chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system, particularly allergies or asthma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosis of diseases involving eosinophil reactions since expression seems to be concentrated in eosinophils and other tissues involved in immunity such as the liver and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in tissues of hematopoietic lineage and to a lesser extent in Hodgkins lymphoma. Any frame shifts in this sequence can easily be clarified using known molecular biology techniques.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and immune deficiency or dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, lymphoid and reticuloendothelial tissues, and cancerous tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/ diagnosis for lymphomas or immune dysfunction or as a therapeutic protein useful in immune modulation based on expression in anergic T-cells and lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in neutrophils and to a lesser extent in activated lymphoid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the cell type present in a biological sample and for diagnosis of diseases and conditions: inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
5 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 323 as residues: Glu-40 to Lys-46.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for modulation of an immune reaction or as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

15 This gene is expressed primarily in brain and to a lesser extent in activated T-cells. It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. Preferred polypeptide fragments comprise the amino acid sequence PRVRNSPEDLGLSLTGDSCKL (SEQ ID NO:617).

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative disorders including ischemic shock, alzheimers and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain, and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
30 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 324 as residues: Ser-5 to Glu-14, Ile-21 to Pro-35, Ser-65 to Asp-81, Cys-89 to Val-96, Lys-136 to Ser-145, Ile-152 to Met-169, and Arg-189 to Lys-196.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic/treatment for cancers of the given tissue or in the treatment of neurological disorders of the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene was also recently cloned by other groups, naming this calcium-activated potassium channel gene, hKCa4. (See Accession No. AF033021, see also, Accession No. 2584866.) This gene is mapped to human chromosome 19q13.2. A second signal sequence likely exists upstream from the predicted signal sequence as described in Table 1. Preferred polypeptide fragments comprise: QADDLQATVAALCVLRGGGPWAG SWLSPKTPGAMGGDLVLGLGALRRRKRL (SEQ NO: 618); or EQEKSLAGWALVAXXGIGL MVLHAEMLWFGGCSAVNATGHLSDTLWLIPITFLTIGYGDVVP GTMWGKIVCLCTGVMGVCC TALLVAVVARKLEFNKAEKHVHNFMMDIQYTKEMKESAAARVLQEAWMFYKHTRRKESHAAR XHQRXLLAAINAFRQVRLKHKRLREQVNSMVDISKMHMILYDLQNLSSSHRALEKQIDTLG KLDALTELLSTALGPRQLPEPSQQSK (SEQ ID NO: 619), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in breast lymph node and T-cells, and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematologic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue, blood cells and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 325 as residues: Arg-13 to Lys-23.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment/diagnosis of hematologic and diseases involving immune modulation based on distribution in the lymph node and T-cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene was recently cloned by another group, calling it PAPS synthase. (See Accession No. c1204135.) Preferred polypeptide fragments comprise the amino acid sequence YQAHVSRNKRQVVGTRGGFRGCTVWLTGLSGAGK (SEQ ID NO: 620).

- 5 Also preferred are the polynucleotide fragments encoding this polypeptide fragment.

It has been discovered that this gene is expressed primarily in benign prostate hyperplasia, Human Umbilical Vein Endothelial Cells and to a lesser extent in smooth muscle and Human endometrial stromal cells-treated with estradiol.

- Therefore, polynucleotides and polypeptides of the invention are useful as
- 10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammation, ischemia, and restenosis, based on endothelial cell and smooth muscle cell expression, and prostate diseases such as benign prostate hyperplasia or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
- 15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate or vessels of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, endothelial cells, smooth muscle, and endometrium, and cancerous and wounded tissues) or bodily
- 20 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 326 as residues: Arg-21 to Asp-26, Lys-35 to Lys-44,
- 25 Glu-49 to Asn-58.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosing diseases or conditions where the endothelial cell lining of the veins and arteries of underlying smooth muscle are involved.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in human 6 week embryo and to a lesser extent in placenta.

- Therefore, polynucleotides and polypeptides of the invention are useful as
- 35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental anomalies or fetal deficiencies. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly developmental in nature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic
5 tissue, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
10 NO. 327 as residues Lys-50 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of developmental abnormalities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

15 This gene is expressed primarily in kidney and amygdala and to a lesser extent in fetal tissues. This gene is mapped to chromosome 14, and therefore is useful in linkage analysis as a marker for chromosome 14.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) present in a biological sample and
20 for diagnosis of diseases and conditions: kidney diseases, neurological disorders and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s). For a number of disorders of the above tissues, particularly of the renal system or developing fetal tissues, expression of this gene at significantly higher or
25 lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, amygdala, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
30 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of conditions affecting the brain, kidneys and fetal development.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: solid tumors similar to ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 329 as residues Ser-51 to Val-56.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of solid tumors of the reproductive system such as ovarian cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in brain medulloblastoma. Preferred polypeptide fragments comprise the amino acid sequence: IRHEQHPNFSLEMHSGSSLLFLPQL ILILPVCAHLHEELNC (SEQ ID NO: 643) and SFFISEEKGHLLQAERHPWVAGALVGVSGLTLTTCSGPTEKPATKNYFLKRLQEMHIRAN (SEQ ID NO: 644), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the CNS or. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating medulloblastoma or similar tumors.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose tissues expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating obesity by regulating the function and number of adipocytes

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

25 This gene is expressed primarily in B cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of the immune system with an emphasis on B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumors of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

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the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of B cell derived
5 tumors based on its expression in b cell lymphomas

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in immune cells and to a lesser extent in fetal tissues

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
15 type(s). For a number of disorders of the above tissues or cells, particularly of the immune expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cells of the immune system, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
20 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:333 as residues Asp-10 to Pro-19, Ser-74 to Tyr-79, Glu-95 to Lys-110.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for treatment of diseases involving alterations in T cell activity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

It has been discovered that this gene is expressed primarily in ovarian tumor.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
35 or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumors of the reproductive organs. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian

and other reproductive tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 334 as residues: Leu-22 to Gln-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of ovarian tumors as it has only been identified in ovarian tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

It has been discovered that this gene is expressed primarily in fetal tissues and to a lesser extent in osteoclastoma cell line

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: osteoporosis or arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of conditions of abnormal bone remodeling due to enhanced activity of osteoclasts. This may be useful as a specific marker for malignancies derived from osteoclasts or their precursors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with a periplasmic ribonuclease which is thought to be important in degrading extracellular polynucleotides

It has been discovered that this gene is expressed primarily in serum treated smooth muscle cells

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular disease such as restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are
5 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
10 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Gln-30 to Lys-36, and Pro-41 to Arg-48.

15 The tissue distribution and homology to ribonucleases indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of pathological conditions of smooth muscle associated with bacterial or viral infiltration

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

20 This gene is expressed primarily in Early Stage Human Brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain development and related diseases. Similarly, polypeptides and antibodies directed to
25 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain development and related diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides
35 and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases affecting human brain development and related diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

It has been discovered that this gene is expressed primarily in human brain tissue.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain diseases and other diseases related to brain diseases, which may be caused by brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain diseases and other diseases related.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

It has been discovered that this gene is expressed primarily in Anergic T-cells.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases, inflammatory diseases and diseases related to T lymph cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
30 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune diseases, inflammatory diseases and diseases related to T lymph cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
35 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for immune diseases,
5 inflammatory diseases and diseases related to T lymph cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

The translation product of this gene shares sequence homology with *Shigella flexneri* positive transcriptional regulator CriR (criR) gene which is thought to be
10 important in regulation of gene expression.

This gene is expressed primarily in human synovial sarcoma and normal human brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: human brain diseases particularly sarcomas of the synovium. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain and synovium and other related human
20 brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., synovial tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
25 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human synovial sarcoma and other related human brain diseases.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed in bone marrow, infant brain, fetal liver and spleen, prostate and to a lesser extent in pineal gland, adipose tissue, kidney, adrenal gland, umbilical vein endothelial cells, and T cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases related to bone marrow or

hematoplastic tissues, prostate, kidney, adrenal gland, and cardiovascular tissue or organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, hematopoietic cells, pineal gland, adipose tissue, kidney, adrenal gland, endothelial cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

This gene is expressed primarily in meningea and to a lesser extent in breast and adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases of the meningea and related brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the meningea and related brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., meningea, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the meningea and related brain diseases.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 31**

This gene is expressed in meningea, fetal spleen, osteoblast and to a lesser extent in activated T-cells, endometrial stromal cells, fetal lung, HL-60, thymus, testis and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: meningeal disease, osteoporosis, immune diseases, and hematoplastic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the
15 above tissues or cells, particularly of the meningeal diseases, osteoporosis, immune diseases, and hematoplastic diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endometrium, lung, thymus, testis, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of
25 meningeal, osteoporosis, immune diseases, hematoplastic diseases, testis diseases and lung diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

This gene is expressed primarily in human thymus and to a much lesser extent
30 in infant brain, T-cells, smooth muscle, endothelial cells, bone marrow, human ovarian tumor and keratinocytes testes, osteoclastoma, breast, and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases involving the
35 thymus, particularly thymic cancer and diseases involving T-cell maturation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the thymus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, brain, and other tissue of the nervous system, blood cells, bone marrow, ovaries, and testes, and other reproductive tissue, mammary
5 tissue, tonsils, melanocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the thymus particularly thymic cancer and diseases involving T-cell maturation.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 33**

This gene is expressed primarily in human tonsils, and placenta, and to a lesser extent in adipocytes, melanocyte, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions: inflammatory diseases, immune diseases, and obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the inflammatory diseases, immune diseases, and obesity, expression of
25 this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., tonsils, placenta, adipocytes, melanocytes, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases such as inflammation, immune diseases, and obesity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed in activated T cells, and to a lesser extent in pituitary, testis, and breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases relating to T cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
10 disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary, testes and other reproductive tissue, mammary tissue, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological disorders.
25 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to neurological disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
30 brain, and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neurological disorders.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the
diseases relating to neurological disorders, expression of this gene at significantly
higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
brain and other tissue of the nervous system, and cancerous and wounded tissues) or
bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the
standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of neurological
20 disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in human ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: ovarian cancer.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
ovarian disorders such as those involving germ cells, ovarian follicles, stromal cells,
30 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., ovary and other reproductive tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
35 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of ovarioopathy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in lymph node breast cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the breast cancer,
expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., mammary tissue and lymphoid tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
15 such a disorder, relative to the standard gene expression level, i.e., the expression level
in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for used as a diagnostic marker for breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

20 This gene is expressed primarily in brain and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neuronal disorders such
as trauma, brain degeneration, and brain tumor. Similarly, polypeptides and antibodies
25 directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the brain, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., brain and other tissue of the nervous system, and cancerous and wounded
30 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for diagnosis and therapeutic treatment of
neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

5 This gene is expressed in early stage human embryo, adrenal gland tumor, and immune tissues such as fetal liver, fetal spleen, T-cell, and myeloid progenitor cell line and to a lesser extent in ovary, colon cancer, and a few other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis including
10 adrenal gland tumor, colon cancer and various other tumors, developmental and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer tissues, early stage human tissues, and immune system,
15 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, blood cells, bone marrow, ovary and other reproductive tissue, and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and therapeutic treatment of immune and developmental disorders, and tumorigenesis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in fetal lung, endothelial cells, liver, thymus and a few other immune tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders such as immune deficiency and autoimmune diseases, pulmonary diseases, liver diseases, and tumor matasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal lung, liver, endothelial cells, and immune tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues and cell types (e.g., lung, endothelial cells, liver, thymus, and other tissue of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune disorders and pulmonary and hepatic diseases. Its promoter may also be used for immune system and lung-specific gene therapies. The expression of this gene in endothelial cells indicates that it may also involve in angiogenesis which therefore may play role in tumor matasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed primarily in liver, thyroid, parathyroid and to a lesser extent in fetal lung, stomach and early embryos.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic regulation, obesity, hepatic failure, hepatocellular tumors or thyroiditis and thyroid tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive/endocrine system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, thyroid, parathyroid, lung, stomach, and embryonic tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and the extracellular locations indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of digestive/endocrine disorders, including metabolic regulation, hepatic failure, malabsorption, gastritis and neoplasms.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

This gene is expressed primarily in Schizophrenic adult brain, pituitary, front cortex, hypothalamus and to a lesser extent in retina, adipose and stomach cancer and placenta.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal tissue, adipose, stomach, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
- 15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nerve
- 20 system, including schizophrenia, neurodegeneration, and neoplasia. Additionally, a secreted protein in brain may serve as an endocrine.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

- The translation product of this gene shares sequence homology with GTP
- 25 binding proteins which are thought to be important in signal transduction and protein transport.

This gene is expressed primarily in umbilical vein and microvascular endothelial cells, GM-CSF treated macrophage, anergic T cells, osteoblast, osteoclast, CD34+ cells and to a lesser extent in gall bladder.

- 30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: bone formation and growth, osteonecrosis, osteoporosis, angiogenesis and/or hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
- 35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoiesis systems, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues and cell types (e.g., endothelial cells, blood cells, bone, and gall bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene
5 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to GTP binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of bone formation and growth, osteonecrosis, osteoporosis, and/or
10 hematopoiesis because its involvement in the growth signaling or angiogenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with signal sequence receptor gamma subunit which is thought to be important in protein
15 translocation on endoplasmic reticulum.

This gene is expressed primarily in adrenal gland, salivary gland, prostate, and to a lesser extent in endothelial cells and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions: protein secretion. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the secretory organs, expression of this gene at significantly higher or lower levels may be
25 routinely detected in certain tissues and cell types (e.g., adrenal gland, salivary gland, prostate, endothelial cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution and homology to SSR gamma subunit indicate that polynucleotides and polypeptides corresponding to this gene are useful for endocrine disorders, prostate cancer, xerostomia or sialorrhea.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 46

This gene is expressed primarily in osteoclastoma cells and to a lesser extent in melanocyte, amygdala, brain, and stomach.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ossification, osteoporosis, fracture, osteonecrosis, osteosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, amygdala, brain and other tissue of the nervous system, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in intervention of ossification, osteoporosis, fracture, osteonecrosis and osteosarcoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The translation product of this gene shares sequence homology with proline rich proteins which is thought to be important in protein-protein interaction.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological and psychological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system and endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to proline-rich proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful in intervention

and detection of neurological diseases, including trauma, neoplasia, degenerative or metabolic conditions in the central nerve system. Additionally, the gene product may be secreted by the brain as an endocrine.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 49**

The translation product of this gene shares sequence homology with the AOCB gene from *Aspergillus nidulans* which is important in asexual development.

This gene is expressed primarily in infant brain and to a lesser extent in the developing embryo, trachea tumors, B-cell lymphoma and synovial sarcoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative diseases, leukemia and sarcoma's. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
15 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, blood cells, trachea, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
20 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in infant brain and sarcoma's and homology to a gene involved in a key step of eukaryotic development (fungal spore formation) indicates
25 that the protein product of this clone could play a role in neurological diseases such as schizophrenia, particularly in infants. The existence of the gene in a B-cell lymphoma indicates the gene may be used in the treatment and detection of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

30 This gene is expressed primarily in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary disorders including lung cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene only in fetal lung indicates that it plays a key role in development of the pulmonary system. This would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung. It may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in hematopoietic cell types and fetal cells and to a lesser extent in all tissue types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in the immune system and hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene predominantly in hematopoietic cells and in the developing embryo indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of lymphomas and disease states affecting the immune system or hematopoiesis disorders such as leukemia, AIDS, arthritis and asthma..

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 52

This gene is expressed primarily in prostate and to a lesser extent in fetal spleen, fetal liver, infant brain and T cell leukemias.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate disorders, prostate cancer, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, and/or prostate gland expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, spleen, liver, brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in prostate indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection or treatment of prostate disorders or prostate cancer. Its distribution in fetal liver and fetal spleen indicates it may play a role in the immune system and its misregulation could lead to immune disorders such as leukemia, arthritis and asthma.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

The translation product of this gene shares sequence homology with dynein.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuro-degenerative diseases of the brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly neuro-degenerative diseases expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution in the brain and homology to dynein, a microtubule motor protein involved in the positioning of cellular organelles and molecules indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection/treatment of neurodegenerative diseases, such as Alzheimers, 5 Huntingtons, Parkinsons diseases and shizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with ubiquitin-conjugation protein, an enzyme which is thought to be important in the processing of 10 the Huntingtons Disease causing gene.

This gene is expressed primarily in brain and to a lesser extent in activated macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 15 biological sample and for diagnosis of diseases and conditions: neurodegenerative disease states including Huntington's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of brain tissues. For a number of disorders of the above tissues or cells, particularly of the neurological systems expression of this gene at 20 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level 25 in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in the brain and its homology to a Huntington interacting protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the regulation of the expression of the Huntington disease gene and other neurodegenerative diseases including 30 spinocerebellar ataxia types I and III, dentatorubropallidoluysian and spinal bulbar muscular atrophy. In addition, the existence of elevated levels of free ubiquitin pools in Alzheimer's disease, Parkinson's disease and amyotrophic lateral sclerosis indicates that the ubiquitin pathway of protein degradation plays a role in these disease states. Thus, considering the gene described here is homologous to a ubiquitin-conjugation 35 protein it may play a general role in neurodegenerative conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in T-cells (anergic T-cells, resting T-Cells, apoptotic T-cells) and lymph node (breast), as well as brain (hypothalamus, hippocampus, pituitary, infant brain, early-stage brain).

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune (e.g. immunodeficiencies, autoimmunities, inflammation, leukemias & lymphomas) and neurological (e.g. Alzheimer's disease, dementia, schizophrenia) disorders. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous, hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood
15 cells, lymphoid tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention or detection of pathologies associated with the hematopoietic and immune systems, such as anemias (leukemias). In addition, the expression in brain (including fetal) might suggest a role in developmental brain defects, neuro-degenerative diseases or behavioral abnormalities
25 (e.g. schizophrenia, Alzheimer's, dementia, depression, etc.).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

This gene is expressed primarily in lung, and to a lesser extent in a variety of other hematological cell types (e.g. Raji cells, bone marrow cell line, activated
30 monocytes).

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary and/or hematological dysfunction. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculo-pulmonary and hematopoietic systems, expression of this

gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
5 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention and detection of pathologies associated with the vasculo-pulmonary system. In addition the expression of this gene
10 in a variety of leukocytic cell types and a bone marrow cell line might suggest a role in hematopoietic and immune system disorders, such as leukemias & lymphomas, inflammation, immunodeficiencies and autoimmunities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

15 The translation product of this gene shares sequence homology with adenylate kinase isozyme 3 (gil163528 GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus]), which is thought to be important in catalyzing the phosphorylation of AMP to ADP in the presence of ATP or inorganic triphosphate.

This gene is expressed primarily in fetal liver, heart and placenta, and to a lesser
20 extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic, cardiovascular or reproductive disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic, cardiovascular and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, heart, and placenta, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for the treatment and diagnosis of conditions related to hepatic function and pathogenesis, in particular, those dealing with liver development and the differentiation of hepatocyte progenitor cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

This gene is expressed primarily in CD34 positive cells (Cord Blood).

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: hematopoietic
differentiation and immune disorders. Similarly, polypeptides and antibodies directed to
these polypeptides are useful in providing immunological probes for differential
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of hematopoietic and immune systems, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., hematopoietic cells, and blood cells, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful in the detection and treatment of conditions
associated with CD34-positive cells, and therefore as a marker for cell differentiation in
20 hematopoiesis, as well as immunological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

The translation product of the predicted open reading frame of this contig has
sequence identity to the murine gene designated Insulin-Like Growth Factor-Binding
25 Protein (IGFBP)-1 as described by Lee and colleagues (Hepatology 19 (3), 656-665
(1994)).

This gene is expressed exclusively in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of hemangiopericytoma and other pericyte or
endothelial cell proliferative disorders. Similarly, polypeptides and antibodies directed
to these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the circulatory and immune systems, expression of this
35 gene at significantly higher or lower levels may routinely be detected in certain tissues
and cell types (e.g., pericyte or endothelial cells, and liver, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Polynucleotides and polypeptides corresponding to this gene are useful as cell growth regulators since IGFBP-1-like molecules function as modulators of insulin-like growth factor activity. In addition, since IGFBP-1 is expressed at high levels following hepatectomy and during fetal liver development, polynucleotides of the present invention may also be used for the diagnosis of developmental disorders. Further, polypeptides of the present invention may be used therapeutically to treat developmental liver disorders as well as to regulate hepatocyte and supporting cell growth following hepatectomy or to treat liver disorders.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hemangiopericytoma and liver disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in schizophrenic frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: nervous system and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the frontal cortex and CNS expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of frontal cortex, neuro-degenerative and CNS disorders

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in human adrenal gland tumor, and to a lesser extent in human kidney, medulla and adult pulmonary tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic, endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and nervous system disorders and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, kidney, brain and other tissue of the nervous system, pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of neurological and endocrine disorders including neoplasia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in human adipocytes, and to a lesser extent in spleen, 12-week old human, and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune, metabolic and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes, spleen, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of immune, developmental and metabolic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

One translated product of this clone is homologous to the mouse zinc finger protein PZF. (See Accession No. 453376; see also Gene 152 (2), 233-238 (1995).) Preferred polypeptide fragments correspond to the highly conserved domains shared between mouse and man. For example, preferred polypeptide fragments comprise the amino acid sequence: LQCEICGFTCRQKASLNWHMKKHDADSFYQFSCNICGKKFEKKDSVVAHKAKSH PEV (SEQ ID NO: 621); ITSTDILGTNPESLTQPSD (SEQ ID NO: 622); NSTSGECLLLEAGM SKSY (SEQ ID NO: 623); CSGTERVSLMADGKIFVGS GSGGTEGLVMNSDILGATTEVLIEDSD SAGP (SEQ ID NO: 624); IQYVRCEMEGCGTVLAHPRYLQHHIKYQHLLKKKYVCPHPSCGRLF RLQKQLLRHAKHHT (SEQ ID NO: 625); QRDYICEYCARAFKSSHNLAVHRMIHTGEK (SEQ ID NO: 626); RSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPNTDQLDY (SEQ ID NO: 627); PFKDDPRDETYKPHLERETPKPRRKSG (SEQ ID NO: 630); QYVRCEMEGCGTVLAHPRYLQ HHIKYQHLLKKKYVCPHPSCGRLFRLQKQLLRHAKHHTD (SEQ ID NO: 629); or residues 151-182 of QRDYICEYCARAFKSSHNLAVHRMIHTGEKHY (SEQ ID NO: 628). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in Rhabdomyosarcoma, melanocyte and colon cancer tissue and to a lesser extent in smooth muscle, pancreatic tumor, and apoptotic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoetic, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striated muscle, melanocytes, colon, smooth muscle, pancreas, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of cancer and hemopoetic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in human adipose and salivary gland tissue and to a lesser extent in human bone marrow and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and hemopoetic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose, salivary gland, bone marrow, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis of metabolic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This translated product of this gene was recently identified as oxytocinase splice variant 1. (See Accession Nos. 2209276 and d1010078.) Preferred polypeptide fragments comprise the amino acid sequence: EMFDSL SYFKGSSLLMLKTYLSEDV FQHAVVLYLHN HSYASIQSDDLWDSFNEVTNQTL DVKRMMKWTWLQKGFPLVT VQKKGKELFIQQRFFLNMK PEIQPSDTRYM (SEQ ID NO: 631). Also preferred are polynucleotide fragments encoding this polypeptide fragment.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in hemopoetic cells, particularly apoptotic T-cells, and to lesser extent in primary dendritic cells and adipose tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of apoptotic T-cells, primary dendritic cells, and adipose tissue present in a biological sample and for diagnosis of diseases and conditions: hemopoetic diseases including cancer and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the oral and intestinal mucosa as well as hemopoetic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases of the immune system, including cancer, hemopoetic and infectious diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in kidney cortex and to a lesser extent in infant brain, heart, uterus, and blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of kidney tissue present in a biological sample and for diagnosis of diseases and conditions: soft tissue cancer, inflammation, kidney fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and endocrines systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, brain, and other nervous tissue, heart, uterus, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and fibroses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

The translation product of this gene shares strong sequence homology with vertebrate and invertebrate protein tyrosine phosphatases.

This gene is expressed primarily in endometrial tumors, melanocytes, myeloid progenitors and to a lesser extent in infant brain, adipocytes, and several hematopoietic stem cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of transformed hematopoietic and epithelial cells present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of skin and endometrium, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, melanocytes, bone marrow, adipocytes, hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and sequence similarity with tyrosine phosphatases indicate that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and hematopoietic disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in osteoclastoma, breast, and infant brain and to a lesser extent in various fetal and transformed bone, ovarian, and neuronal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: degenerative conditions of the brain and skeleton. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of degenerative, neurological and skeletal disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene was originally cloned from tumor cell lines. Recently another group has also cloned this gene, calling it the human malignant melanoma metastasis-suppressor (KiSS-1) gene. (See Accession No. U43527.) Preferred polypeptide fragments comprise the amino acid sequence: LEKVASVGNSRPTGQQLESGLLA (SEQ ID NO: 632); VHREEASCYCQAEPDGL (SEQ ID NO: 633); RPALRQAGGCTREPRQKRWAGL (SEQ ID NO: 634); and AVNFRPQRSQSM (SEQ ID NO: 635). Any frame shifts can easily be resolved using known molecular biology techniques.

This gene is expressed primarily in many types of carcinomas and to a lesser extent in many normal organs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissues(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanomas, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of transformed organ tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. As a tumor suppressor gene, increase amounts of the polypeptide can be used to treat patients having a particular cancer.

The tissue distribution indicates that this gene and the translated product is useful for diagnosing and study of cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

This gene is expressed primarily in striatum and to a lesser extent in adipocytes and hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of striatal cells present in a biological sample and for diagnosis of diseases and conditions: neurological, fat and lysosomal storage

diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striatal tissue, adipocytes, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, study and treatment of neurodegenerative and growth disorders.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 73**

This gene is expressed primarily in bone marrow stromal cells and to a lesser extent in smooth muscle, testes, endothelium, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of bone marrow present in a biological sample and for diagnosis of diseases and conditions: connective tissue and hematopoietic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, stromal cells, smooth muscle, testes and other reproductive tissue, endothelium, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of connective tissue and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed primarily in brain, fetal liver and lung and to a lesser extent in retina, spinal chord, activated T-cells and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of brain and regenerating liver present in a biological sample and for diagnosis of diseases and conditions: CNS and spinal chord injuries, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the nervous and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, pulmonary tissue, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of hematopoietic and
20 neurological conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with GTP binding proteins (intracellular).

25 This gene is expressed primarily in bone marrow, brain, and melanocytes and to a lesser extent in various endocrine and hematopoietic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematopoietic and
30 nervous system conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone
35 marrow, melanocytes, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to nucleotide binding factors indicate that polynucleotides and polypeptides corresponding to this gene are useful for study,
5 diagnosis, and treatment of brain degenerative, skin and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene is expressed primarily in activated T-cells and to a lesser extent in retina, brain, and fetal bone.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of activated T-cells and developing brain present in a biological sample and for diagnosis of diseases and conditions: immune deficiencies and skeletal and neuronal growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and skeletomuscular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, retinal tissue, and bone, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for diagnosis, study and treatment of cancer, urogenital, and brain degenerative diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene is expressed primarily in fetal liver, activated monocytes, osteoblasts
30 and to a lesser extent in synovial, brain, and lymphoid tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of myeloid and lymphoid present in a biological sample and for diagnosis of diseases and conditions: inflammation, immune deficiencies, cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and skeleton, expression of this gene at significantly

higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, blood cells, bone, synovial tissue, brain and other tissue of the nervous system, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
5 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of lymphoid
10 and mesenchymal cancers and nervous system diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

The translation product of this gene shares sequence homology with polymerase polyprotein precursor which is thought to be important in DNA repair and replication

15 This gene is expressed primarily in infant brain and to a lesser extent in tumors and tumor cell lines

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
20 not limited to, especially of the neural system and developing organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system expression of this gene at significantly higher or lower levels may be routinely detected
25 in certain (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to polymerase polyprotein precursor indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers especially of the neural system and developing organs

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed primarily in muscle and endothelial cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., muscle, endothelial cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders of the vascular and neural system including cardiovascular and endothelial.

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

This gene is expressed primarily in placenta and to a lesser extent in fetal liver

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental disorders and disorder of the haemopoietic system, fetal liver and placenta. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developmental disorders and disorder of the haemopoietic system, fetal liver and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of developmental disorders and disorders of the haemopoietic system, fetal liver and placenta.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed primarily in bone marrow, placenta and tissues and organs of the hematopoietic system.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the bone and haemopoietic system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, bone and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, placenta, and hematopoietic cells, and cancerous and
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the
20 immune, bone and hematopoietic system

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

The translation product of this gene shares sequence homology with secretory carrier membrane protein which is thought to be important in protein transport and
25 export. Any frame shifts in coding sequence can be easily resolved using standard molecular biology techniques. Another group recently cloned this gene, calling it SCAMP. (See Accession No. 2232243.)

This gene is expressed primarily in prostate, breast and spleen, and to a lesser extent in several other tissues and organs.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the breast prostate and spleen. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly disorders of the breast prostate and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell

types (e.g., prostate, mammary tissue, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secretory carrier membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the breast, prostate and spleen.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 83**

This gene is expressed primarily in developing organs and tissue like placenta and infant brain and to a lesser extent in developed organs and tissue like cerebellum and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, heart, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the neural system including neurological disorders and cancer.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with ATPase 6 in *Trypanosoma brucei* which is thought to be important in metabolism.

This gene is expressed primarily in tumor and fetal tissues and to a lesser extent in melanocytes, kidney cortex, monocytes and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: metabolism disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, melanocytes, kidney, blood cells, ovary and other tissue of the reproductive system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATPase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of metabolism disorders, especially in fetal and tumor tissue growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with the immunoglobulin superfamily of proteins which are known to be important in immune response and immunity.

This gene is expressed primarily in stromal cells, colon cancer, lung, amygdala, melanocyte and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells, colon, lung, amygdala, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune system disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

The translation product of this gene shares sequence homology with transcription initiation factor eIF-4 gamma which is thought to be important in gene transcription.

This gene is expressed primarily in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in tumor tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to transcription initiation factor eIF-4 gamma indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene regulation in tumorigenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

The translation product of this gene shares sequence homology at low level in prolines with secreted basic proline-rich peptide II-2 which is thought to be important in protein structure or inhibiting hydroxyapatite formation in vitro.

This gene is expressed primarily in endometrial tumor and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular/skeletal and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample

taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secreted basic proline-rich peptide II-2 indicate that polynucleotides and polypeptides corresponding to this gene are useful for inhibiting hydroxyapatite formation or establishing cell/tissue structure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

This gene is expressed primarily in: amniotic cells induced with TNF in culture; and to a lesser extent in colon tissue from a patient with Crohn's Disease; parathyroid tumor; activated T-cells; cells of the human Caco-2 cell line; adenocarcinoma; colon; corpus colosum; fetal kidney; pancreas tumor; fetal brain; early stage brain, and anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system; e.g., tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., amniotic cells, colon, kidney, pancreas, parathyroid, brain and other tissue of the nervous system, blood cells, hematopoietic cells, liver, spleen, bone, testes and other reproductive tissue, brain and other tissue of the nervous system, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for modulating tumorigenesis and other immune system conditions such as disorders in immune response.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

This gene is expressed primarily in fetal liver/spleen and hematopoietic cells and to a lesser extent in brain, osteosarcoma, and testis tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, liver, spleen, bone, testes, and other reproductive tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

The translation product of this gene shares weak sequence homology with mouse Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in infant and adult brain and fetal liver/spleen and to a lesser extent in smooth muscle, T cells, and a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, spleen, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and its homology to Gcapi protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders in neuronal, hematopoietic, immune, and endocrine systems.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

This gene is expressed primarily in brain and hematopoietic cells and to a lesser extent in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorder in nervous, hematopoietic, immune systems and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of disorders in the nervous, hematopoietic, and immune systems.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

The translation product of this gene shares sequence homology with neuroendocrine-specific protein A which is thought to be important in neurologic systems.

30 This gene is expressed primarily in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neural disorders and degeneration disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central or peripheral nervous systems, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to neuroendocrine-specific protein A indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neural disorders and degeneration disease.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 93

The translation product of this gene shares sequence homology with collagen-like protein and prolin-rich protein which are thought to be important in connective tissue function and tissue structure.

15 This gene is expressed primarily in fetal liver/spleen and brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuronal or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the nervous system, and
25 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to collagen-like protein and proline-rich
30 proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for supporting brain and hematopoietic tissue function and diagnosis and treatment of disorders in these functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

35 This gene is expressed primarily in embryonic tissues and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system (e.g., tumors), expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancer.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 95**

This gene is expressed primarily in brain tumor, placenta, and melanoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor or melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain or melanocytes, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, placenta, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the translation product of this gene is useful in the diagnosis and treatment of brain tumors and melanoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 96

The translation product of this gene shares sequence homology with a yeast membrane protein, SUR4, which encodes for APA1 that acts on a glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose.

This gene is expressed primarily in fetal liver, and to a lesser extent in placenta and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of fetal liver or defects of glucose-regulated ATPase activities in tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune/hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, placenta, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to yeast SUR4 membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of defects of fetal liver or defects of glucose-regulated ATPase activities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

This gene is expressed primarily in fetal liver, brain, and amniotic fluid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the fetal immune system and adult brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune system and adult brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., amniotic fluid, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for detecting defects of the fetal immune and hematopoietic systems since fetal liver is

the predominant organ responsible for hematopoiesis in the fetus. In addition, the gene product of this gene is thought to be useful for detecting certain neurological defects of the brain.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 98**

The translation product of this gene shares sequence homology with an yolk protein precursor, Vitellogenin which is thought to be important in binding lipids such as phosvitin.

This gene is expressed primarily in amniotic cells and fetal liver.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in amniotic cells, fetal liver development and the fetal immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
20 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to vitellogenin indicate that the protein
25 product of this clone is useful for treatment and diagnosis of defects in amniotic cells, fetal liver development and the fetal immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

This gene is expressed primarily in placenta, endometrial tumor, osteosarcoma
30 and stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumor of the endometrium or bone, and osteosarcoma. Similarly, polypeptides and antibodies
35 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the obstetric system (e.g. placenta,

endometrium) and the bones, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endometrium, bone, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors and abnormalities of the endometrium, and the bones because of its abundance in the aforementioned tissues..

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatocellular tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of hepatocellular cancer because of its abundant expression in this tissue.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in Corpus Colosum, fetal lung and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the Corpus Colosum or defects of the fetal lung. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Corpus Colosum and brain in general, and fetal lung, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of the Corpus Colosum and brain in general, and defects of fetal lung.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 102**

This gene is expressed primarily in T cells and stromal cells, and to a lesser extent in adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of T cell immunity and stromal cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, stromal cells, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of T cell immunity and stromal cell development because of its abundant expression in these tissues.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 103**

This gene is expressed primarily in infant brain and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides
5 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, especially brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, cancerous and
10 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful
15 for detecting defects of the brain, especially in young children.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

This gene is expressed primarily in human osteoclastoma and to a lesser extent in human pancreas tumor.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly osteoclastoma and pancreatic tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
25 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in transformed tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone and pancreas, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of some types of tumors, particularly pancreatic cancer and
35 osteoclastoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

This gene is expressed primarily in fetal liver/spleen, and to a lesser extent in activated T-Cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
10 immune system, expression of this gene at significantly higher or lower levels may be
routinely detected in certain tissues and cell types (e.g., liver, spleen, and blood cells,
and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
having such a disorder, relative to the standard gene expression level, i.e., the
15 expression level in healthy tissue or bodily fluid from an individual not having the
disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis or treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 107

This gene is expressed primarily in human embryo and to a lesser extent in
spleen and chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: leukemia. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
number of disorders of the above tissues or cells, particularly of the immune or
hemopoietic systems, expression of this gene at significantly higher or lower levels may
30 be routinely detected in certain tissues and cell types (e.g., embryonic tissue, spleen,
and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
an individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
35 disorder.

The tissue distribution indicates that the protein product of this clone is useful
for the diagnosis and treatment of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene is expressed primarily in placenta, and to a lesser extent in early stage human brain and in lung.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: fetal developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
10 or cell type(s). For a number of disorders of the above tissues or cells, particularly in fetal and amniotic tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, brain and other tissue of the nervous system, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this is useful for production of growth factor(s) associated with fetal development. Preferred
20 polypeptides comprise the full-length polypeptide shown in the sequence listing, truncated however, at the amino terminus and beginning with QTIE.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

This gene is expressed primarily in fetal spleen, and to a lesser extent in B-Cell
25 lymphoma and T-Cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
35 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the treatment and diagnosis of human lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

5 The translation product of this gene shares sequence homology with sarcoma amplified sequence (SAS), a tetraspan receptor which is thought to be important in malignant fibrous histiocyoma and liposarcoma.

This gene is expressed primarily in human osteoclastoma, and to a lesser extent in pineal gland and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: malignant fibrous histiocyoma and liposarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, pineal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to sarcoma amplified sequence (SAS) indicate that the protein product of this clone is useful for treatment of, osteosarcoma,
25 malignant fibrous histiocyoma and liposarcoma and related cancers, particularly sarcomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 111

The translation product of this gene shares sequence homology with 6.8K
30 proteolipid protein, mitochondrial - bovine.

This gene is expressed primarily in Wilm's tumor and to a lesser extent in cerebellum and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: Wilm's tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the immune or renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids
5 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to 6.8K proteolipid protein indicate that
10 the protein product of this clone is useful for diagnostic and therapeutics associated with tumors, particularly Wilm's tumor disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 112

This gene is expressed primarily in embryonic tissue and to a lesser extent in
15 osteoblasts, endothelial cells, macrophages (GM-CSF treated), and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
20 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, bone, endothelial cells, blood cells and bone marrow, and cancerous and wounded tissues) or
25 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treatment or diagnosis of immune disorders. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: MITDVQLAIFANMLGVSLFLLVVLVLYHYVAVNNPKKQE (SEQ ID NO: 636).

FEATURES OF PROTEIN ENCODED BY GENE NO: 113

35 This gene is expressed primarily in hepatocellular tumor, and to a lesser extent in fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors, particularly hepatocellular tumors. Similarly, polypeptides and antibodies directed to these

5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

10 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful

15 for diagnosis and treatment of tumors, particularly hepatocellular tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 114

The translation product of this gene exhibits a very high degree of sequence identity with the human Pig8 gene which is thought to be important in p53 mediated

20 apoptosis. The sequence of this gene has since been published by Polyak and colleagues (Nature 389, 300-306 (1997)). In addition, the predicted translation product of this contig exhibits very high sequence homology with a murine gene denoted as EI24 which is also thought to be important in p53 mediated apoptosis.

This gene is expressed primarily in infant brain and activated T-cells and to a

25 lesser extent in bone marrow, fetal liver, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and tissue damage by radiation and anti-cancer drugs. Similarly,

30 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the

35 nervous system, blood cells, bone marrow, liver, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human Pig8 and murine EI24 genes indicate that polynucleotides and polypeptides corresponding to this gene are useful for preventing apoptosis in patients being treated with anti-oncogenic drugs such as etoposide, hydroperoxycyclophosphamide, and X-irradiation, since this protein product is upregulated in cells undergoing such treatment where p53 was overexpressed. It may also be useful in the treatment of hematopoietic disorders and in boosting numbers of hematopoietic stem cells by interfering with the apoptosis of progenitor cells. The mature polypeptide is predicted to comprise the following amino acid sequence:

EEMADSVKTFLLQDLARGIKDSIWGICTISKLDARIQKKREEQRRRRASSVLAQRRRAQSIERKQES
EPRIVSRIFQCCAWNGGVFWFSLLLFYRVFIPVLQSVTARIIGDPSLHGDVWSWLEFFLTISFSA
LWVLPFLVLSKVVNAIWFQDIADLAFEVSGRKPFPSPSVSKIADMLFNLLLQALFLIQGMFVSL
FPIHLVGQLVSLHMSLLYSLYCFEYRWFNKGIEMHQRLSNIERNWPYYFGFGLPLAFLTAMQ
SSYIISGCLFSILFPLFIISANEAKTPGKAYLFQLRLFSLVVFLSNRLFHKTIVYLQSALSSSTSAEK
FPSHPSPAKLKATAGH (SEQ ID NO: 637). Accordingly, polypeptides comprising the foregoing amino acid sequence are provided as are polynucleotides encoded such polypeptides.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 115

This gene is expressed primarily in stromal cells and to a lesser extent in multiple sclerosis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: affecting the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of multiple sclerosis and other autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 116

This gene is expressed primarily in the gall bladder

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: gall stones or infection
of the digestive system. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the digestive system or renal system, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., gall bladder and tissue of the digestive system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
15 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for possible prevention of digestive disorders
where there may be a lack of digestive enzymes produced or in the detection and
20 possible prevention of gall stones.

FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with dystrophin
gene which is thought to be important in building and maintenance of muscles.

25 This gene is expressed primarily in placenta and to a lesser extent in fetal brain
and fetal liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: muscular dystrophy,
30 Duchenne and Becker's muscular dystrophies. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the skeletal muscle system, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., placenta, brain and other tissue of the nervous system, muscle,
35 liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to the dystrophin gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diseases related the degenerative myopathies that are characterized by the weakness and atrophy of muscles without neural degradation; such as Duchenne and Becker's muscular dystrophies.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 118**

This gene is expressed primarily in olfactory tissue and to a lesser extent in cartilage.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: connective tissue diseases; chondrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue and cartilage, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 15
20
25

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for tumors of connective tissues, osteoarthritis and the treatment and diagnosis of chondrosarcoma.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 119**

This gene is expressed primarily in Activated Neutrophils and to a lesser extent in fetal spleen, and CD34 positive cells from cord blood.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: allergies, defects in hematopoiesis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
- 35

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoiesis system the, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and
5 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for reducing the allergic effects felt by allergy suffers by neutralizing the activity of the immune system, especially since neutrophils are abundant in persons suffering from allergies and other inflammatory conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 120

15 The translation product of this gene shares sequence homology with poly A binding protein II which is thought to be important in RNA binding for transcription of RNA to DNA

This gene is expressed primarily in colon and to a lesser extent in brain and immune system.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: colon cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the immune and digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., colon, tissue and cells of the immune system, and brain or other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to poly A binding protein II indicate that polynucleotides and polypeptides corresponding to this gene are useful for detection
35 and treatment of colon cancer and other disorders of the digestive system..

FEATURES OF PROTEIN ENCODED BY GENE NO: 121

The translation product of this gene shares sequence homology with thymidine diphosphoglucose 4.6 dehydrase which is thought to be important in the metabolism of sugar.

5 This gene is expressed primarily in fetal liver and spleen and to a lesser extent in infant brain.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diabetes. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the
15 nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution and homology to thymidine diphosphoglucose 4.6 dehydrase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of persons with diabetes since it appears that this protein is needed in the metabolism of sugar in to its more basic components.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 122

 The translation product of this gene shares sequence homology with ceruloplasmin which is thought to be important in the metabolism and transport of iron and copper. Ceruloplasmin also contains domains with homology to clotting factors V and VIII. Defects in the circulating levels of ceruloplasmin (aceruloplasminemia) have
30 been associated with certain disease conditions such as Wilson disease, and the accompanying hepatolenticular degeneration.

 This gene is expressed primarily in brain and retina and to a lesser extent in endothelial cells.

 Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases marked by defects in iron metabolism; aceruloplasminemia not characterized by defects in the

known ceruloplasmin gene locus; nonclassical Wilson disease; movement disorders; and tumors derived from a brain tissue origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, retina, and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, retinal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ceruloplasmin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of patients with aceruloplasminemia, or other defects in iron and/or copper metabolism. Mutations in this locus could also be diagnostic for patients currently experiencing or predicted to experience aceruloplasminemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 123

This gene is expressed primarily in brain and B cell lymphoma and to a lesser extent in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: B cell lymphoma; tumors and diseases of the brain and/or spleen; hematopoietic defects. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in neuronal,

hematopoietic, and immune systems. It could potentially be useful for neurodegenerative disorders and neuronal and/or hematopoietic cell survival or proliferation.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 124**

This gene is expressed primarily in osteoclastoma, dermatofibrosarcoma, and B cell lymphoma and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer in particular osteoclastoma, dermatofibrosarcoma, and B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, immune, and circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, epidermis, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers and lymphoma; osteoporosis; and the control of cell proliferation and/or differentiation.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 125

This gene is expressed primarily in immune tissues and hematopoietic cells, particularly in activated T cells and neutrophils, spleen, and fetal liver, and to a lesser extent in infant adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in T cell activation; hematopoietic disorders; tumors of a hematopoietic and/or adrenal gland origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and/or endocrine systems, expression of this gene at significantly higher

or lower levels may be routinely detected in certain tissues and cell types (e.g., cells and tissues of the immune system, hematopoietic cells, blood cells, liver, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune and/or hematopoietic disorders;
10 diseases related to proliferation and/or differentiation of hematopoietic cells; defects in T cell and neutrophil activation and responsiveness; and endocrine and/or metabolic disorders, particularly of early childhood.

FEATURES OF PROTEIN ENCODED BY GENE NO: 126

15 This gene is expressed primarily in placenta and endothelial cells and to a lesser extent in melanocytes and embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial
20 cell origin; angiogenesis associated with tumor development and metastasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and developing embryo, expression of this gene at significantly higher or lower levels
25 may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, melanocytes, and embryonic tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of developmental disorders; inhibition of angiogenesis; and vascular patterning.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 127

This gene is expressed primarily in endothelial cells and hematopoietic tissues, including spleen, tonsils, leukocytes, and both B- and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial cell and/or hematopoietic origin; leukemias and lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, hematopoietic cells, spleen, tonsils, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the manipulation of angiogenesis; the differentiation and morphogenesis of endothelial cells; the proliferation and/or differentiation of hematopoietic cells; and the commitment of hematopoietic cells to distinct cell lineages.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 128

This gene is expressed primarily in kidney medulla and to a lesser extent in spleen from chronic myelogenous leukemia patients, prostate cancer, and some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a kidney origin; chronic myelogenous leukemia; prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, spleen, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of kidney disorders and cancer, particularly chronic myelogenous leukemia and prostate cancer. It may also be useful for the enhancement of kidney tubule regeneration in the treatment of acute renal failure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 129

This gene is expressed primarily in adult and infant brain and to a lesser extent in mesenchymal or fibroblast cells, as well as tissues with a mesenchymal origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and of mesenchymal cells and tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; and fibrosis, based upon the expression of this gene within those tissues. Fibrosis is considered as mesenchymal cells and fibroblasts are the primary cellular targets involved in this pathological condition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 130

This gene is expressed primarily in hepatocellular cancer and to a lesser extent in fetal tissues as well as testes tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, fetal tissue, and testes and other
5 reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 131

This gene is expressed only in infant early brain.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: development and diseases of the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
25 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the brain in children and in
30 treating nervous system disorders such as Alzheimer's disease, schizophrenia, dementia, depression, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 132

This gene is expressed primarily in brain and to a lesser extent in glioblastoma.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Alzheimer's disease,

schizophrenia, depression, mania, and dementia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating brain disorders such as Alzheimer's disease, schizophrenia, depression, mania, and dementia.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 133**

The translation product of this gene shares sequence homology with ribitol dehydrogenase of bacteria which is thought to be important in metabolism of sugars.

This gene is expressed primarily in macrophage and to a lesser extent in T-cell lymphoma and lung.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tissue destruction in inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to ribitol dehydrogenase indicate that polynucleotides and polypeptides corresponding to this gene are useful for altering macrophage metabolism in diseases such as inflammation where macrophages are causing excess tissue destruction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 134

This gene is expressed primarily in pancreatic tumor and to a lesser extent in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
10 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and connective tissue systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pancreas, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing various cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 135

This gene is expressed primarily in T cell lines such as Raji and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune system disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or
30 lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
35 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing inflammatory diseases

such as rheumatoid arthritis, sepsis, inflammatory bowel disease, and psoriasis, as well as neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 136

5 The translation product of this gene shares high sequence homology with SAR1 subfamily of GTP-binding proteins which is thought to be important in vesicular transport in mammalian cells.

 This gene is expressed primarily in serum-stimulated smooth muscle cells and to a lesser extent in a T-cell lymphoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases affecting vesicular transport. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
20 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to GTP-binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene therapy
25 in treating the large number of diseases involved in defective vesicular transport within cells..

FEATURES OF PROTEIN ENCODED BY GENE NO: 137

 The translation product of this gene shares sequence homology with a protein
30 found in *C. elegans* cosmid F25B5.

 This gene is expressed primarily in a fetal tissues and to a lesser extent in melanocytes.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: abnormal fetal development, especially of the pulmonary system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal pulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, pulmonary tissue, and melanocytes, and
5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for treatment and diagnosis of diseases affecting the pulmonary system, such as emphysema.

FEATURES OF PROTEIN ENCODED BY GENE NO: 138

This gene is expressed primarily in gall bladder and to a lesser extent in smooth
15 muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: digestive system disease and gall bladder problems. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., gall bladder and tissue of the digestive system, and smooth muscle, and cancerous and
25 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treating diseases of the digestive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 139

This gene is expressed primarily in placenta and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal fetal development. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developing tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing abnormal fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 140

15 This gene is expressed primarily in smooth muscle and to a lesser extent in ovary, prostate cancer, and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hypertension and
20 atherosclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth
25 muscle, ovary and other reproductive tissue, prostate, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the circulatory system, such as hypertension, atherosclerosis, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 141

35 This gene is expressed primarily in fetal spleen and to a lesser extent in placenta and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and other diseases affecting blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen, placenta, bone marrow, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the generation of red and white blood cells and for the diagnosis of disease of these cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 142

The predicted translation product of this contig is a human homolog of the murine tetracycline/sugar transporter molecule recently reported by Matsuo and colleagues (Biochem. Biophys. Res. Commun. 238 (1), 126-129 (1997)).

This gene is expressed primarily in synovium and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: rheumatoid arthritis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and lymphatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, such as rheumatoid arthritis, leukemia, neutropenia, inflammatory bowel disease, psoriasis, sepsis, and the like.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 143

This gene is expressed primarily in placenta and to a lesser extent in melanocyte, fetal liver and spleen, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal early development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, melanocytes, liver, spleen, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of abnormal early development phenomena and diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and blood systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

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expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in hematopoiesis and bone marrow regeneration as it is most abundant in fetal tissues responsible for the generation of hematopoietic cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 145

The translation product of this gene shares sequence homology with protein tyrosine phosphatase which is thought to be important in transducing signal to activate cells such as T cell, B cell and other cell types.

This gene is expressed primarily in T cells and tissues in early stages of development and to a lesser extent in cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic and fetal tissue, undifferentiated cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the protein tyrosine phosphatase family indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 146

This gene is expressed primarily in T cell and to a lesser extent in B cell, macrophages and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating the immune system therefore can be used in treating diseases such as autoimmune diseases and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 147

This gene is expressed primarily in placenta and to a lesser extent in endothelial cells, testis tumor, ovarian cancer, uterine cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, testis and ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 148

This sequence has significant homology to mouse torsin A. Recently, another group cloned the human Torsin A gene. (See, Accession No. 2358279; see also Nature Genet. 17, 40-48 (1997).)

This gene is expressed primarily in osteoclastoma, T-cell, and placenta and to a lesser extent in fetal lung, fetal liver, fetal brain, adult brain and tumor tissues

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disease conditions in hematopoiesis and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, bone, placenta, lung, liver, and brain and other tissues of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating blood related diseases such as deficiencies in red blood cell, white blood cell, platelet and other hematopoiesis cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 149

This gene is expressed primarily in T cell, prostate and prostate cancer, endothelial cells and to a lesser extent in monocyte, dendritic cell, bone marrow, salivary gland, colon cancer, stomach cancer, pancreatic tumor, uterine cancer, fetal spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, prostate, endothelial cells, dendritic cells, bone marrow, salivary gland, colon, stomach, pancreas, uterus, spleen and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 150

- 5 This gene was recently cloned by another group, calling it eIF3-p66. (See Accession No. 2351378.) This gene plays a role in RNA binding and macromolecular assembly, and therefore, any mutations in this gene would likely result in a diseased phenotype. Preferred polypeptide fragments comprise the amino acid sequence:
- 10 MAKFMTPVIQDNPSGWGPCAVPEQFRDMPYQPFSGDRLGKVADWTGATYQDKRYTNKYSS
QFGGGSQYAYFHEEDESSFLVDTARTQKTAYQRNMRFAQRNLRRDKDRRNMLQFNLQILP
KSAKQKERERIRLQKKFQKQFQVGRQKWDQKSQKPRDSSVEVRSDWEVKEEMDFPQLMKMRY
LEVSEPQDIECCGALEYDKAFDRITRSEKPLRXXKRIFHTVTTTDDPVIRKLAKTQGNVFATD
AILATLMSCTRSVYSWDIVVQRVGSKLFFDKRDNSDFDLLTVSETANEPQDEGNSFNSPRNL
AMEATYINHNFSQQCLRMGKERYNFPNPNPFVEDDMDKNEIASVAYRYSGLGDDIDLIVRC
15 EHDGVMTGANGEVSFINIKTLNEWDSRHCNGVDWRQKLD SQRGAVIATELKNNSYKLARWTC
CALLAGSEYLKLGYSRYHVKDSSRHVILGTQQFKPNEFASQINLSVENAWGILRCVIDICMKL
EEGKYLIKDPNKQVIRVYSLPDGTFSS (SEQ ID NO: 638), as well as N-terminal and C-terminal deletions of this polypeptide fragment.

- 20 This gene is expressed primarily in T cell, bone marrow, embryo and endothelial cells and to a lesser extent in testis tumor and endometrial tumor.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful
- 25 in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
- 30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune disorders and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 151

This gene is expressed primarily in testis and to a lesser extent in T cell, spinal cord, placenta, neutrophil and monocyte.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: male reproductive and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testis and other reproductive tissue, blood cells, tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating immune and reproductive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 152

The translation product of this gene shares sequence homology with tyrosyl-tRNA synthetase which is thought to be important in cell growth.

This gene is expressed primarily in brain, liver, keratinocytes, tonsils, and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, keratinocytes, tonsils, heart expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissues of the nervous system, liver, keratinocytes, tonsils and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to tyrosyl-tRNA synthetase indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating
5 cell growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 153

This gene is homologous to the *Drosophila* transcriptional regulator dre4. (See Accession No. 2511745.) Dre4 is a gene required for steroidogenesis in *Drosophila*
10 melanogaster and encodes a developmentally expressed homologue of the yeast transcriptional regulator CDC68. Preferred polypeptide fragments comprise the amino acid sequence: KKRHTDVQFYTEVGEITTDLGKHQHMHDRDDLYAEQMEREMRHKLTAFKN FIEKVEALTKEELEFEVPPFDLGFNGAPYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFXR VQFHLKNFDMVTVYKDYSKKVTMINAIPVASLDPIKEWLNNSCDLKYTEGVQSLNWTKIMKTIVD
15 DPEGFFEQGGWSFL (SEQ ID NO: 639), as well as N-terminal and C-terminal deletions of this fragments. Also preferred are polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in fetal liver, spleen, placenta, lung, T cell, thyroid, testes.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor, heart and liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal liver, spleen, placenta, lung, T cell, thyroid, testes expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, lung, blood cells, thyroid, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
30 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 154

This gene is expressed primarily in brain and to a lesser extent in fetal heart, testis, spleen, lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: heart, liver and spleen diseases, immunological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, fetal heart, testis, spleen, lung expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, heart, testes and other reproductive tissue, spleen, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 155

Activation of T cells through the T cell antigen receptor (TCR) results in the rapid tyrosine phosphorylation of a number of cellular proteins, one of the earliest being a 100 kDa protein. This gene is the human equivalent of murine valosin containing protein (VCP). VCP is a member of a family of ATP binding, homo-oligomeric proteins, and the mammalian homolog of *Saccharomyces cerevisiae* cdc48p, a protein essential to the completion of mitosis in yeast. Both endogenous and expressed murine VCP are tyrosine phosphorylated in response to T cell activation. Thus we have identified a novel component of the TCR mediated tyrosine kinase activation pathway that may provide a link between TCR activation and cell cycle control.

25

This gene is expressed primarily in brain, liver, spleen, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, spleen, placenta expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, spleen, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

35

an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to VCR indicate that polynucleotides and polypeptides corresponding to this gene are useful for treating cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 156

10 The translation product of this gene shares sequence homology with rat growth response protein which is thought to be important in cell growth. A group recently cloned the human homolog of this gene, calling it insulin induced protein 1. (See Accession No. 2358269, see also, Genomics 43 (3), 278-284 (1997).) Preferred polypeptide fragments comprise the amino acid sequence: RSGLGLGITIAFLATLITQF LVYNGVYQYTSPDFLYIRSWLPCIFFSGGVTVGNIGRQLAMGVPEKPHSD (SEQ ID NO: 640), as well as N-terminal and C-terminal deletions of this polypeptide fragment. Also
15 preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain, liver, placenta, heart, spleen, lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, placenta, heart, spleen.
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, placenta, heart, spleen, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
30 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to growth-response protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 157

This gene is expressed primarily in Glioblastoma, endometrial tumor, lymphoma and pancreas tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Glioblastoma, Endometrial tumor, lymphoma and pancreas tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, lymphoid tissue, pancreas, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
15 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 158

20 The translation product of this gene shares sequence homology with IGE receptor which is thought to be important in allergy and asthma.

This gene is expressed primarily in T cell, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: allergy and asthma and other immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower
30 levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
35 disorder.

The tissue distribution and homology to IgE receptor indicate that polynucleotides and polypeptides corresponding to this gene are useful for allergy and asthma.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 159**

The translation product of this gene shares sequence homology with immunoglobulin heavy chain which is thought to be important in immune response to the antigen.

10 This gene is expressed primarily in activated neutrophil and to a lesser extent in activated T cell, monocyte and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: infection, inflammation and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are
15 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin heavy chain variable region indicate that polynucleotides and polypeptides corresponding to this gene are
25 useful for making the ligand to block specific antigen which cause certain disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 160

The translation product of this gene shares sequence homology with mouse X inactive specific transcript protein which is thought to be important in X chromosome
30 inactivation.

This gene is expressed primarily in HSA172 cell and to a lesser extent in normal ovary tissue, ovarian cancer, frontal cortex and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: ovarian tumor, schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovary and other reproductive tissue, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to X inactive specific transcript protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive system tumors and CNS tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 161

15 This gene is expressed primarily in adipose cell and to a lesser extent in liver and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity and liver
20 disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose cell, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose cells, liver, and
25 prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of obesity and liver disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 162

35 The translation product of this gene shares sequence homology with yeast ubiquitin activating enzyme homolog which is thought to be important in protein posttranslation processing.

This gene is expressed primarily in stromal cell and to a lesser extent in retina, H. Atrophic Endometrium, colon carcinoma and myeloid progenitor cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development, neuronal growth disorders and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal cells, endometrium, colon, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ubiquitin-activating enzyme homolog indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of some type of tumors, fucosidosis and neuronal growth disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 163

This gene is expressed primarily in primary breast cancer and hemangiopericytoma and to a lesser extent in adult brain and cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer, leukemia and cerebellum disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of various tumors and disease involved in neural system.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 164**

The translation product of this gene shares sequence homology with proline rich proteins. Recently, another group has also cloned this gene, calling it CD84 leukocyte antigen, a new member of the Ig superfamily. (See Accession No. U82988, see also, Blood 90 (6), 2398-2405 (1997).)

10 This gene is expressed primarily in Weizmann olfactory tissue and osteoclastoma and to a lesser extent in anergic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ostsis and immune
15 disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue, bone, and
20 blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution and homology to the Ig superfamily indicate that the protein product of this clone is useful for treatment of osteoporosis, autoimmune disease, and other immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 165

30 This gene is expressed primarily in atrophic endometrium and colon cancer and to a lesser extent in some fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly,
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, colon, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors, specifically endometrium and colon tumors.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 166

This gene is expressed primarily in human primary breast cancer and to a lesser extent in activated monocyte. Although the predicted signal sequence is identified in Table 1, other upstream sequences are also relevant. Preferred polypeptide fragments comprise
15 the amino acid sequence: VTQPKHLSASMGGSV EIPFSFYYPWELAXXPXVRISWRRGHFHG QSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQSVYFCRVELDTRRSG (SEQ ID NO: 641), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in
30 healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 167

35 This gene is expressed primarily in fetal tissues and to a lesser extent in adult lung. This gene has also been mapped to chromosomal location 9q34, and thus, can be used as a marker for linkage analysis for chromosome 9.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 168

The translation product of this gene shares sequence homology with Ig Heavy Chain which is thought to be important in immune response.

This gene is expressed primarily in prostate cancer tissue specifically

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The translation product of this gene shares sequence homology with cytosolic acyl coenzyme-A hydrolase, which is thought to be important in neuron-specific fatty acid metabolism. The gene represented by this contig has since been published by Hajra and colleagues (GenBank Accession No. U91316).

This gene is expressed primarily in human pituitary gland and to a lesser extent in colorectal cancer tissue. This gene has also been observed in the LNCAP cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hyperlipidemias of familial and/or idiopathic origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly blood, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to rat cytosolic acyl coenzyme-A hydrolase indicate that polynucleotides and polypeptides corresponding to this gene are useful for the detection or treatment of hyperlipidemia disease states by virtue of the ability of specific drugs to activate the enzyme.

FEATURES OF PROTEIN ENCODED BY GENE NO: 170

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene which is thought to be important in organism development.

This gene is expressed primarily in human synovial sarcoma tissue, bone marrow, and to a lesser extent in human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of bone, specifically synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, connective tissues and possibly immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, bone marrow, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another

tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to *Caenorhabditis elegans* indicate that polynucleotides and polypeptides corresponding to this gene are useful as a diagnostic and/or therapeutic modality directed at the detection and/or treatment of connective tissue sarcomas or other related bone diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 171

10 The translation product of this gene shares sequence homology with beta1-6GlcNAc transferase which is thought to be important in the transfer and metabolism of beta1-6, N-acetylglucosamine. This gene product has previously been shown to suppress melanoma lung metastasis in both syngeneic and nude mice, decreased invasiveness into the matrigel, and inhibition of cell attachment to collagen and laminin
15 without affecting cell growth.

This gene is expressed primarily in human testes and prostate tissues, and to a lesser extent in kidney, medulla, and pancreas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at
25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, prostate, kidney, pancreas, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to beta1-6GlcNAc transferase indicate that the protein product of this clone is useful for the development of diagnostic and/or therapeutic modalities directed at the detection and/or treatment of cancer, the metastasis
35 of malignant tissue or cells. Defects in this potentially secreted enzyme may play a role in metastasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 172

This gene is expressed primarily in fetal spleen and liver.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders,
Wilm's tumor disease, hepatic disorders, and hematopoietic disorders. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the hematopoiesis and
immune systems, expression of this gene at significantly higher or lower levels may be
routinely detected in certain tissues and cell types (e.g., spleen and liver, and cancerous
and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in
healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the treatment and identification of fetal defects
along with correcting diseases that affect hematopoiesis and the immune system.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 173

The translation product of this gene shares sequence homology with ret II
oncogene which is thought to be important in Hirschsprung disease and many types of
cancers.

25 This gene is expressed in multiple tissues including the lymphatic system, brain,
and thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for identification of the tissue(s) or cell type(s) present in a biological sample
and for diagnosis of diseases and conditions: Hirschsprung disease and multiple
30 cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful
in providing immunological probes for identification of the tissue(s) or cell type(s). For
a number of disorders of the above tissues or cells, particularly of the immune and
central nervous system, expression of this gene at significantly higher or lower levels
may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue,
35 thyroid, and brain and other tissue of the nervous system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ret II oncogene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of various cancers. It would also be useful for the diagnosis and treatment of Hirschsprung disease. Preferred polypeptides of the invention comprise the amino acid sequence: MEAQQVNEAESAREQLQXLHDQIAGQKASKQELETelerLKQEFHYIEDLY RTKNTLQSRIKDRDEEIQKLRNQLTNKTLSSSQSELENRLHQLTETLIQKQTMLESLSSTEKNSL VFQLERLEQQMNSASGSSSNGSSINMSGIDNGEGTRLRNVPVLFNDTETNLAGMYGKVRKAAS
 10 SIDQFSIRLGIFLRRYPIARVVFVIYMALLHLWVMIVLLTYTPEM HHDQPYGK (SEQ ID NO: 642).

FEATURES OF PROTEIN ENCODED BY GENE NO: 174

The translation product of this gene shares sequence homology with testis enhanced gene transcript which is thought to be important in regulation of human development.

This gene is expressed primarily in infant brain and to a lesser extent in a variety of other tissues and cell types, including the prostate, testes, monocytes, macrophages, dendritic cells, keratinocytes, and adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological, developmental, immune and inflammation disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, prostate, testes and other reproductive tissue, blood cells, keratinocytes, and adipocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to testis enhanced gene transcript indicate that the protein product of this clone is useful for diagnosis and treatment of disorders involving the developing brain and the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 175

This gene is expressed primarily in prostate and to a lesser extent in various other tissues, including placenta.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, especially of the prostate. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
- 10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
- 15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of prostate disorders and cancer. It may also be useful for
- 20 the diagnosis and treatment of endocrine disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 176

- The translation product of this gene shares sequence homology with *Saccharomyces cerevisiae* YNT20 gene which is thought to be important in
- 25 mitochondrial function.

This gene is expressed at a particularly high level in muscle tissue.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases related to such tissues and cell types
- 30 including: muscle wasting diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
- 35 types (e.g., muscle and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the YNT20 gene indicate that this protein is useful for treatment and detection of neuromuscular diseases caused by loss of mitochondrial function. For example this gene or its protein product could be used in replacement therapy for such diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in the brain and to a lesser extent in kidney, placenta, smooth muscle, heart and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuromuscular diseases, degenerative diseases of the central nervous system, and heart disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, central nervous system, and heart, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, kidney, placenta, muscle, heart and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

This gene or its protein product could also be used for replacement therapy for the above mentioned diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 178

The translation product of this gene shares sequence homology with caldesmon which is thought to be important in the cellular response to changes in glucose levels.

This gene is expressed primarily in multiple tissues including brain and retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: central nervous system disorders and retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the CNS disorders and retinopathy, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and retinal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to caldesmon indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of retinopathies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 179

The translation product of this gene shares sequence homology with mouse fibrosin protein which is thought to be important in regulation of fibrinogenesis in certain chronic inflammatory diseases.

This gene is expressed primarily in amniotic cells and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast cancer and abnormal embryo development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to fibrosin indicate that the protein product of this clone is useful for treatment of breast cancer. This gene or its protein product could be used in replacement therapy for breast cancer. In addition the protein product of this gene is useful in the treatment of chronic inflammatory diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 180

This gene is expressed several infant tissues including brain and liver and various adult tissues including brain, lung, liver, testes, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, brain cancer, lung cancer, liver cancer and cancers of the reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, hepatic system, and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, liver, testes and other reproductive tissue, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene product indicates that the protein product of this clone is involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 181

This gene is expressed primarily in activated monocytes and to a lesser extent in melanocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of immune system diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, melanocytes, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 182

This gene is expressed primarily in placenta and several tumors of various tissue origin and to a lesser extent in normal tissues including liver, lung, brain, and skin,

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers of all kinds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 10 of the above tissues or cells, particularly of the central nervous system, respiratory system and skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, lung, brain and other tissues of the nervous system, and skin, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
- 15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The high expression of this gene in multiple tumors indicates that the protein product of the clone may be involved in cell growth control and therefore would be
- 20 useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

FEATURES OF PROTEIN ENCODED BY GENE NO: 183

- 25 The translation product of this gene shares sequence homology with the mouse Ndr1 gene which is thought to be important in cancer progression.

This gene is expressed multiple cell types and tissues including brain, lung, kidney, bone marrow, liver, and spleen.

- Therefore, polynucleotides and polypeptides of the invention are useful as
- 30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and endocrine
- 35 systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, kidney, bone marrow, liver and spleen, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to Ndr1 gene, which is thought to be involved in cancer progression, indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 184

This gene is expressed primarily in early stage human brain and liver and to a lesser extent in several other fetal tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain and liver cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
20 type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
25 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in infant and embryonic brain.

- Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of degenerative nervous system disorders and brain cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 186

This gene is expressed primarily in multiple tissues including placenta, fetal lung, fetal liver, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers including liver, brain and lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, pulmonary system, and hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, lung, liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	11	582	1	582	177	177	313	1	18	19	22
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	197	1020	296	830	442	442	499	1	18	19	22
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	12	465	1	465	81	81	314	1	30	31	128
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	198	524	229	343		196	500	1	20	21	33
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	13	474	1	474	1	1	315	1	24	25	28
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	199	332	1	319	35	35	501	1	24	25	28

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
4	HCUFQ22	97897 02/26/97 209043 05/15/97	ZAP Express	14	314	1	298	122	122	316	1	34	35	64
5	HCUFV01	97897 02/26/97 209043 05/15/97	ZAP Express	15	613	1	613	30	30	317	1	18	19	21
6	HCUGA50	97897 02/26/97 209043 05/15/97	ZAP Express	16	356	1	356	239	239	318	1	22	23	39
7	HCUIM14	97897 02/26/97 209043 05/15/97	ZAP Express	17	414	185	414	278	278	319	1	26	27	33
8	HLD0U93	97897 02/26/97 209043 05/15/97	pCMVSPORT 3.0	18	469	1	469	77	77	320	1	44	45	88
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	19	550	1	550	129	129	321	1	21	22	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	200	376	9	376		1	502	1	8	9	15
10	HSAXR76	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	20	741	55	741	190	190	322	1			27
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	21	991	1	991	62	62	323	1	30	31	64
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	201	1192	253	1137		409	503	1			19
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	22	653	1	653	64	64	324	1	30	31	196
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	202	589	1	513	109	109	504	1			29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
13	HLMV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	23	1486	596	1418	102	102	325	1	54	55	252
13	HLMV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	203	847	1	839	87	87	505	1	30	31	75
13	HLMV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	204	852	75	850		690	506	1			10
13	HTXEF04	209235 09/04/97	Uni-ZAP XR	205	1354	54	1354	100	100	507	1	33	34	207
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	24	2323	1017	2039	1242	1242	326	1	21	22	68
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	206	1378	113	1226	303	303	508	1	25	26	36
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	25	683	1	683	304	304	327	1	30	31	84

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	207	1166	281	884	567	567	509	1	18	19	19
16	HHFFL33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	26	2036	14	1959	214	214	328	1	20	21	36
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	27	717	1	717	70	70	329	1	30	31	63
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	208	697	2	697	33	33	510	1	31	32	32
18	HMDAE90	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	28	495	1	495	39	39	330	1	24	25	35
19	HOUAW01	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	29	556	1	556	116	116	331	1	19	20	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
20	HBJAE44	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	30	434	1	434	78	78	332	1	35	36	40
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	31	715	1	715	87	87	333	1	30	31	111
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	209	932	274	932	387	387	511	1	27	28	28
22	HOGCO71	97897 02/26/97 209043 05/15/97	pCMVSPORT 2.0	32	486	1	486	137	137	334	1	21	22	106
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	33	725	1	725	436	436	335	1	30	31	50
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	210	661	1	647	81	81	512	1	25	26	26

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
24	HSKNJ72	97897 02/26/97 209043 05/15/97	pBluescript	34	437	1	437	85	85	336	1	30	31	48
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	35	943	1	943	196	196	337	1	30	31	41
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	211	592	1	534	72	72	513	1	24	25	33
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	36	604	1	604	375	375	338	1	20	21	76
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	212	938	1	509		17	514	1	30	31	47
27	HSAUZ47	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	37	349	1	349		201	339	1	20	21	31

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
28	HSSDM73	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	38	672	1	672	22	22	340	1	38	39	42
29	HBMVK68	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	39	1908	135	1908	309	309	341	1	20	21	26
30	HMKDC66	97898 02/26/97 209044 05/15/97	pSport1	40	458	93	458	147	147	342	1	24	25	26
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	41	1153	500	1153	427	427	343	1	30	31	157
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	213	1079	502	896		739	515	1	23	24	43
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	42	1983	1092	1983	27	27	344	1	11	12	520

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	214	3791	2757	3357		2030	516	1			3
33	HTOJN06	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	43	1406	1	695		19	345	1	19	20	39
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	44	1391	851	1153	74	74	346	1	30	31	234
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	215	1334	822	1036		638	517	1	18	19	174
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	45	1569	768	1569	14	14	347	1	19	20	169
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	216	1511	770	1404	844	844	518	1	32	33	43

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
36	HHPBD40	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	46	1924	1	1681	62	62	348	1	19	20	43
37	HOVCL83	97898 02/26/97 209044 05/15/97	pSport1	47	475	252	396	141	141	349	1	37	38	78
38	HBCAY62	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	48	346	1	346	61	61	350	1	19	20	24
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	49	1366	882	1300	177	177	351	1	30	31	274
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	217	642	192	581		448	519	1			13
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	50	1405	110	1404	61	61	352	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	218	1241	1	1241	172	172	520	1	21	22	30
41	HLHCK50	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	51	504	207	485	222	222	353	1			3
42	HRSAN45	97899 02/26/97 209045 05/15/97	ZAP Express	52	777	1	214	113	113	354	1	24	25	52
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	53	602	1	419	41	41	355	1	59	60	132
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	219	1080	186	686	399	399	521	1	26	27	47
44	HMAABL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	54	1749	222	1749	166	166	356	1	30	31	204

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT 3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
44	HMABL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	220	1258	149	1190	254	254	522	1	18	19	26
45	HSKDK47	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	55	1896	596	1614	650	650	357	1	33	34	47
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	56	1753	555	1753	414	414	358	1	18	19	73
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	221	1693	554	1693		526	523	1	25	26	58
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	57	1220	690	1024	128	128	359	1	30	31	102
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	222	1196	712	1163		1097	524	1			19

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
48	HFCAl74	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	58	1049	362	1049	335	335	360	1	33	34	48
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	59	1776	854	1737	189	189	361	1	30	31	179
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	223	1791	979	1791	1164	1164	525	1	18	19	40
50	HLFBC91	97899 02/26/97 209045 05/15/97	pBluescript SK-	60	443	1	443	164	164	362	1	21	22	25
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	61	2888	1909	2888	90	90	363	1	30	31	224
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	224	2517	1597	2517	1953	1953	526	1	18	19	57

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	62	1851	1568	1736	139	139	364	1	30	31	349
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	225	2424	299	2309		530	527	1	17	18	21
53	HHTLC66	97899 02/26/97 209045 05/15/97	ZAP Express	63	3542	883	3492	964	964	365	1	25	26	467
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	64	883	237	883	229	229	366	1	30	31	152
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	226	1080	242	1033	436	436	528	1	24	25	39
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	65	1541	1	1541	236	236	367	1	30	31	373

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	227	1336	4	1336	946	946	529	1	25	26	128
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	66	732	41	698	163	163	368	1	18	19	83
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	228	2043	1133	1756	1262	1262	530	1	20	21	82
57	HKTAG35	209011 04/28/97	Uni-ZAP XR	67	629	1	629	264	264	369	1			21
57	HMEFX42	97899 02/26/97 209045 05/15/97	Lambda ZAP II	229	540	25	536	227	227	531	1			20
58	HHFHN61	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	68	1751	375	1751	95	95	370	1	19	20	227
59	HCWFEF90	97899 02/26/97 209045 05/15/97	ZAP Express	69	508	1	508	22	22	371	1	30	31	79

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	230	448	9	448		1	532	1	22	23	75
60	HHGCM20	97899 02/26/97 209045 05/15/97	Lambda ZAP II	70	245	1	245	93	93	372	1	1	2	51
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	71	361	1	361	1	1	373	1	30	31	61
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	231	407	1	407	210	210	533	1	17	18	60
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	72	713	8	713	169	169	374	1	30	31	40
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	232	830	190	580	329	329	534	1	28	29	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	73	862	1	862	67	375	1	30	31	44
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	233	932	138	905	287	535	1			2
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	74	4602	4162	4525	730	376	1	30	31	203
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	234	2786	2406	2739	2577	536	1	22	23	36
65	HSGBA84	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	75	1255	1	1195	112	377	1	28	29	29
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	76	475	1	475	13	378	1	30	31	136

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	235	458	1	458	26	26	537	1			14
67	HTGCP16	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	77	465	25	299	74	74	379	1	33	34	41
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	78	1907	1627	1730	26	26	380	1	30	31	468
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	236	591	1	444	251	251	538	1			18
69	HETGJ09	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	79	1168	136	1168	267	267	381	1	20	21	29
70	HOBNC61	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	80	1285	132	1285	292	292	382	1	27	28	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
71	HFFAH94	97900 02/26/97 209046 05/15/97	Lambda ZAP II	81	1290	768	1054	701	701	383	1	21	22	138
72	HBIAB95	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	82	684	1	684	119	119	384	1	30	31	74
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	83	2024	1609	1953	200	200	385	1	30	31	521
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	237	1286	391	959		1204	539	1	9	10	11
74	HEBEG68	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	84	931	14	537	85	85	386	1	25	26	137
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	85	825	59	802	66	66	387	1	30	31	186

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	238	734	1	734	1	1	540	1	37	38	108
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	239	809	80	794		294	541	1	15	16	106
76	HTXDU73	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	86	1238	36	918	17	17	388	1			1
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	87	1460	9	1458	166	166	389	1	53	54	299
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	240	2201	841	2080	507	507	542	1	43	44	136
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	241	1661	311	1520	390	390	543	1	35	36	424

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
78	HTEIY30	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	88	1395	567	1395	639	639	390	1	36	37	49
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	89	1186	352	1186	540	540	391	1	49	50	61
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	242	1146	329	1146	564	564	544	1	21	22	39
80	HPMFL27	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	90	1821	1203	1614	1503	1503	392	1	30	31	79
81	HMWDN32	97900 02/26/97 209046 05/15/97	Uni-Zap XR	91	862	253	862	359	359	393	1	32	33	36
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	92	696	349	696	98	98	394	1	30	31	180

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	243	1350	265	1230	348	348	545	1	32	33	58
83	HFFFW36	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	93	1886	1	1759	197	197	395	1			21
84	HE2PL77	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	94	1774	742	1772	785	785	396	1	21	22	60
85	HSDFV29	209076 05/22/97	Uni-ZAP XR	95	2503	1	1648	206	206	397	1	32	33	152
85	HCQAV53	97901 02/26/97 209047 05/15/97	Lambda ZAP II	244	1529	72	911	191	191	546	1	20	21	33
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	96	2801	418	2801	234	234	398	1	30	31	480
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	245	1537	1	1537	125	125	547	1	21	22	367

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of AA of ORF
87	HLHDR57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	97	1631	916	1631	1	1	399	1	1	2	423
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	98	504	26	504	197	197	400	1	23	24	78
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	246	506	1	499	183	183	548	1	32	33	77
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	99	1416	145	1416	456	456	401	1	18	19	74
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	247	1348	84	1348	363	363	549	1	21	22	47
90	HSHCI16	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	100	2847	1	2847		2	402	1			20

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
91	HTSEL31	97901 02/26/97 209047 05/15/97	pBluescript	101	1394	608	1346	602	602	403	1	23	24	87
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	102	794	1	794	518	518	404	1	30	31	92
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	248	1766	42	1766	356	356	550	1	30	31	168
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	249	2664	47	1708		147	551	1	18	19	124
93	HODASS9	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	103	1544	898	1531	975	975	405	1			21
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	104	871	106	871	248	248	406	1	34	35	174

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	250	865	97	865	258	258	552	1	19	20	177
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	105	404	1	404	16	16	407	1	21	22	64
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	251	2082	852	2074	829	829	553	1	22	23	72
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	106	1542	506	1542	122	122	408	1	51	52	280
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	252	1482	508	1482		633	554	1	15	16	45
96	HCUHB01	209215 08/21/97	ZAP Express	253	834	1	834	82	82	555	1	40	41	251
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	107	2327	1528	2327	465	465	409	1	30	31	284

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	254	1508	885	1508		988	556	1			19
98	HAQBT94	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	108	1062	157	1062	172	172	410	1	28	29	187
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	109	2539	275	2501	903	903	411	1	30	31	237
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	255	2514	592	2431	176	176	557	1	30	31	217
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	256	2357	465	2288		1151	558	1	12	13	82
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	110	1751	969	1751	4	4	412	1	46	47	192

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	257	689	218	655	314	314	559	1	18	19	95
100	HEONN58	209119 06/12/97	pSportI	258	2377	5	2377	25	25	560	1	28	29	54
101	HCRAM28	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	111	1117	1	1117		1	413	1	19	20	21
101	HIBEK16	209627 02/12/98	Other	259	1193	69	1135	242	242	561	1	24	25	108
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	112	1313	128	1313	271	271	414	1	30	31	51
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	260	1262	26	1262	35	35	562	1	35	36	50
103	HEBDJ82	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	113	1654	553	1654	709	709	415	1			32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	114	1171	540	1171	337	337	416	1	30	31	163
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	261	1179	626	1161	335	335	563	1	30	31	253
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	262	1162	629	1131	942	942	564	1			18
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	115	842	373	800	100	100	417	1	65	66	174
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	263	735	290	735			565	1			
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	264	783	416	783		413	566	1	33	34	73

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	116	1640	187	1470	581	418	1	30	31	50
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	265	1638	301	1405	119	567	1	30	31	263
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	266	1455	148	1188	438	568	1	24	25	70
107	HE6DK18	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	117	952	418	906	499	419	1	28	29	120
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	118	1256	21	1079	301	420	1	30	31	159
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	267	1086	25	1050	227	569	1	23	24	34

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	119	1143	171	1051	175	175	421	1	50	51	154
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	268	1003	21	1003	115	115	570	1	34	35	104
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	269	1234	174	1015	232	232	571	1	27	28	132
110	HSXBL78	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	120	1782	1	1720	138	138	422	1	32	33	204
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	121	610	18	609	50	50	423	1	30	31	67
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	270	574	1	566	337	337	572	1	27	28	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
112	HOEAP41	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	122	526	185	375	143	143	424	1	21	22	25
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	123	2081	1179	1976	48	48	425	1	30	31	299
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	271	1731	889	1626	886	886	573	1	18	19	28
114	HTXGS75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	124	1717	764	1640	76	76	426	1			13
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	125	804	1	804	145	145	427	1	15	16	198
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	272	1320	77	637	280	280	574	1	22	23	40

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	126	431	1	431	73	73	428	1	38	39	47
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	273	515	1	515	43	43	575	1	20	21	30
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	127	3752	3465	3752	748	748	429	1	30	31	370
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	274	2995	2738	2995	2777	2777	576	1	18	19	29
118	HASAS24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	128	1144	669	1144	896	896	430	1			30
119	HSIDN55	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	129	1830	1234	1830	1265	1265	431	1			24

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
120	HGBGZ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	130	1864	1505	1741	1578	432	1	37	38	53
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	131	2041	1	1214	46	433	1	35	36	176
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	275	1990	8	1128	71	577	1	16	17	92
122	HOECP43	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	132	2012	853	1986	1127	434	1	22	23	77
123	H2CBV31	97902 02/26/97 209048 05/15/97	pBluescript SK-	133	1669	670	1632	962	435	1	25	26	32
124	HPCAD23	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	134	1565	281	1565	274	436	1	25	26	30

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
125	HSPAG15	97902 02/26/97 209048 05/15/97	pSport1	135	2007	1101	2007	1124	437	1	39	40	69
126	HELGH31	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	136	1291	1	1180	107	438	1			19
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	137	1906	1	1906	184	439	1	30	31	43
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	276	2436	572	2436	726	578	1	30	31	42
128	HLYAU95	97902 02/26/97 209048 05/15/97	pSport1	138	1935	1044	1794	1183	440	1	18	19	33
129	HHSCV65	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	139	1446	572	1347	585	441	1	25	26	53

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
130	HTTAD57	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	140	1109	639	1109	676	442	1	24	25	64
131	HEBGA37	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	141	497	9	497	95	443	1			34
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	142	269	1	269	1	444	1	30	31	89
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	277	782	408	781	571	579	1	31	32	70
133	HSGSC60	97902 02/26/97 209048 05/15/97	Lambda ZAP II	143	1269	55	1262	55	445	1	25	26	350
134	HPMGD24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	144	1944	97	1871	306	446	1	16	17	49

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	145	1021	526	1021	74	74	447	1	30	31	278
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	278	961	524	961	545	545	580	1	23	24	110
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	146	1285	5	1285	116	116	448	1	30	31	199
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	279	1228	9	1228	324	324	581	1	26	27	30
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	147	1386	169	1272	165	165	449	1	30	31	258
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	280	1327	169	1208	160	160	582	1	23	24	71

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
138	HMWGI25	97902 02/26/97 209048 05/15/97	Uni-Zap XR	148	2098	721	2044	784	784	450	1	18	19	87
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	149	1847	1689	1847	241	241	451	1	33	34	315
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	281	799	1	799		243	583	1	12	13	47
140	HMSKE75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	150	1569	113	1517	417	417	452	1	21	22	52
141	HCMESH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	151	1540	538	1540	48	48	453	1	30	31	383
141	HCMESH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	282	2196	270	2196	294	294	584	1	32	33	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
142	HTWCB92	97902 02/26/97 209048 05/15/97	pSport1	152	1719	690	1575	6	6	454	1	52	53	186
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	153	863	1	863	195	195	455	1	26	27	163
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	283	1185	277	1166	621	621	585	1			19
144	HFAMG13	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	154	1101	1	512	40	40	456	1	21	22	46
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	155	2031	669	2031	411	411	457	1	23	24	105
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	284	1634	615	1485	878	878	586	1	20	21	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	156	1981	1458	1809	1592	1592	458	1	23	24	70
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	285	1795	1458	1749	1562	1562	587	1	33	34	69
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	157	915	45	912	22	22	459	1	22	23	155
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	286	858	46	858	224	224	588	1	30	31	77
147	HSJAP03	209139 07/03/97	Uni-ZAP XR	287	915	1	915	22	22	589	1	22	23	155
148	HSKGO26	97903 02/26/97 209049 05/15/97	pBluescript	158	2117	51	1422	32	32	460	1	23	24	332
149	HCQAV96	97903 02/26/97 209049 05/15/97	Lambda ZAP II	159	2395	1509	2382	1440	1440	461	1			5

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
150	HSHCC16	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	160	2120	1223	2108	1416	1416	462	1			14
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	161	900	482	900	46	46	463	1	30	31	285
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	288	1517	783	1517	1062	1062	590	1			24
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	162	1003	1	1003	288	288	464	1	30	31	80
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	289	3865	217	1195	281	281	591	1	16	17	38
153	HTSFQ12	97903 02/26/97 209049 05/15/97	pBluescript	163	2196	1607	2180	1611	1611	465	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	164	1945	271	1840	299	299	466	1	63	64	96
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	290	1910	279	1818	355	355	592	1	39	40	69
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	165	2933	489	2871	258	258	467	1	30	31	399
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	291	3276	486	2838		525	593	1	45	46	308
156	HJPCJ76	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	166	2243	343	2221		341	468	1			1
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	167	1816	1130	1816	284	284	469	1	31	32	273

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	292	1695	1098	1548	1306	1306	594	1			22
158	HMKBA64	97903 02/26/97 209049 05/15/97	pSport1	168	945	1	787	208	208	470	1	18	19	192
159	HNFIP24	97903 02/26/97 209049 05/15/97	pBluescript	169	902	46	816	19	19	471	1	26	27	234
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	170	1883	798	1869	1001	1001	472	1	45	46	105
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	293	1501	438	1501	510	510	595	1			24
161	HAWBA28	97903 02/26/97 209049 05/15/97	pBluescript SK-	171	2100	1642	2100	1722	1722	473	1	23	24	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	172	1930	187	1930	65	65	474	1	30	31	571
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	294	2683	183	2683	431	431	596	1			24
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	173	1509	962	1451	122	122	475	1	30	31	312
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	295	1454	961	1420	976	976	597	1			1
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	174	3173	2197	2972	51	51	476	1	21	22	329
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	296	828	52	828	305	305	598	1			8

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	175	991	374	970	60	60	477	1	24	25	178
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	297	2416	1387	2413	1473	1473	599	1	18	19	25
166	HFKFX55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	176	1290	499	1290		688	478	1	25	26	52
167	H2LAO11	97903 02/26/97 209049 05/15/97	pBluescript SK-	177	2290	1	2290	173	173	479	1	22	23	62
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	178	549	1	549	11	11	480	1	21	22	27
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	298	545	1	545	17	17	600	1	21	22	27

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	179	1509	294	1352	92	92	481	1	30	31	339
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	299	1530	385	1530	562	562	601	1	23	24	61
170	HCF AE79	97904 02/26/97 209050 05/15/97	pSport1	180	1316	985	1250	995	995	482	1	26	27	32
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	181	777	1	777	51	51	483	1	30	31	48
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	300	997	244	997	300	300	602	1	23	24	29
172	HODCW06	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	182	791	1	791	14	14	484	1	29	30	38

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
173	HFTAR26	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	183	1405	346	1405	575	575	485	1	20	21	61
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	184	1596	75	1596	131	131	486	1	24	25	346
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	301	2345	75	2345	233	233	603	1	56	57	69
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	185	2293	355	2288	67	67	487	1	30	31	237
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	302	2369	2	1946		60	604	1	9	10	24
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	186	1212	462	1180	257	257	488	1	30	31	200

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	303	1181	424	1149	663	663	605	1	23	24	35
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	187	1605	770	1554	166	166	489	1	30	31	351
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	304	1537	719	1515		787	606	1	43	44	130
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	188	1516	960	1516	8	8	490	1	30	31	265
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	305	1493	1	1261	54	54	607	1	18	19	23
179	HAQAF27	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	189	681	287	681		401	491	1			25

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	190	1014	703	1014	360	360	492	1	30	31	159
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	306	577	1	577	175	175	608	1			6
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	191	2779	2207	2630	1153	1153	493	1	30	31	279
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	307	2860	163	2860	21	21	609	1	30	31	232
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	308	876	275	876	302	302	610	1	32	33	34
182	HETBY74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	192	1923	30	1923	45	45	494	1	33	34	193

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	193	2346	1160	2286	178	178	495	1	30	31	205
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	309	2025	840	2025	971	971	611	1	18	19	21
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	194	3054	2004	3054	434	434	496	1	11	12	147
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	310	3026	1966	3026		2131	612	1			9
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	195	907	152	907	297	297	497	1	30	31	64
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	311	712	67	712	107	107	613	1	18	19	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	196	1290	84	809	225	225	498	1	30	31	94
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	312	1289	785	1289	927	927	614	1	28	29	30

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
- 10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

- 15 Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
- 20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- 25 In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
- 30 shown in Table 1.

- As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
- 35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 "Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994);
20 SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991).) While there exists a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans. (Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).) Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers," Martin J. Bishop, ed., Academic Press, San Diego, (1994), and Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).
25 Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. 215:403 (1990), Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711 (using the local homology algorithm of Smith
35 and Waterman, Advances in Applied Mathematics 2:482-489 (1981).)

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, 95% identical to a reference sequence, the parameters are set so that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990).) The term "sequence" includes nucleotide and amino acid sequences. In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB search of a DNA sequence to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, and Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, and Window Size=500 or query sequence length in nucleotide bases, whichever is shorter. Preferred parameters employed to calculate percent identity and similarity of an amino acid alignment are: Matrix=PAM 150, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, and Window Size=500 or query sequence length in amino acid residues, whichever is shorter.

As an illustration, a polynucleotide having a nucleotide sequence of at least 95% "identity" to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone, means that the polynucleotide is identical to a sequence contained in SEQ ID NO:X or the cDNA except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the total length (not just within a given 100 nucleotide stretch). In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to SEQ ID NO:X or the deposited clone, up to 5% of the nucleotides in the sequence contained in SEQ ID NO:X or the cDNA can be deleted, inserted, or substituted with other nucleotides. These changes may occur anywhere throughout the polynucleotide.

Further embodiments of the present invention include polynucleotides having at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone. Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the polynucleotides having at least 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity

will encode a polypeptide identical to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference polypeptide, is intended that the amino acid sequence of the polypeptide is identical to the reference polypeptide except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the total length of the reference polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

Further embodiments of the present invention include polypeptides having at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone. Preferably, the above polypeptides should exhibit at least one biological activity of the protein.

In a preferred embodiment, polypeptides of the present invention include polypeptides having at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98%, or 99% similarity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an

organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.

Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

5 Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988
10 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

 Moreover, ample evidence demonstrates that variants often retain a biological
15 activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible
20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

25 Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form
30 are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

 Thus, the invention further includes polypeptide variants which show
35 substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make

phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

5 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid
10 substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham
15 and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the
20 protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues
25 Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues,
30 where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino
35 acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

10 In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

20 Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, and 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, and 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about"

includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

5 In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

10 Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if
15 it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is
20 meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred,
25 as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

30 Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular
35 locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

5 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
10 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

 Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of
15 immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4- polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86
20 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion
25 proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified,
30 would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol.
35 Chem. 270:9459-9471 (1995).)

 Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In

preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the claimed invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS,

293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A,
5 pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

10 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the
15 present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity
20 chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids,
25 tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be
30 non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most
35 proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes
5 known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention
10 can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic
15 cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can
20 be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using
25 fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to
30 mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross
35 hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage

analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the

present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute
5 biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags"
10 which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an
15 individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely
20 small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from
25 polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the
30 present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present
35 invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers
5 for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The
10 following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-
15 3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and
20 technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-
25 radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with
30 an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the
35 subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20

millicuries of ^{99m}Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The
5 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene
10 expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to
15 supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired
20 response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such
25 as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention could be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a
30 recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

35 The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules

may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

5 A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells
10 from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

15 A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic
20 cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency
25 (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood
30 coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks
35 (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from

inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Bimaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.
- Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillois, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect
5 any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis,
10 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide
15 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide
20 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

25 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal
30 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and
35 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat

disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

5 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or
10 small molecules.

 Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural
15 receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

 Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell
20 membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

25 The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

 Alternatively, the assay can be carried out using cell-free preparations,
30 polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

35 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The

antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

5 All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

10 Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

15

Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

20 A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

25 A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

30 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

35

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of
5 SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3'
10 Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of
15 the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide
20 at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

25 Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
30 ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising
35 a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1. for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining

whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence
5 selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

10 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions
15 beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the
20 amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence
25 at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
30 ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
35 Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the

amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
5 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
10 least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a
15 polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in
20 the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
25 and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining
30 whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of
35 polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an

amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
and a complete amino acid sequence of a protein encoded by a human cDNA clone
identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
ATCC Deposit Number shown for said cDNA clone in Table 1.

5 Also preferred is the above method wherein said step of comparing sequences is
performed by comparing the amino acid sequence determined from a polypeptide
molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a
biological sample which method comprises a step of detecting polypeptide molecules in
10 said sample, if any, comprising an amino acid sequence that is at least 90% identical to
a sequence of at least 10 contiguous amino acids in a sequence selected from the group
consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as
defined in Table 1; and a complete amino acid sequence of a secreted protein encoded
by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained
15 in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type
of a biological sample, which method comprises a step of detecting polypeptide
molecules comprising an amino acid sequence in a panel of at least two amino acid
sequences, wherein at least one sequence in said panel is at least 90% identical to a
20 sequence of at least 10 contiguous amino acids in a sequence selected from the above
group.

Also preferred is a method for diagnosing in a subject a pathological condition
associated with abnormal structure or expression of a gene encoding a secreted protein
identified in Table 1, which method comprises a step of detecting in a biological sample
25 obtained from said subject polypeptide molecules comprising an amino acid sequence in
a panel of at least two amino acid sequences, wherein at least one sequence in said panel
is at least 90% identical to a sequence of at least 10 contiguous amino acids in a
sequence selected from the group consisting of: an amino acid sequence of SEQ ID
NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid
30 sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA
Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number
shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules
includes using an antibody.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide
sequence which is at least 95% identical to a nucleotide sequence encoding a
polypeptide wherein said polypeptide comprises an amino acid sequence that is at least

90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated

polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
20	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
25	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation

of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors
5 contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., *Focus* 15:59 (1993).) Vector lacmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
10 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
15 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
20 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
25 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
30 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
35 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection

agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to

remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

5 This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

10

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
15 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
20 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
25 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
30 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5'
35 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of

conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

10 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product
15 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

20 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are
25 identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The
30 cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by
35 centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic

agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high
5 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with
10 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in
15 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes
20 an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number XXXXXX.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence,
25 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
30 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible
35 enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

- 5 The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at
10 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

15 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

 Following high speed centrifugation (30,000 xg) to remove insoluble particles,
25 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

 To clarify the refolded polypeptide solution, a previously prepared tangential
30 filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a

stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem
5 columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column
10 volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
15 Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

20 In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and
25 Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated
30 homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription,
35 translation, secretion and the like, including a signal peptide and an in-frame AUG as

required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

25 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

35 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),

pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., *J. Biol. Chem.* 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., *Biochem. et Biophys. Acta*, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., *Biotechnology* 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Bebbington et al., *Bio/Technology* 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., *Cell* 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the

naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested
5 with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid
10 pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that
15 confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri
20 dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 -
25 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins.
30 These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the
35 polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having

more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in

5 Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

10 For example, if pC4 (Accession No.209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that
15 the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a
20 heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

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GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAC
25 CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
30 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
35 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)
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Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

10 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at 20 about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are 25 selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

30 Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a 35 mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody

whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

- 5 It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of
- 10 recombinant DNA technology or through synthetic chemistry.

- For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art.
- 15 (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

20

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

- The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in
- 25 Examples 13-20.

- First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well
- 30 (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

- Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml
- 35 DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

5 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of

10 transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off

15 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (see below) with 2mm glutamine and 1x penstrep.

20 (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B

25 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

30 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an

35 activity in a particular assay.

HGS-CHO-5 medium formulation:**Inorganic Salts**

CaCl ₂ (anhyd)	116.6 mg/L
CuSO ₄ ·5H ₂ O	0.00130
Fe(NO ₃) ₃ ·9H ₂ O	0.050
FeSO ₄ ·7H ₂ O	0.417
KCl	311.80
MgCl ₂	28.64
MgSO ₄	48.84
NaCl	6995.50
NaHCO ₃	2400.0
NaH ₂ PO ₄ ·H ₂ O	62.50
Na ₂ HPO ₄	71.02
ZnSO ₄ ·7H ₂ O	.4320

5 Lipids

Arachidonic Acid	.002 mg/L
Cholesterol	1.022
DL-alpha-Tocopherol-Acetate	.070
Linoleic Acid	0.0520
Linolenic Acid	0.010
Myristic Acid	0.010
Oleic Acid	0.010
Palmitic Acid	0.010
Palmitic Acid	0.010
Pluronic F-68	100
Stearic Acid	0.010
Tween 80	2.20

Carbon Source

D-Glucose	4551 mg/L
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Amino Acids

L- Alanine	130.85 mg/ml
L-Arginine-HCL	147.50
L-Asparagine-H ₂ O	7.50
L-Aspartic Acid	6.65
L-Cystine-2HCL-H ₂ O	29.56
L-Cystine-2HCL	31.29
L-Glutamic Acid	7.35
L-Glutamine	365.0
Glycine	18.75
L-Histidine-HCL-	52.48

H ₂ O	
L-Isoleucine	106.97
L-Leucine	111.45
L-Lysine HCL	163.75
L-Methionine	32.34
L-Phenylalanine	68.48
L-Proline	40.0
L-Serine	26.25
L-Threonine	101.05
L-Tryptophan	19.22
L-Tyrosine-2Na-2H ₂ O	91.79
L-Valine	99.65

Vitamins

Biotin	0.0035 mg/L
D-Ca Pantothenate	3.24
Choline Chloride	11.78
Folic Acid	4.65
i-Inositol	15.60
Niacinamide	3.02
Pyridoxal HCL	3.00
Pyridoxine HCL	0.031
Riboflavin	0.319
Thiamine HCL	3.17
Thymidine	0.365
Vitamin B ₁₂	0.680

Other Components

HEPES Buffer	25 mM
Na Hypoxanthine	2.39 mg/L
Lipoic Acid	0.105
Sodium Putrescine-2HCL	0.081
Sodium Pyruvate	55.0
Sodium Selenite	0.0067
Ethanolamine	20uM
Ferric Citrate	0.122
Methyl-B-Cyclodextrin complexed with Linoleic Acid	41.70
Methyl-B-Cyclodextrin complexed with Oleic Acid	33.33
Methyl-B-Cyclodextrin complexed with Retinal Acetate	10

5

Adjust osmolarity to 327 mOsm

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>ISRE</u> <u>Ligand</u>	<u>JAKs</u>				<u>STATs</u>	<u>GAS(elements) or</u>
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
5	<u>IFN family</u>						
	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
15	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
	>>Ly6)(IgH)						
25	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
30	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
35	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-
40	CAS>IRF1=IFP>>Ly6)						
	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
45	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to
 5 bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:
 5':GCGCCTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCG
 10 AAATGATTTCCTCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in
 15 the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:
 5':CTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATG
 20 ATTTTCCTCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
 CTAATCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC
 CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGC
 CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
 TGCAAAAAAGCTT:3' (SEQ ID NO:5)

25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can
 30 be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and
 35 XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a

neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI

+ 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

5 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

10 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophane covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat pheochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)
5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

20

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating diseases. For example, inhibitors of NF- κ B could be used to treat those diseases
5 related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
10 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)
15 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)
Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:
20 5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTC
CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
25 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not
30 preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

- Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

- As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

- Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

- Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

- Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4

15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular

signaling even which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

5 The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In
10 addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

15 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

20 Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

25 Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine
30 (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento,
35 CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are

used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium.

- 5 Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim
- 10 (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation,
- 15 the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

- Generally, the tyrosine kinase activity of a supernatant is evaluated by
- 20 determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 25 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 30 components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 35 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This

allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
5 above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
10 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine
15 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
20 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then
25 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
30 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodynce filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
35 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and
5 Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

10

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from
15 these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

20 PCR products is then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

25 PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals is identified by mutations not present in unaffected individuals.

30 Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the
35 corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera
5 (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and
10 translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

15 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

20 For example, antibody-sandwich ELISAs are used to detect soluble polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the
25 polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

30 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

35 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on

the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale).
Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

5 The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for
10 purposes herein is thus determined by such considerations.

 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 $\mu\text{g/kg/day}$ to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day , and
15 most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 $\mu\text{g/kg/hour}$ to about 50 $\mu\text{g/kg/hour}$, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes
20 and the interval following treatment for responses to occur appears to vary depending on the desired effect.

 Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal
25 patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

30 The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al.,
35 Biopolymers 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D-(-)-3-hydroxybutyric

acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; 5 EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

10 For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the 15 formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the 20 carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that 25 enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or 30 immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, 35 poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of

about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile.

5 Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized
10 formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or
15 more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the
20 present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by
25 administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

30 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

5 For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

10

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and
15 separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS,
20 penicillin and streptomycin, is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

25 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified
30 using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions
35 appropriate for ligation of the two fragments. The ligation mixture is then used to

transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

5 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

10 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the
15 titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is being produced.

20 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Human Genome Sciences, Inc. et al.
- (ii) TITLE OF INVENTION: 186 Human Secreted Proteins
- 10 (iii) NUMBER OF SEQUENCES: 644
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Human Genome Sciences, Inc.
- 15 (B) STREET: 9410 Key West Avenue
- (C) CITY: Rockville
- (D) STATE: Maryland
- 20 (E) COUNTRY: USA
- (F) ZIP: 20850
- 25 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- 30 (B) COMPUTER: HP Vectra 486/33
- (C) OPERATING SYSTEM: MSDOS version 6.2
- 35 (D) SOFTWARE: ASCII Text
- (vi) CURRENT APPLICATION DATA:
- 40 (A) APPLICATION NUMBER:
- (B) FILING DATE: March 6, 1998
- 45 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- 50 (A) APPLICATION NUMBER:
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- 55

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

30	GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG	60
	AATTCGAGGG TGCACCGTCA GTCCTCCTCT TCCCCC AAA ACCCAAGGAC ACCCTCATGA	120
35	TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGACGT AAGCCACGAA GACCOCTGAGG	180
	TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG	240
	AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT	300
40	GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG	360
	AGAAAACCAT CTCCAAGCC AAAGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC	420
45	CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT	480
	ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA	540
	CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTCTCT CTACAGCAAG CTCACCGTGG	600
50	ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC	660
	ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCCC	720
55	GACTCTAGAG GAT	733

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10 Trp Ser Xaa Trp Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GC GCCTCGAG ATT TCCCGA AATCTAGATT TCCCGAAAT GATT TCCCGG AAATGATTTC 60
30 CCCGAAATAT CTGCCATCTC AATTAG 86

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 GCGCAAGCT TTTTGCAAAG CCTAGGC 27

(2) INFORMATION FOR SEQ ID NO: 5:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

60 CTCGAGATTT CCCCAGAAATC TAGATTTCCC CGAAATGATT TCCCGAAAT GATT TCCCGG 60

AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
GCCCCTAACT CCGCCAGTT CCGCCATTC TCGCCCAT GGCTGACTAA TTTTITTTAT 180
5 TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60
CCATCTCAAT TAG 73

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60
CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120
CAGTTCGGCC CATCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG CAGAGGCCGA 180
GCCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240
CTTTTGCAAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCAGGAGGT AATTCTACC AGAAATTTCC AGAGCATTAT GTAGGTAGAA AAAAATGCAA 60
GCAAGCTGTT AAAGATCTTG GATCCATTA TATAGTATGT ATAGCTGAAA TCTGTAATTC 120
AATCACTTPT TCTCTTTTAT CCTCTAACCA AAAAATGTGT TAATTTTGCA TCCCAAATGT 180
TTTTAATCTT TGTATATTTT TTA AAAATCC TTTCTCCTC ATCATGCTT TTTTGTGGT 240
TGTAATAGA CTTACTTGCA CTTTGAAGAT GAGTTACTCC TTGTCATCTT ACAAATATGT 300
GATATGGTAA TTTTCATAAC AGATGTCAGT TTTGAACCAA GAATGGTGA TTTGTTTATA 360
AGAAAAAAC TGGCTTCATT TCTGTGAAAT TGCTCTTGA AAATTTCTTT TTACACGTGT 420

AAGCCAACTG AGATACCGTG ATGGTGTGA TTTCTTTCAA TGATGCTTAC CATCTATTTT 480
AGCCACTGAG CCTTTTATTA TTGTCTATT TGTAAGTTT ATTTGTCTTA ACTCATTTAA 540
5 TAAATATACT GTTTATCTGT TTCTGAAAAA AAAAAAAAAA AA 582

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

20

GTITGGGGT GAGGCCGAGC TGCTGCGGGG CTTCGTGCGC GGCCAGGACA CAGCTACTCG 60
CACGGCGGCG GCGCCTGGCT ATGATGTTCC TCACCCAGGG CGGCCTCTG CCCTCTACTC 120
25 GTGCCAGGCC CACTTGCCAG GCAGGAGCCC TCCCCAAGCC TTCAGGGCTG CTCGGAGTCA 180
CCTGTTGGAA TGGACTAAAA GGACCCTTGT GTGGGAACAG GTGCTCCCCA AACACCCTGC 240
TGCTGGCTGC CAGGCAGGCC CTCTGGAAGG GAAGGGGAG GACTCATCAG GACCTCCCTG 300
30 GACCCCTGCA GGGCAGGCAG CTGCGGCCG AGCCCAAGCA TTTGGCTCTG CTGCCCCCAA 360
GGGACAGGA AGCCTCTTGG GCCTCTTCCC TTCTGGACA AGGCCCCCTG CCTTTGCCTC 420
35 ACATAAACTG TACAGTATTT TCATTAAAG CCTCTTTCAT AAAAA 465

40

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

50

ATGCAATCC TGCTCACAGC CTTCCTGTTG GTGCCACTTC TGGCTCTTTG TGATGTCCCC 60
ATATCCCTAG GCTTCTCCCC CTCCTAGAAG GGCTTCTTGA TAGATTAGAA AATAAGAATG 120
AGTGACATTT CCTATGTGCA TATAAGAAGG AGCCACAAGA CATGTCTTTT AAATAAAAGG 180
55 ACAGTGTCCA TCCTTTTAGC TGCCGAATAG AACCTTGGTC TCATCCTCCT GGAGCTAGGC 240
CTTTAAACA GCTTCTGTGT TTCTCATTTG TCTCAGTGT TTGCCAGGGT TTTATCGAA 300
60 AGATAATGTT CCGTTTAAAA TATTTCTTAA TGAGCCCGG CGTGGTGGCT CACGCCTGTA 360

ACCCTAGCAM TTGGGGGCTG AGCGGGTGA TCACGAGGTC AGGAGATCGA GACCATCCTG 420
5 GSTAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA AAAAAAAAAA AAAA 474

10 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
20 TTATGTTGGG GAGCAAGACC TGATAGCCAG CCTTTACATG GGAGTATAAT TCTGTCCTCC 60
ATCTCATAAG CCCAGTACC TGAGCCAGAA TGATTATAAC CAACCACACT GTCTCTTTAT 120
CATGGATGGC TTTAGCAGTA GGTATTMTTC ATCATTGCCA TTTGTAGCTC TACAGTGGTT 180
25 TATAGTAATT TCTCATCTTT TAAGTCTCTC CCTCAGTGCC TGTGTTATC AAATCATTG 240
CTCTCTCANG CAGTTGAGCT CTGCATTCTC CCYTATGGGG GAGAGCTGTG TTGGAGAGAG 300
30 AGAATATNAC TTCC 314

35 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
45 CTCATATTGC CGTCTGGCTA AAAGTGAACA TGCCATTGAT CAATCTGCTT TTATTATATT 60
ATGTTCCCTAA TGGTGGCAAG CAAGACAAGA AGTAGAAAGA AAGATGGTGT AAGCTCAAGA 120
ACCCACTAAA TCTATCCTAT GGCTGGGTT CACCCAGCCT GCTTTGTGGA TTTTGTCTCA 180
50 CTATAACAGA GCTCCCAAGG AGACTGCAGA GTCAGCTCCC TTAAGCACTG TAACTAAAGC 240
CTAACTCTTC CGTCCACCC AACAATGTYC CCAGCTCATC CTCTTTCCCR AAGTCCOCTT 300
TCTGCCCCAG ATGCGAATTG CATTTAACTA ATCCTCAAGT GAAATGTCCA CACAGRATTG 360
55 CATTTTAATT AGCATACCAT AGTTTTTGTG CAAATTTGCT TTCAGARGAC TCCCATTGCA 420
GCTGCTCAGA GACGCTAANG GCAGGGCCTC TTGA/WGCTTT CCCGATAGCT TTCAGCTGCA 480
60 ATAGCTCTTA GGCAGAATGC CATGAGCGTC CTGCCCAACT GTATTACTGG GGAACACCTG 540

ATTTGGCTAGA AGTTGATCCT CCGTAACTT TTCTGAGTTC TTTACATTTA CTCGTGAAAC 600
CCAAATATGC CAC 613

5

10 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCCCCCCAT TGAACCCCTGG GCTGTGAAAG TTTTTCCTG TGTGGGTCGT TCTGTGTGGC 60
GCCTGGTGTG TGGKTCCCAA CTCCTGTTC AAAGTGGCAG CAGCCAATCA TGAAGCGCCC 120
TTATTTTATG TTGCAGATGA CCAGGTCTCC CCCCCACAGC CTCTGTCTGG TCCCTCATG 180
GTGAGTGGTC TGCCTGCCA AGGAGCCTGA TTGGTGGGAA ATGGCATCAT CTAATATGAT 240
GGGAAGGCAT TTGGTCCTGG TTATGTTTAT TACAACATCA TTGCACTCTG GGAATCCAGT 300
CCCTGAAAAC GTAATTTGTG GTGTTACCAA AGGACCACAG GGGAAAAAAA AAAAAA 356

30

35 (2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAAACTANAT CCCGGGGCTT TTAACNGGTA CTTGGGAAAT AAGTATTGGG TAATCACTAA 60
GNGGACATG ACTGCACCAA ACCAAAGCTA TAGAAAGAAA TGATTGACTT TTTAAATAT 120
ATTCACATTA ACTGTCCTAG GATACTTCTC TTGAGGCTTT GGAAAACTTC TTCCTTGAAA 180
TTTGATATC CACTCCAGTT CTGTCACCAA AGATTTTAAT CTTGAGATCG CAATTTCTC 240
TCTCCAGAA AAAAGTACTA CAACAGGCTC AAGGATATG CTTTGGTGGT CAAGGGATTA 300
CACTATGGTT TTCTTCTGT TCACAATGGT ATTTACAGGA GACCTGTGCA TCAGAGGACG 360
TACTGAACTA TCTTTATGAC TTTGATTGTG ATCAGAGGTT TAAAAAAA AAAA 414

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60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10 AATCACCATT GCAATACAAA TGATCTGCCT GGTGAATGYT GAGCTGTACC CCACATTCGT 60
CAGGAACYTC GGAGTGATGG TGTGTCCTC CCTGTGTGAC ATAGGTGGGA TAATCACCCC 120
15 CTTCATAGTC TTCAGGCTGA GGGAGGTCTG GCAAGCCTTG CCCCTCATTT TGTTCGCGT 180
GTTGGGCTG CTTGCCGCGG GAGTGACGCT ACTTCTTCCA GAGACCAAGG GGGTCGCTTT 240
GCCAGAGACC ATGAAGGACG CCGAGAACCT TGGGAGAAAA GCAAAGCCCA AAGAAAACAC 300
20 GATTTACCTT AAGGTCCAAA CTCAGAACC CTCGGGCACC TGAGAGAGAT GTTTTGGCGC 360
GATGTCGTGT TGGAGGGATG AAGATGGAGT TATCCTCTGC AGAAATTCCT AGACGCCTTC 420
25 ACTTCTCTGT ATTCTTCCTC ATACTGCCT ACCCCCCAAT TAATATCAG 469

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

40 CCCCCCCCC CCCCCACACT TTCAGGAGTC ACCCCCCAGC ATTTGGGGTT GGGTTGGCCC 60
TACTCCAGCC TGGAGCTCCC TGAGGGAGCC TGCCTCCCT GCTCCCAATC CCCGCTACTG 120
GTGCAGGGAT GCAGCCTGGA GCTGGCGTCC TTGTTCTGGG CCTGCTGCTG CCGCCACCCC 180
45 AGAGCCCCAG CCTGTCCTGA ATGACATCA GTGCTTCCCT GAACTGCCTC CCCCACCCCT 240
GGGCATTATC CCAGGAAACT TTATGTTTTC TAGAAGCTAA GCAGCTGCTG GGAATCAGGG 300
50 ACTGGTGAG GTAGGCTGAG TGGCAGCTCA GTCTAGAAG GTCTCTGAAG ATCTGGACTG 360
AGGACCTTGC TACTCCCCAA GCCAGAGCCC ATCAGCCAGG CCTGCTGTGA GCCACCTGCC 420
TGTGGAGTGC TGAGCTCAAC CAAAGGCTGG CAAGCTCTGG GCCTCATTTA AGGGATTCTG 480
55 ATGAGCCGAT GGCCCTGGA GGCAGCCCAT TAAAGCATCT GGCTCGTTTT TGGAAAAAAA 540
AAAAAAAAA 550

(2) INFORMATION FOR SEQ ID NO: 20:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTGAAGAG TGTACAGTAC AGGATTATTA TAATGAAAGT TTATATCAAC AGGGTTTCGT	60
15 TGGCTCTGCA TATATTATAA GCAAAGAGA TTGGTAAAGT GCCACAGTAT TCCAGATAAC	120
TTTTCAAGTG CGGCCTTCT TCTCGTCTT TAATTTGAAA CCTAGATACA TGCAGTAAAA	180
ACTAGGAGAA TGACTTTTAC CCTTGGGGAC AGCCAAGTTT TGGTGATAAA CCTATTTCCT	240
20 AGCATGCCTT CAGGAAGTTG TGCCAGACCC TAGATTGTGA AGGACCCACT GTTCTTCTGT	300
TGTACGAGCT CCCTGAACCA TTGTTTCAGAG GACCAATGTC ACATCGCTTC ATGGGCATGG	360
25 NCCATGGGAG CATCTGGGTG ATAYCTGTCT ACAGTATTGG CTCTTCTGCG AGGCTGATAC	420
ACAAGGCCTC TCTCCACAT GATCATTTGC AAACCTCCCC CAGCCCCTAC CATCCAATGT	480
GGAAGGAAAA CAAGAACTGC CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT	540
30 TCGGGCTGTC ACCTTCCTCC TCCCCTTCT GTATCCTCAG AGATGCTGCG TGGATGTTTC	600
CTTAACCTCA GCTGACTTCC CTGTGAATGT CTAATGCTAG TTCAGGGCCT CCAGGCATTG	660
35 ATTTGTACAG TGGTAACCTC CAATGAGGCT TCTGTTATCA TTTGGTGTGC TTTYTCTGTC	720
ATTAAAAGAA ATGATTTTCC C	741

40

(2) INFORMATION FOR SEQ ID NO: 21:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGTC TCCCCTGGGG AAGTTTTTCT TTTTCAGGAG GGAGGAGGGC TTTCCAGGT	60
AATGTGTCTA GAGTGTGGG CAGAAAATCT GGGACCACAC CACACCAGTT CTCTCCTTAA	120
55 TCCACGTCAT TTGCCTCTA TCCCAGCTAT GTTCCAGTG TCCTCTGGGT GTTCCAAGA	180
GCAACAAGAA ATGAATAAAT CTCTGGTGAG TTGTTTATTT GTTCTTCACT TTGTTTACA	240
60 CTGTATTTTC TGAGTTTATG GGTGTCTGTG AATTAAAAAG GAAAAGTAGA AATAAGTAAA	300

ACTCAGGTTG AAGGAAATAT ACATAAATAA GATAAAGCTG ACCTGTAGAT ATAGCAGGTT 360
ATAAAGCTTA GAGTTGTCTA AGTTGAGTGC AAATTTTCCT CTGATCTTTC TGATGCCGAA 420
5 CAAAAAGCA GTCATGTTTG TTATGTGATT GGAATGGAAC CCGAGAAGAG AGCATGCTGT 480
GTTCTTGTGG GACAGGAAAG CTGCGTGCA CCAAGTCTGA ACCACCACCT TCATGGTGAC 540
10 ATAGATTATG TGCTGGAACA TATTCACAC CGGCCTGGCA GTAAACACTT GTAGTGTGTG 600
GCAGTGAAA CGGTCATCTT CCGCTAAAGC ACGGCGTGT GTGCAGCGGA AATGGTCATC 660
TGCTGCTAAA ACACAGCTTC CATCGTAATG TATGCTCCTT ACTCAAAGAG TGTGGTCCCA 720
15 AACAGCCTTT GGGAGGTCCT CCTTGATTCA TGGATGAAAC CTGGAACATC TTGAGGACTG 780
AGTTAACCAT AGGTCCTTAA ATAACCTCTC ACACGTTTTT CTTAGTTTAT CTCTACATGC 840
20 AGGGTGTGCA GCAGCCTGTT CAAAGTCATA TTTCTGGGA AATATTTCCA GTGTTTATTT 900
GCACTTTAGC CCACTCTGTG TAGCCTTATT TCTTCTAAAC TCACCATTAA TCTGAATAAT 960
AGTCAAATTT AGGGGGACTG TATTTGCCTT A 991
25

30 (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCACGCGTCC GGAATPCCCC TGAGGATCTT GGGCTATCTT TGACAGGGGA TTCTTGAAG 60
40 TTGATGCTTT CTACAAGTGA ATATAGTCAG TCCCCAAGA TGGAGAGCTT GAGTTCTCAC 120
AGAATTGATG AAGATGGAGA AAACACACAG ATTGAGGATA CGGAACCCAT GTCTCCAGTT 180
45 CTCAATTCTA AATTTGTTCC TGCTGAAAT GATAGTATCC TGATGAATCC AGCACAGGAT 240
GGTGAAGTAC AACTGAGTCA GAATGATGAC AAAACAAAGG GAGATGATAC AGACACCAGG 300
GATGACATTA GTATTTTAGC CACTGGTTGC AAGGCAGAG AAGAAACGGT AGCAGAAGAA 360
50 GTTTGTATTG ATCTCACTTG TGATTCGGGG AGTCAGGCAG TTCCGTCACC AGCTACTCGA 420
TCTGAGGCAC TTTCTAGTGT GTTAGATCAG GAGGAAGCTA TGGAAATTAA AGAACACCAT 480
55 CCAGAGGAGG GGTCTTCAGG GTCTGAGGTG GAAGAAATCC CTGAGACACC TTGTGAAAGT 540
CAAGGAGAGG AACTCAAAGA AGAAAATATG GAGAGTGTTC CGTTGCACCT TTCTCTGACT 600
GAAACTCAGT CCAAGGGTT GTGTCTTCGG AGGCATCCAA AAAAAAAAAA AAA 653
60

(2) INFORMATION FOR SEQ ID NO: 23:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15 GGCAGGCTGA CGACCTGCAA GCCACAGTGG CTGCCCTGTG CGTGCTGCGA GGTGGGGGAC 60
CCTGGGCAGG AAGCTGGCTG AGCCCCAAGA CCCCAGGGGC CATGGGCGGG GATCTGGTGC 120
TTGGCCTGGG GGCCTTGAGA CGCCGAAAGC GCTTGCTGGA GCAGGAGAAG TCTCTRCCCG 180
20 GCTGGGCACT GGTGCTGGCA SGARCTGGCA TTGGACTCAT GGTGCTGCAT GCAGAGATGC 240
TGTGTTTCGG GGGGTGCTCG GCTGTCAATG CCACTGGGCA CCITTCAGAC ACACITTTGGC 300
TGATCCCCAT CACATTCTTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC ACCATGTGGG 360
25 GCAAGATCGT YTGCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC CTGCTGGTGG 420
CCGTGGTGGC CCGGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC AACTTCATGA 480
30 TGGATATCCA GTATACCAA GAGATGAAGG AGTCCGCTGC CCGAGTGCTA CAAGAAGCCT 540
GGATGTTCTA CAAACATACT CGCAGGAAGG AGTCTCATGC TGCCCGCANG CATCAGCGCA 600
35 ANCTGCTGGC CGCCATCAAC GCGTTCGCC AGGTGCGGCT GAAACACCGG AAGCTCCGGG 660
AACAAGTGAA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT GACCTGCAGC 720
AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG GCGGGGAAGC 780
40 TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT CCAGAACCCA 840
GCCAGCAGTC CAAGTAGCTG GACCCACGAG GAGGAACCAG GCTACTTTCC CCAGTACTGA 900
GGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCCAGCCCTG AACAAAGCAC CTCAAGTGCA 960
45 AGGACCAAAG GGGGCCCTGG CTTGGAGTGG GTTGGCTTGC TGATGGCTGC TGGAGGGGAC 1020
GCTGCTAAA GTGGGKAGGC CTTGGCCAC CTGAGGCCCC AGGTGGGAAC ATGGTCACCC 1080
50 CCACTCTGCA TACCCTCATC AAAAACACTC TCACTATGCT GCTATGGACG ACCTCCAGCT 1140
CTCAGTTACA AGTGCAGGCG ACTGGAGGCA GGAATCCTGG GTCCCTGGGA AAGAGGGTAC 1200
TAGGGGCCCG GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT 1260
55 GGGTATGAGG CTGGGCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA 1320
CCATTTTTC AGAGCTGCAG AGAGCACCTG GTGGGAGGA AGAAGTGTA CTCACCAGCC 1380
60 TCTGCTCTTA TCTTTGTAAT AATGTTAAA GCCAGAAAAA AATAAAAAA AAAAAAAAAA 1440

AACTCGAGGG GGGCCCRKAC CCAATCWCCC TATAGTAKAC GTANNN

1486

5

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTTCGCGGTT TCTCCTGCCA GGGGAGGTCC CGGCTTCCCG TGGAGGCTCC GGACCAAGCC 60

CCTTCAGCTT CTCCTCCCG ATCGATGTGC TGCCGCCGCC GCCGCCGCC TCCCGCGTCC 120

20

TTCGGTCTCT GCTCCCGGA CCCGGCTCCG CGCAGCCAGC CAGCATGTGC GGGATCAAGA 180

AGCAAAAGAC GGAGAACCAG CAGAAATCCA CCAATGTAGT CTATCAGGCC CACCATGTGA 240

25

GCAGGAATAA GAGAGGGCAA GTGGTTGGAA CAAGGGGTGG GTTCCGAGGA TGTACCGTGT 300

GGCTAACAGG TCTCTCTGGT GCTGGGAAA ACAACGATAA GTTTTGCCCT GGAGGAGTAC 360

TTGTCTCCCA TGCCATCCCT GTTAATTCCT GGATGGGGAC AATGTCCGTC ATGGCCTTAA 420

30

CAGAATCCCC CAGATGGCTT CATGGCCCC AAAGCATGGA AGGTCCTGAC AGATTATTAC 480

AGGTCCTGAC AGAAGAACTA AGCCTTTGGT CCAGAGTTTC TTTCTGAAGT GCTCTTTGAT 540

35

TACCTTTTCT ATTTTATGA TTAGATGCTT TGTATTAAAT TGCTTCTCAA TGATGCATTT 600

TAATCTTTTA TAATGAAGTA AAAGTTGTGT CTATAATTAA AAAATATAT ATATATATAC 660

ACACACACAT ATACATACAA AGTCAACTG AAGACCAAT CTTAGCAGGT AAAAGCAATA 720

40

TTCTTATACA TTTCATAATA AAATTAGCTC TATGTATTTT CTAATGCACC TGAGCAGGCA 780

GGTCCAGAT TTCTTAAGGC TTTGTTTGAC CATGTGTCTA GTTACTTGCT GAAAAGTGAA 840

45

TATATTTTCC AGCATGTCTT GACAACCTGT ACTCTTCCAA TGTCATTTAT CAGTTGTAAA 900

ATATATCAGA TGTGTCTCTT TCTGTACAAT TGACAAAAA AAAAATTTT TTTTCTCACT 960

CTAAAAGAGG TGTGGCTCAC ATCAAGATTC TTCCTGATAT TTTACCTCAT GCTGTACAAA 1020

50

GCCTTAATGT TGTAAATATA TCTTACGTGT TGAAGACCTG ACTGGAGAAA CAAAATGTGC 1080

AATAACGTGA ATTTATCTT AGAGATCTGT GCAGCCTATT TCTGTCACAA AAGTTATATT 1140

55

GTCTAATAAG AGAAGTCTTA ATGGCCTCTG TGAATAATGT AACTCCAGTT ACACGGTGAC 1200

TTTAATAGC ATACAGTGAT TTGATGAAAG GACGTCAAAC AATGTGGCGA TGTCGTGGAA 1260

AGTTATCTTT CCCGCTCTTT GCTGTGGTCA TTGTGTCTTG CAGAAAGGAT GGCCCTGATG 1320

60

	CAGCAGCAGC GCCAGCTGTA ATAAAAAATA ATTACACTA TCAGACTAGC AAGGCACTAG	1380
	AACTGGAAAA GACCACAGAA AACAAAGAAT CCAACCCCTT CATCTTACAG GTGAACAAAC	1440
5	TGTGATGATG CACATGTATG TGTTTTGTAA GCTGTGAGCA CCGTAACAAA ATGTAAATTT	1500
	GCCATTATTA GGAAGTGCTG GTGGCAGTGA AGAAGCACCC AGGCCACTTG ACTCCCAGTC	1560
10	TGGTGCCCTG TCTACACCAG ACAACACAGG AGCTGGGTCA GATTCCCTC AGCTGCTTAA	1620
	CAAAGTTTCT CGAACAGAAA GTGCTTACAA AGCTGCCTTC TCGGATACTG AAAGGTCGAG	1680
	TTTTCTGAAC TGCCTGATT TTATTGCAGT TGAAAAAATA AAAAAGCTAT TCCAAAGATT	1740
15	TCAAGCTGTT CTGAGACATC TTCTGATGGC TTTACTTCCT GAGAGGCAAT GTTTTACTT	1800
	TATGCATAAT TCATTGTTGC CAAGGAATAA AGTGAAGAAA CAGCACCTTT TAATATATAG	1860
20	GTCTCTCTGG AAGAGACCTA AATTAGAAAG AGAAAACTGT GACAATTTTC ATATTCTCAT	1920
	TCITAAAAAA CACTAATCTT AACTAACAAA AGTTCTTTTG AGAATAAGTT ACACACAATG	1980
	GCCACAGCAG TTTGTCTTTA ATAGTATAGT GCCTATACTC ATGTAATCGG TTACTCACTA	2040
25	CTGCCTTTAA AAAAAAAAC CAGCATATTT ATTGAAAACA TGAGACAGGA TTATAGTGCC	2100
	TTAACCGATA TATTTTGTGA CTTAAAAAT ACATTTAAAA CTGCTCTTCT GCTCTAGTAC	2160
30	CATGCTTAGT GCAAAATGATT ATTTCTATGT ACAACTGATG CTGTCTCTTA TTTTAATAAA	2220
	TTTATCAGAG TGAAAAAATA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	2323
35		

(2) INFORMATION FOR SEQ ID NO: 25:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	GGCAGGAGCC TGTGTGGTCA TGTTCCTCGT GGTGCAGTAC CTGACATGAG CCAGCCACGC	60
50	TCAGTGGCTG AACAGCATTC CCACAGCCTG CAAGTGTGTG TGTGTGTGAA AGAGAGAGGG	120
	GGGCCCAGAG CCGCCTTTTG AAATGTTTGC CTGTCTGAAC TGTGAAGACA CTTGGGAGTG	180
55	ATTGTGGTCT AATTTCCAAC CTGCTCTGTT TTCTGTGACA TCTTGGAGGG GAGCTAGTGC	240
	CACACCATGC GCGGTGCTTA GAAATGAAAA AGTCCCGGGT CTGTCTCTCT CACTCTCGCT	300
	CTCATGGGGG AGGGAAAGAA TGGCTTTGGT GGCTTTGTTC ACACAGCTGA TGCCTGCTGG	360
60	GAAGGTGTCC ACAGTGAGCC TGTGTGCAGG ACTGTCCACA CGGTTACAC TTGTCACCAT	420

CAGGCCTTTC TGGTCCTGAT AGGGTGGAGC AAAAGTGGAA AGGAAAGGAA AGAGGCTTTT 480
 CTCACAGCCA TTATATTAAA TAGTAGGTCG ATTCACATCT CGTGCTCCTG GCCACCTTCC 540
 5 CCTGTGCCTC AGTGACATGT AGATGACTGA CTGCCAATAC TTGTCACCAT TCCCTGGAAG 600
 CAGCTACCTA GGGGAAACAA GATGTAGTGC TATTGCCGAT AACAAGTAAG ATTTTCCACA 660
 10 CTAAAAAAA AAAAAAAAAA AAA 683

15 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2036 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

25 CTGAGAAAGG AAAGCATTCG GATCTGCTGC AAAACACAT ATATCCATAA AGACTCATGT 60
 TATTAGAAA ACAGATTGTG AACACAATCA CATTCGCATG AATCCTTTAA AAGGAAGAAG 120
 ACCTTAAAGT ATCTGCAAAT CTGAATTCTT ATTTATTCCT TCACTGAATA TAGAAACAAT 180
 30 GGTATCTGTA TTATTAGAGA TATTATTTTG GATATGTTAC TTATTAACCT GCTATGGCTG 240
 GTAACCATGA TAAAGTCTGT TATTAATAAC AACATAATTC TTTTTTTAAA GAAGAAAAGC 300
 35 TTATTTTCA TTGACAGTGT ATAGATTTAT CTACTTAGTT GTGTTTGCT ATTAGTGTTT 360
 TAAATTTTIT TTTAAGTTGA GTGTTTGATA AATTTTAAGA CCCTGTCCCC ACCTTGTTTT 420
 GAGTCTGTG TTGACTACAG GTATATAGCY CAWTTTAAAA ATCCTAAAGC AAAAGAATTT 480
 40 TATTTATAAA AGAATCMAMC MGTTCATGC ATGAGGCTGT GAAGTCAGAT ATTTAGTAAT 540
 AAAAGCAGCA GTGCCTTTTT TTGTATTTAC CCATTGACCC CCACCAAATG CAACTGTTTT 600
 45 ATATTAAGAA AATAGTAACA ATTTTAAAT CTCAGAGTAA AATCTATTT ACTACATGCT 660
 TTTCCCCCT TGTCTGATT TAAGCAGTGT GACTTGGCA TCTCTACAT GTCTTAGGGA 720
 CAGTGGTGT CTACAATATT ATCATGTATG ATGTTTATT GTTGCTTTTT ATTCATAGTG 780
 50 GCTTCTTACC AGAAACAGTA GGAAGAAACA CATGAACTGT GTACAAGACA TGAAACATTG 840
 CTGCTGATAT GTTGTTTTTT CACATGCTTT TGAGTTTTCA CTTTTTAAAC GAGAGCCAGC 900
 55 AAGCAAAATA GATGTGGCTG GGTCTGCCTG TCCGGCGGCG TTTTGCACC GAGCTCTCAA 960
 ATCTGTGTA TTGAGGGTTC CTTTTGGTA CTCAGGATTG GAGCTACAGC TGGGCCCCC 1020
 TCTCTCCCAT TCGTTTGAAG AGACACTGAG GGAAACAAGG GTTCTTTTTG AGGTGTCCTT 1080
 60

	GGCTGCCTTT TACGGGATGG GAGCCTTCTC CGGATCTTTT GTTCTTCTGC ACCTCTTGTA	1140
	GCTACTGCCG GTGCAAGGTT GTAGATGTTA TTCCCCAGGA GCCTGGGCTK GGGGGCTGAG	1200
5	CTGGGCTGAA TGCAAAAGCA TGCAACCAGA AGGCGGGCAA GGGGAGGAAA AGCAGGCCTG	1260
	GCCTCATTTG TCCCCTGGAG ATGTCTGTAG CAGTCAGCTC CAGCTTGGGC CTGGGGAAGC	1320
	AGCCTGACCA AGGCGCTCAG GTGTGCCTGT TACAAGAAGA ACCTGCAGAA GGATAATTTG	1380
10	CACATGGAGC TGTGATAACA CTAATGTTGA TTTTMTTTT TTTTACAAGT CATCAGRGAT	1440
	GTTTGCAAAG TGAGTTTAT TTTTMTGTAA TTCCPTTATC TTTACTTAAA GGTGAATGTG	1500
15	TATTCCTCTG GGAGGAATAG GAAGAAAACA GGAATGTTAA TAATGTCGAA CAGAAAACCT	1560
	CCTCCCTTAT TAATATATAA TCYTCATGTA TTTATGCCNT AATGTAAGCT GACTTTTAAA	1620
	AAGCTTTCCT TTGTTGCATG CCTGTGCAG GCATCTGTAT TGTACATGCA TGCCTTTCGT	1680
20	CCTGTTTTC TGTATAAAGT TAGTGAACAA AGAAATATTT TTGCCCTAGT TCATGTTGCC	1740
	AAGCAATGCA TATTTTTTAA ATTTGTCATA TATGGAAAGA GCATGTTTGT TACATGTAAA	1800
25	AGCTTTACTG ATATACAGAT AACTAATGT TTGAAGATGC TGTCTTTTGC AAGGTACAG	1860
	TTTTCAAATG TTGTTACCAG TGAAACACCC TTGTGGTTTA AACTTGCTAC AATGTATTTA	1920
	TTATTCATTT CCTCCCATGT AACTAAGAAT CATGGCTATA TTTTCATATCA ACGTTATATT	1980
30	GAAAGTGAAG GGAAATGATT AATACAAGGT TTTGTAACAA AAAAAANAA ANNAAA	2036

35

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

45

	GGCAGGAGAT AACATAGGCA CAATAATACT GTATGTCTAC TTCTAGGATT ATAAGGAATT	60
	AACATTGAGA TGACATTTCC ATTTGAGAAG AAAATAGTTG CTTTCAGTGC CTTTATTG	120
50	ATTCCTGGAG AGAGCAGACT CGCACCAACA TTCAACCCCA GCGCTGATAT GACAGTAATC	180
	CTCAGAGGCA GAGCCAGCA CAAAACAGCA ATGCTAGAAA GTTACAATTG GAAAGTTTCC	240
55	TGCCAGCTTC GGAATGACA CTGCAAAGCT GATGCCAGAA ACTGCCAGAG TAATTCTCCT	300
	CATTACTGCT CTACCCACCC ACTTTAGCT CCCCAAATTA ACTAGTGCAG TTGACTAATC	360
	CTCTTTACCT TTATCATTTA GGTGAGGCAT TGCACAAAA CTCTCGACTT TGCCATATAA	420
60	GGGCTGTGGT TCTCTGTGGT CCTGGATAAG AGGCATCACC ATTATCTGGA AACATGCAGT	480

AAATGCAGAT TCTTCATCTT CTCCCCAGAC CTCCTGAGTT AGAAATTCAC AAGTTCTCCA 540
GGTGATCTCA TACATGCTAA AGTTTGAGAA CCATTGAGTA AAGTTAATGC ATTAAGAAGA 600
5 GATTAGATAG GGATGGTGGC GTATCTTCCT ACAGTTTCCC TGTAAACAAG AAAGTCAGAG 660
GTCAGTTGAT CAGACATTAG ATTATTTATT GCTAAACTA AAAAAAATTA AAAAAA 717
10

(2) INFORMATION FOR SEQ ID NO: 28:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAATTCGGCA CGAGCAGCAT CCTAATTTTA GTTTGGAGAT GCATTCTAAA GGATCTTCTC 60
25 TATTGCTTTT TCTCCACAA TTAATCTTGA TTCTGCCTGT CTGTGCACAT TTGCATGAGG 120
AACTGAACCTG TTGTTTTCAT AGGTAAATGA GAGACTGAGT TTTTTCATTT CTGAAGAGAA 180
AGGGCATTTG CTCCTACAAG CTGAAAGGCA CCCCTGGGTG GCTGGGGCCC TCGTGGGAGT 240
30 TTCTGGGGGA TTGACCCCTA CAACATGCAG TGCCCTACA GAAAAACCTG CAACTAAAAA 300
TTATTTTTTA AAAAGGCTCC TCCAGGAAAT GCATATAAGG GCTAATCACC CAGTATTTTG 360
35 ARGCTTCGAA GARGTAATAR AMCCCTGGAG AGAGAACTG AGACATGTAA GAGGGTGGGA 420
ATGACTCAGT GGTGGCACAC TATGGAGTCC TGCCACAAG TAGCACACAT CAACCCACTA 480
40 CACAGAAATC CTAGG 495

(2) INFORMATION FOR SEQ ID NO: 29:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AGCTTAACGT CATGATTCAT TAGGGGAATG CAAGGCAAAA CCATGATGAG AATGCCCTTA 60
55 GACACCTCTT AGAAGAGCTG CTAGAAAGGC AGACAGCACC AAGCGCTTAA ATGAGATGGG 120
GGCACTGGTG CTTCTTCTGT GCCTACTGGT AGGGGTGCAG CAGAGTGGTT CAGTCTGGGA 180
60 CAGTTAGCTG GACATCACGT GGACCCAACA CACGCATTTC CTGGGTACT TACCAAGGAG 240

AATAGAAAGC AGGCAGATCT TTACAGCAGC TCTTACCTGW TTGCAAAACA ATGGAAATGC 300
5 CCACATGTCC ACAAACAAGT KTGTGGTCTG CCTGTGCCAT GAAGCACAGT GTGGCTGAGC 360
GTCAAGAGTC CCCACACTCA AAGGAGGCAG CAGATACAGG GCTGCACACT GTGTGATTCC 420
ACACATGTGA CATCTCTGGAC ACGGACATGC TGGATGGCAA AACGAGCATC GGGCTGAGAG 480
10 GACTGCTGAG AAGGGGAACG GGGCTGCTGG GATGTGGGT GATTGTAGCA GTAGCTCATG 540
GAGATGTGAC CTCAAA 556

15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTAAATGGTG ACTGTGGCTT TGTGAGACA GGCCCCAAAT GGTAGGTGTG AACACAACAT 60
GCACAGAATG AGGAGACATG CAGAGTGCTG AAATACTGTC CTGGACAGAT GTGTTACATG 120
30 ACTTTCCTTTT CAGCTTATTT CTGTGGCCTG CCTTTGAAGA TAGAGCTTTG TTGATATTTA 180
CATTAAACCA AATTGTATAA YTATGTTCCA TTCTGACATG TTATTTAGCA AARGAAAAAR 240
35 GAGTAATTCT ACATCAGCAT CTTTAGTGCA TGCTAAAAGA TTAAAAATGT CTTTGGGGA 300
ACATGTTTTG TATACATAAA TGTTTAGATA GAAATATTTA TAGAATNCTC TATGTGAGTA 360
TTNATCTCCC TATGTATATT TATATCTAGA TGTGTCAATC TTTGTATTGA TATGAAATGC 420
40 TATGAATAGT GAGA 434

45

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCACGCGTCC GATCTCAGC CTCCGACACT ATTGCGAGCC ATACACAACC TGGTGCAGG 60
AAACGTACTC CCAAATAAG CCCAAGATGC AAAGTTGGT TCAATGGGGG TTAGACAGCT 120
60 ATGACTATCT CCAAATGCA CCTCCTGGAT TTTTCCGAG ACTTGGTGTG ATTGGTTTTG 180

CTGGCCTTAT TGGACTCCTT TTGGCTAGAG GTTCAAAAAT AAAGAAGCTA GTGTATCCGC 240
CTGGTTTCAT GGGATTAGCT GCCTCCCTCT ATTATCCACA ACAAGCCATC GTGTTTGCCC 300
5 AGGTCAGTGG GGAGAGATTA TATGACTGGG GTTACGAGG ATATATAGTC ATAGAAGATT 360
TGTGGAAGGA GAACTTTCAA AAGCCAGGAA ATGTGAAGAA TTCACCTGGA ACTAAGTAGA 420
10 AAATCCATG CTCTGCCATC TTAATCAGTT ATAGGTAAAC ATTGGAATC CATAGAATAA 480
ATCAGTATTT CTACAGAAAA ATGGCATAGA AGTCAGTATT GAATGTATTA AATTGGCTTT 540
CTTCTTCAGG AAAAAGTAGA CCAGACCTCT GTTATCTTCT GTGAAATCAT CCTACAAGCA 600
15 AACTAACCTG GAATCCCTTC ACCTAGAGAT AATGTACAAG CCTTAGAACT CCTCATCTCT 660
ATGTTGCTAT TTATGTACCT AATTAAAACC CAAGTTAAAA AAAAAAAAAA AAAAA 715
20

(2) INFORMATION FOR SEQ ID NO: 32:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
GAGCCAGTGC CGGCGAAAGG GGACCTTCCT CTACTTCCTG CCACAGACCC TGTCCCACA 60
35 CACTTCCTGC CCCTGCTCTG CTGGGAGGCC ACTTCCTCCC CCAGTGCTGG ATTCCACCCC 120
CAGCTACCC TCAAACATGG CCCCCTCTCT CCTCTGCTT GCCCTCTCT GCTCCCTGGA 180
GGCTGTTCTG TCCTCCCTC TTGAAAAGCA ATGCCAGCTT CCTGGGATCT TCTGCCAACT 240
40 CCAGCTACCA TGCCCTTTGC TCCTGTCAGC TCAGCTCCTC AAGGGAATTG TCTAMCCTCG 300
GTGTCTGCT TCCCTCCCTC AACCTCCTCA CCCTGCTCCA AGCTGGCATC TGCCCTCCA 360
45 CTGCACAGAA CGGNTCCCCC ACCACCTGCC TTTACAGGA GGAAGCAGCA ACATGGAAGA 420
ANCGAACTAT AGGGGCTACA ANGATGCTCA GCTCTGATCC CGAAGGCAA AAGNATCTTT 480
GGGCAC 486
50

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 725 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5 GTTCCTCTGG TAATAATTAG GTTATTCCCA GAAGCACAGT GTCATCTCTT AAATAAAAGC 60
 TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA AGATTCCCCC TAGGGTTGAT 120
 ATGTGTCTAA TTCATTTTAT AAAAATTATT CTTGTCTTCA TTTTAAAGCT TTGGCTATAT 180
 10 AGTCAGAAAT GTCCTAAATA ACAAATATT TTGTATTTAA TTAGGGAAG ACTAAAGGA 240
 AGAAAAATGA AAACTCAGTC TTTATGTAAG CTCCAAGGAT ATTAGGGCTT AAAGGGCTTT 300
 TCTAGTTTTA TGAGAATTTG TACTACTGAT TTTTATATAT TCCTGTTTTT GATGAACAGA 360
 15 TCTCTGGGGA AATTGTTGAG TTACAATGGC ATTTCACTGT GATCCCTCTC AAGCTCAGAT 420
 CAGTCTATA ACCCAATGAC AACCTGTCTC TTTGGTTTAC TGTCTGTGA AATGTCAGCT 480
 20 CAAGTTTCCC AGAAGTCGTG TGTTTATGAT GAGTCAGAGT GCTTTTCCTC GGTGGGACAG 540
 TTGCTGGCCC TCTTAATTTT GGTTATGTG CTTCOAAGTA TCTAAACCTC CAGTCTGATC 600
 TGTATATGCT ATCCTAACTG TTAATTGTAT TATGATTAT GTTGATTATC TTGCTTGAAG 660
 25 GTTCATACTT TTCAATTTGA TAGAAATAAA GTTTTTTCT GCTTATAAAA AAAAAAAAAA 720
 AAAAA 725
 30

(2) INFORMATION FOR SEQ ID NO: 34:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CACACAGCAT GCTGCCCTCA GACGTGTCCA TCCTGTACCA CATGAAAACG CTGCTGCTCC 60
 45 TGCAAGATAC TGAGAGATTG AAGCATGCTC TGGAAATGTT CCCAGAACAT TGCACGATGC 120
 CTCCTGCTPT TATTGGCTCT TGTGAAATC AAATTGGAAG ATCTTCAGTC CCAGCTGCAC 180
 CCAACGTGGA AAAGTATTCC AGGTCCATCC CCAAGGAACC AACACCGATG ACATGGACTC 240
 50 AGGAATCTTA TAACCTACGT GGACTCTTTC CATCCGTACA TTGTCGTGCA CATGCCACTC 300
 ATCACCTGGC GTGCCAGAT CCTCGCARGG CAACACCCTG TGATAATTCC AGGTGATTCT 360
 55 CTACATCTGC AGCTTGAGGT TAGCCTCATA TCACATTACA TTCTCACTAN AACNAAAAA 420
 AAAAAAAAAA AACTCNA 437

60

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGCACGAGCT GGAACAGAGA CTAAATCCCA CGAAACTGAC ATTGTTAAAC AACTAAAAAC 60
AGAAGTACTT ACCTCTTGAA GATTTAATAT ATAATGGITG ACATGATACA TGTACATGAT 120
15 GAATGACCAG ATGCTTATGG TCTACATTTT CCTTTATCCT GTTAGTATTA CCTTCCTTAA 180
TCTTTGTICA TTAACATGCT AATTCCTCTT CAGTGTITAT TTTCTAGTGA CAGAATGCTA 240
20 ACATTTCTTA CACCCTGGCA GAAGGGAGAG AAATGTGTTT TGGGGTGGGT AACTAAATTT 300
TTGAGTGAAA TATCATAAGA TGANAATGGA AANAAGGAGA CACAAANAGT TATNACAAAA 360
AAACAATGGT TTTTITAGCC ATTTGACTGG CTCTTTAAAT AGTCTACAAG ACATTCACGT 420
25 TTAACATCAC TTTTAGTGAA ATAAAATGTG CCATACTAGT ATGTGCTTCA AAAGGGCAAA 480
TGTGCTTTAG TGCCCTAAGG CTAAATTTTG GTCATTTGAC ATCAGAGATG TTGTAAGTAT 540
30 TGCACCTAAT ACGCACCTAT TTNTCAATAG TGTATTTTTT TGGNTAGCAT TTTTTTTACC 600
ACTATNTTGT TGATAGCTTT TTGTCTNTN AGGTTGNAAN ATGACAGTGC TNATNTCAAA 660
CAGATTACCC ATNTGCAGAA CTAAGGGAAG CNATTTATGT ATGAAAGNAA TTNTTGAATT 720
35 NGTCATTNTC AACCNITGNA TTAAAGCTTA GACTAAATAG TAATATATNG TGGGNAGGAT 780
TTTGTTTTTG TGATATTTNT GTGNATTAAG GNATAGATGT TAACCNITAT TTTGTAGNAA 840
40 AGTGANTTGT ATGTGGTTAA TTATAAATAA AACTGGTACC AGGNAAAAAA AAAAAAAAAN 900
NAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAA 943

45

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCACGAGAA ATCTTCATGC TGTAGTCACT CCAGACCATG GAGTGGCTTT CCAGCTGAAT 60
GAATCCTATG TCTCGCGTGC AGGTGGTTGG TTTTCAATGT TCTTGCTAAT TTTTTTTCTA 120
60

TTGGATCTTG GGAGTTTCT TGTGTTGCTC CTGTGTTTGC CCAGCTTTAA TAAAACCAGG 180
 CGCAAACAAA AACCATAGCA TTCTGAACAA TAGGGGGCCC ACATTGGACC CAGTATGTCA 240
 5 CTTTAATGGA CTTCAAGAAA AAATCTGAAT GGAAAAATG AACTAGGAA TGTATACTCC 300
 ACACATTTTA TGCCATATAA TGGTGTGTTT TCCTAATTTT GTTCTTGTG GCGAAATGTG 360
 GCTTTCAAAT TAAAATGACC TTTTCTTCTT TGAAACTTTT TGTTTTGACT TGTATAATTA 420
 10 AGGGTTTGA AAGATTCATA ATTCTGAGAG AGGTTTGCAA CCAGGAGATA CAAAGAAGTC 480
 TCAGTAGTAA TCTGTTCAT GTGCTTTTAC AGCCAGCTAC ATTTAAGGAT GTATTAGTTA 540
 15 CAGAAATTAT ATGTCTGTGT ATGTGTCTCT ACTCAATAAA GTACATGCCT CCACAAAAAA 600
 AAAA 604

20

(2) INFORMATION FOR SEQ ID NO: 37:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGAGTGCCC GGGAGCCCCG AGGCCCTGCC CCTAAGAAGG ATATCTYTRA CCGCTCCCTT 60
 GTCCACACCC TAACCCCCCA GCTGCTCAGG CAGTGGGCAC ATGGCAGGGG CCTCACTGGG 120
 35 GGCACATAGA GCATTTGGGG GACTGCGAGT GCTCACCTTT GACTTCCTGC AGGTCGGGGG 180
 AAAACCAGAT CATGATGACC AAAGTYTACA TATCTTTGAT CTTTCATGGT CTGATCCTGC 240
 40 CCTCCCTGGG TCTCACCAGG TATATGCCAC CACYTTCTGY TCTAAATTCA GAATAAGAGT 300
 CACATCAGGA GAGCACTGTC CCCAGGANAA TGCAAACGGG TTGGCAGCA 349

45

(2) INFORMATION FOR SEQ ID NO: 38:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTAGTCGTTG CGGTGCCCCG GATGGCGAAG ATCTCGCCGT TTGAAGTCGT AAAACGCACC 60
 TCGGTACCGG TGCTTGTTGG TTTGGTGATT GTWATCGTTG CTACAGAGCT GATGGTGCCA 120
 60

GGAACGGCAG CAGCGGTCAC AGGCAAGTAA ATAGTAATGC CGGAGCAAGT TTCCTCCGGC 180
TTTATCATGT CACCCACTGT GGTATATGCG TTGTGGTCTG CCAACTTTGC CGTGAACAAT 240
5 TTCAGCAATA ATCAGATGGC GGCTGGCGCA ATATTCAAGA TAACGCCTGG CAGTGGTGCG 300
GCTGATGGTT CAGTGCTGCG GSCACCGTTT YTGCCGTATG TTGCACACCA GGNTCTTTAA 360
10 ACAGTTTTCG SACC CGCTTT AGCGTCAAGG GTTCAATGCC GGTCGGTAGC TCGTCTTAG 420
GTTCAACCGCG AGCATAAGCA TTAACATCT CATCAATTTG CTCTGGCTG GCGCTATCAA 480
TACTTTCCAG CATATGTTTA CGCTGGCGGA AACGGGTTAG CGTTTGCCCC ARCMGWTCAT 540
15 AGGCAATGGG CTTAATGAGA TAATCAAATA CACCACAACG TACGGCTTCA GACACCGTTT 600
CCATATCGCT GGCTGCAGTG GTAAACACCA CGTCGCCGGG ATAATGCGCC TGCACCAGTT 660
CATGCAGTAA AT 672
20

(2) INFORMATION FOR SEQ ID NO: 39:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGAGTTGATA TTTTATAGAA CAGTAATTTT ACTTTTAAGG AAATTGGCTA GCTCTTTGAC 60
35 TNNAGAGCTG TAGGAAGCTC AACATTTCTT TGTAGAGAAC GTTGCTTTT TTGGATTGTA 120
CAGGTATAAA AACATTGCTT TTGTTGAATT GTATAGGTGT AAAAAGGGAA TAACTGTATG 180
40 CAGGTTTGAA AAGGAAATGT GCTTTAGGCA TGAGTCATAA GATGCCATTG TACTTGTAGG 240
CATTTTATTT TCCTTTAGAA ATGGACATCA GCTCTTCTCT TCTGACTGGT AACACATAGC 300
CCCAAAGCAT GAGATTATTT TTCATTGGGT TTTTATGTT GTTTAGTTT GGTTTGTTAC 360
45 GCCAGCCCAG TCTGTCTGCG GAACACTGAC TCTGCTCTCT AATGAGAACA AAGTTAGAAA 420
TCTGCCGATA ACCTAAAATA ATTTAGAAAT GAATTAATAA TGTGAAATCG GGTAAAGTG 480
50 ATGATGATAA AATAGCATGC AAGAAACAAG CTCCTTCCAT CAGACTTGGC TACTGTTTTC 540
TTCTGGTACG ATTTGGTTTG GAAGAGCCTC TTGTTTCCTT CTCTTTGGGG TATGTCCTTCG 600
TTTCTTAATA TGTTTGTAAC ATTATGAGA TATAATTAC ATACCTTACA ATTCATTAT 660
55 TTTAAGGGTA CAATTTAGTG GTTTTATAGT TATTCACAAA GTTGTAAC CGTGACCACA 720
GTCAATTTTA GAACATTTG TTACCCCAA AAGAAACCCT GTACCTTGA GCAGTCACCT 780
60 CTCATTTTCT CCCAGTGCCC ACCCATCCC CGAGCCCCKG GAACCACTAA TCTATTCTC 840

5 TCTCTGTAGA TTTGCTTATT CTGGTCATTT CATATAAATG GAATTCTACA ATATTGGGTC 900
TTTTGGGACT GGCTTCCCAA ATATGATTTT CTATATGGAG TGAGAAAATT CTTCTCATCT 960
TGAGAACTCT TATTGCTGTG AAAGGGAGTG GTTGGTAAAA TCAATAGATT TCAGGCAAGA 1020
GGGCCAGATA CCTAACAGGT TTTTCTCCGT GAATCTTATG CTGAGTAGTT TTTCTCATA 1080
10 ACCAAGCATT TATGATATAT TACTACTTAT AATACTGTGG CTAGTCTCTA GAATGGATGT 1140
TGAAATCTTT GCCTCCTCAG TCGGGAAGAG TCCTGCTAAA AATCAGGCTA AAAATCAGGC 1200
CAAAAATCAG GCCAAATGAC TTGGCAAATA ATTGACAAAG TGGTTTTTAC GTGTGTCTAT 1260
15 CTTTGCTAGC AGCTTGATA CCTCAGGCCA GGTGAGCTCC CCAAATTTCT TTTTTCATT 1320
ACTCCAGTGA GTTCTGCTG TCTTTTTCAA GTATGTACCA TAGGACTTAA AGGTGATTTG 1380
20 GATGCGTTGT AACACTGCTA AATATGCTAA GTACAGAATT TTATCTACAG TACTGTGAGA 1440
CAGTCAATTA TTGCCTAGGG TAGTTCAAAA ATATGATGTG AGCTAGTTAA GCCTTTGCTT 1500
GACTGATTTT AGTGATATTC AGAAGTGTGT ACCAATCAAG GCTCTTTAAA ATACGGAACG 1560
25 ACTCACTTAA TAACCAGGGA ACCAGCCAAA TACTGTGCAG CCGCAGAATA TGCATATCAA 1620
TGAGTTGGAG GTGATTATTC TCTGTAATC CTAATGATT GTTTTCTAAG CATTTGTGGT 1680
30 TCTCAGTGGC TTGACAGCAT CTTCTGGT GTATGTGGCC TGTTTACATG ATGTATTGAA 1740
TAATGTTGTT TGTGTGAGC ATCAATGCCT GTAACACCAA ACTAAACACG TGTTTTGGG 1800
ATATGTTTCC AATCTTTAAA TGACCTTGCC CTGTCCAATA AATAAATGAT TGTCTCACCC 1860
35 TGTAAAAAA AAAAAAATT AAAAAACTG GGNGGGGGC CCGGTACN 1908

40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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60

CCTCAAAAAA AAAAANGAAA GGAAAGAGGT CTCTACACAA GCCCGTGATT CTTCATGGCA 60
AGGGATAACA TCAGAAATGT TTCATTYCK GCTATTAGTT TCCATTCTT TCCCCATCCA 120
GGCATAAAGA GAAACAAAAG ACAATGATGG TATTCTCTGT GTCCTCAGCT TTGGCACTTT 180
TGTGATGTT GCTAAGGAGC AGTGACCTTG CTA AAAAGAC TGAATAATCC ACCCACTGAA 240
TAGCTAACCT GGGGAGGAAA TGAAAATTC CTTGTGGAT CTCCCCAAT CCATTGTTGT 300

CACCAGGCCC TCCCAGAACC TCCTCAGTTC CTTCACAGTG CAACCCCTGTG TACTTGGCCC 360
GCAACCCAAT AGTATTGTGC CTCACCTCAC CTTCATGGG CAACTGCCCT CCCTTCTGGA 420
5 CATAAAACCT CATATTTTAA ATNAAGTTGA AATTTGAA 458

10 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

20 GGCACAGAGC CTCGACCCA GGTGGTCTGG AGCCTGCCCG GAGAGTGGTG GCATCTGAGA 60
GGCTGGTCGT GGACTGTGGT TGGGGGAGGT GGGAGCTGTT TTAACCGTGT GCCCCTCTCT 120
CTGTGCCGGC GTGGGCATCC CCCGGGGCAG TGAACCCCG GCGCTCCTCC AGCTTCCGAG 180
25 TCCAGCCAGC CTGGGCGCGG GCGCGCCCC GAGACACCCG AGGAGTCCGT TCCTCCCTGG 240
TTACGTGGAC TGTGGAGCTG GTCTCTTGTG GCTCAGCGCC GTGCGGAGGT TGAAGCGTAC 300
30 CTGCGGAGGT CGCACCAGGG CGTGAGGAGG AGGAGGAAGG GCATGAGCCG AGCTTGAGGA 360
ATCCGTGCTC CAAACTCTAC ACTCAAGGAT GCACTGCGCA ACTCTGGTGG CGATGGGCTG 420
GGCAGATGT CCTTGGAGTT CTACCAGAAG AAGAAGTCTC GCTGGCCATT CTCAGACGAG 480
35 TGCATCCCAT GGGAAAGTGTG GACGGTCAAG GTGCATGTGG TAGCCCTGGC CACGGAGCAG 540
GAGCGGCAGA TCTGCCGGA GAAGGTGGGT GAGAACTCT GCGAGAAGAT CATCAACATC 600
40 GTGGAGGTGA TGAATCGGCA TGAGTACTTG CCCAAGATGC CCACACAGTC GGAGGTGGAT 660
AACGTGTTTG ACACAGGCTT GCGGGACGTG CAGCCCTACC TGTACAAGAT CTCCTTCCAG 720
ATCACTGATG CCTTGGGCAC CTCAGTCACC ACCACCATGC GCAGGCTCAT CAAAGACACC 780
45 CTGCCCTCTG AGCGTCGCTG GATCTCTGGG AGCTCCTTGA TGGCTCCCAG ACCTTGGCTT 840
TTGGGAATTG CACTTTTGGG CCTTTGGGCT CTGGAACCTG CTCTGGGTCA TTGGTGAGAC 900
50 TTGGAAGGGG CAGCCCCCGC TGGCTTCTTG GTTTTGTGGT TGCCAGCCTC AGGTCATCCT 960
TTTAATCTTT GCTGACGGTT CAGTCTGCC TCTACTGTCT CTCCATAGCC CTGGTGGGGT 1020
CCCCCTCTT TCTCCACTGT ACAGAAGAGC CACCCTGGG ATGGGAATA AAGTTGAGAA 1080
55 CATGAGTTTG GGCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
AAAAAAAAA AAA 1153

(2) INFORMATION FOR SEQ ID NO: 42:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1983 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGCACGAGAG GGGCCGAGCC GACAAGATGT TCTTGCTGCC TCTTCCGGCT GCGGGGCGAG 60
15 TAGTCGTCCG ACGTCTGGCC GTGAGACGTT TCGGGAGCCG GAGTCTCTCC ACCGCAGACA 120
TGACGAAGGG CCTTGTTTGA GGAATCTATT CCAAAGAAAA AGAAGATGAT GTGCCACAGT 180
TCACAAGTGC AGGAGAGAAT TTTGATAAAT TGTTAGCTGG AAAGCTGAGA GAGACTTTGA 240
20 ACATATCTGG ACCACCTCTG AAGGCAGGGA AGACTCGAAC CTTTTATGGT CTGCATCAGG 300
ACTTCCCCAG CGTGGTGCTA GTTGGCCTCG GCAAAAAGGC AGCTGGAATC GACGAACAGG 360
25 AAAACTGGCA TGAAGGCAAA GAAAACATCA GAGCTGCTGT TGCAGCGGGG TGCAGGCAGA 420
TTCAAGACCT GGAGCTCTCG TCTGTGGARG TGGATCCCTG TGGAGACGCT CAGGCTGCTG 480
CGGAGGGAGC GGTGCTTGGT CTCTATGAAT ACGATGACCT AAAGCAAAAA AAGAAGATGG 540
30 CTGTGTCCGC AAAGCTCTAT GGAAGTGGGG ATCAGGAGGC CTGGCAGAAA GGAGTCCTGT 600
TTGCTTCTGG GCAGAAGTTG GCACGCCAAT TGATGGAGAC GCCAGCCAAT GAGATGACGC 660
35 CAACCAGATT TGCCGAAATT ATTGAGAAGA ATCTCAAAAG TGCTAGTAGT AAAACCGAGG 720
TCCATATCAG ACCCAAGTCT TGGATTGAGG AACAGGCAAT GGGATCATTG CTCAGTGTGG 780
CCAAAGGATC TGACGAGCCC CCAGTCTTCT TGGAAATTCA CTACAAAGGC AGCCCCAATG 840
40 CAAACGAACC ACCCCTGGTG TTTGTTGGGA AAGGAATTAC CTTTGACAGT GGTGGTATCT 900
CCATCAAGGC TTCTGCAAAT ATGGACCTCA TGAGGGCTGA CATGGGAGGA GCTGCAACTA 960
45 TATGCTCAGC CATCGTGTCT GCTGCAAAGC TTAATTGACC CATTAATATT ATAGGTCTGG 1020
CCCCCTTTTG TGAAAATATG CCCAGCGGCA AGGCCAACAA GCCGGGGGAT GTTGTTAGAG 1080
CCAAAAACGG GAAGACCATC CAGGTTGATA ACACTGATGC TGAGGGGAGG CTCATACTGG 1140
50 CTGATGCGCT CTGTTACGCA CACACGTTTA ACCCGAAGNT CATCCTCAAT GCCGCCACCT 1200
TAACAGGTGC CATGGATGTA GCTTTGGGAT CAGGTGCCAC TGGGGTCTTT ACCAATTTCAT 1260
55 CCTGGCTCTG GAACAACTC TTCGAGGCCA GCATTGAAAC AGGGGACCGT GTCTGGAGGA 1320
TGCCCTCTCTT CGAACATTAT ACAAGACAGG TTGTAGATTG CCAGCTTGCT GATGTTAACA 1380
ACATTGGAAA ATACAGATCT GCAGGAGCAT GTACAGCTGC AGCATTCTCTG AAAGAATTCTG 1440
60

	TAAGTCATCC TAAGTGGGCA CATTAGACA TAGCAGGCGT GATGACCAAC AAAGATGAAG	1500
	TTCCCTATCT ACGGAAAGGC ATGACTGGGA GGCCACAAG GACTCTCATT GAGTCTTAC	1560
5	TTCTGTTTCAG TCAAGACAAT GCTTAGTTCA GATACTCAA AATGTCTTCA CTCTGTCTTA	1620
	AATGGACAG TTGAACCTAA AAGGTTTTG AATAAATGA TGAAATCTT TTAACGAGA	1680
10	CAAAGGATGG TATTTAAAAA TGTAACAC AATGAAATTT GTATGCCTTG ATTTTMTTTT	1740
	CATTTCACAC AAAGATTTAT AAAGTAAAG TTAATATCTT ACTTGATAAG GATTTTAAAG	1800
	ATACTCTATA AATGATTAAA ATTTTAGAA CTTCCTAATC ACTTTTCAGA GTATATGTTT	1860
15	TTCATTGAGA AGCAAAATTG TAACTCAGAT TTGTGATGCT AGGAACATGA GCAAACTGAA	1920
	AATTACTATG CACTTGTGAG AAACAATAAA TGCAACTTGT TGTGCAAAAA AAAAAAAAAA	1980
20	AAA	1983

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35	ATGATGATGA CTTTGAAGAC GATTTTATTC CTCTTCCTCC AGCTAAGCGC CTTGAGGTTA	60
	ATAGTTGGAA AAGACTCTAT AGATATTGAC ATTTCTTCAA GGAGAAGAGA AGATCAGTCT	120
	TTAAGGCTTA ATGCCTAAGC NCTGGTCTT AACTTGACCT GGGATAACTA CTTTAAAGAA	180
40	ATAAAAAATT CCAGTCAATT ATTCCTCAAC TGAAAGTTTA GTGGCAGCAC TTCTATTGTC	240
	CCTTCACCTA TCAGCATACT ATTGTAGAAA GTGTACAGCA TACTGACTCA ATTCCTAAGT	300
45	CTGATTTGTG CAAATTTTFA TCGTACTTTT TAAATAGCCT TCTTACGTGC AATTCTGAGT	360
	TAGAGGTAAA GCCCTGTTGT AAAATAAAGG CTCAAGCAAA ATTGTACAGT GATAGCAACT	420
	TTCCACACAG GACGTTGAAA ACAGTAATGT GGCTACACAG TTTTMTTAAAC TGTAAGAGCA	480
50	TCAGCTGGCT CTTTAAATATA TGACTAAACA ATAATTTAAA ACAATCATA GTAGCAGCAT	540
	ATTAAGGTTT TCTAGTATGC TAATATCACC AGCAATGATC TTTGGCTTTT TGATTTATTT	600
55	GCTAGATGTT TCCCCCTTGG AGTTTGTGCA GTTTCACACT GTTTGCTGGC CCAGGTGTAC	660
	TGTTTGTGGC CTTTGTAAAT ATCGCAAACC ATTTGGTTGGG AGTCAGATTG GTTCTTAAA	720
	AAAAAAAAA AAAACGACAT ACGTGACAGC TCACTTTTCA GTTCATTATA TGTACCGAGG	780
60	GTAGCAGTGT GTGGGATGAG GTTCGATACA GNCGTATTTA TTGCTTGTCA TGTAAATTAA	840

AAACCTTGTA TTAACTCTT TTCAATCCTT TTAGATAAAA TTGTTCTTTG CAAGAATGAT 900
 5 TGGTGCTTAT TTTTCAAAA ATTTGCTGTG AACACGTGA TGACAACAAG CAACATTTAT 960
 CTAATGAAC TACAGCTATCT TAATTGGTT CTCAAGTTT TCTGKTGCAC TTGTAAAATG 1020
 CTACAAGGAA TATTAAAAA ATCTATTCAC TTAACTTAT AATAGTTTAT GAAATAAAAA 1080
 10 CATGAGTCAC AGCTTTTGTG CTGTGGTAAC CTATAAAAA AGTTTGTCTT TGAGATTCAA 1140
 TGTAAAGAAC TGAACAACAT GTATATGTTG TAAATATTTG TGTGTTGTGA GAAATTTTGG 1200
 TCATAAGAAA TTAAAGAAC TTACCAGGAA GGTTTTTAAG TTAGAAATAT TCCATGCCAA 1260
 15 TAAATAGGA AATTATAAAT ATATAGTTT AAGCCTGCAT CAGTGGGAGT CTTGGCTATG 1320
 TAGTTATGTA GTTATTATGN AACCACCAAG ATTTTMTTGG CTATTTACCG TAACCAAAGG 1380
 20 GGCCGATTAA NTGGTTTGAA GNCTTG 1406

25 (2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

35 GGGCTGAAG GCGGCRGCC AGTCCGAGC AGTGCTCGCT CCTGCTCGG GCGCTGCGGC 60
 CCCGGCGTC GCCATGACCA GTGAGCTGGA CATCTTCGTG GGAACACGA CCCTTATCGA 120
 CGAGGACGTG TATCGCCTCT GGCTCGATGG TTAAGCGGTG ACCGACGCGG TGGCCCTGCG 180
 40 GGTGCGCTCG GGAATCCTGG AGCAGACTGG CGCCACGGCA GCGGTGCTGC AGAGCGACAC 240
 CATGGACCAT TACCGCACCT TCCACATGCT CGAGCGGCTG CTGCATGCGC CGCCAAGCT 300
 45 ACTGCACCAG CTCATCTTCC AGATTCCGCC CTCCCGCAG GCACTACTCA TCGAGAGGTA 360
 CTATGCCTTT GATGAGGCCT TTGTTGCGGA GTGCTGGG AAGAAGCTGT CCAAAGGCAC 420
 CAAGAAAGAC CTGGATGACA TCAGACCAA AACAGGCATC ACCCTCAAGA GCTGCCGGAG 480
 50 ACAGTTTGAC AACTTTAAAC GGGTCTTCAA GGTGTTAGAG GAAATGCGGG GCTCCCTGGT 540
 GGACAATATT CAGCAACACT TCCTCCTCTC TGACCGGTTG GCCAGGGACT ATGCAGCCAT 600
 55 CGTCTTCTTT GCTAACAACC GCTTTGAGAC AGGAAGAAA AACTGCAGT ATCTGAGCTT 660
 CGGTGACTTT GCCTTCTGCG CTGAGCTCAT GATCCAAAAC TGGACCCTTG GACCCGTCGA 720
 60 CTCACAGATG GATGACATGG ACATGGACTT AGACAGGAAT TTCTCCAGGA CTTGAAGGAG 780

CTCAAGGTGC TAGTGGCTGA CAAGGACCTT CTGGACCTGC ACAAGAGCCT GGTGTGCACT 840
 GCTCTCOGGG AAAGCTGGGC GTCTTCTCTG AGATGGAAGC CAACTTCAAG AACCTGTCCC 900
 5 GGGGGCTGGT GAACGTGCCG CCAAGCTGAC CCACAATAAA GATGTCAGAG ACCTGTTTGT 960
 GGACCTCGTG GAGAAGTTTG TGGAAACCTG CCGCTCCGAC CACTGGCCAC TCAGCGACGT 1020
 GCGGTTCCTC CTGAATCAGT ATTCAGCGTC TGTCCAATCC CTCGATGGCT TCCGACACCA 1080
 10 GGCCCTCTGG GACCGCTACA TGGGCACCCT CCGCGGCTGC CTCTGCGCC TGTATCATGA 1140
 CTGAGGTGCC TCCCAACGTC CGCCACGCT GACAATAAAG TTGCTCTGAG TTTGGAGACT 1200
 15 GGTCTCTGCT CCGGGGAGCA AGTGGGGGGC GTGCAGATGT GCCTGTGTCT GTCTCTGAGC 1260
 ACCTGGTGTC CGTGTACAAG GATGGATGTG TNCNGTGGCT CCTTGGGAAC TGAGACATAT 1320
 CTCAGGGAAT GGTGTCTGTG CTCAGCCCAT CCACCAGAAG AGTCTGCTCA CAAAAAAAAA 1380
 20 AAAAAAAAAA A 1391

25

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35

GGCACGAGTG GAGATGGCTG CGGCCGTGGC GGGGATGCTG CGAGGGGGTC TCCTGCCCCA 60
 GGCGGGCCGG CTGCCTACCC TCCAGACTGT CCGCTATGGC TCCAAGGCTG TTACCCGCCA 120
 40 CCGTCGTGTG ATGCACCTTC AGCGGCAGAA GCTGATGGCT GTGACTGAAT ATATCCCCCC 180
 GAAACCAGCC ATCCACCCAT CATGCCTGCC ATCTCCTCCC AGCCCCCAC AGGAGGAGAT 240
 AGGCCTCATC AGGCTTCTCC GCCGGGAGAT AGCAGCAGTT TTCCAGGACA ACCGAATGAT 300
 45 AGCCGTCTGC CAGAAATGTG CTCTGAGTGC AGAGGACAAG CTTCTTATTG CGACACCAGC 360
 TGCGGAAACA CAAGATCCTG ATGAAGGTCT TCCCCAACCA GGTCTGAAA GCCCTTCCTG 420
 50 GAGGATTCCA AGTACCAAAA TCTGCTGCCC CTTTTGTGG GGCAACAT GCTGCTGGTC 480
 AGTGAAGAGC CCAAGGTCAA GGAGATGGTA CGATCTTAA GGGACTGTGC CATTCCTGCC 540
 GCTGCTAGGT GGCTGCATTG ATGACACCAT CCTCAGCAGG CAGGGCTTTA TCAACTACTC 600
 55 CAAGCTCCCC AGCCTGCCCC TGSTCAGGG GGAGCTTGTA GGAGGCCTCA CCTGCCTCAC 660
 AGCCCAGACC CACTCCCTGC TCCAGCACCA GCCCCPCCAG CTGACCACCC TGTTGGACCA 720
 60 GTACATCAGA GAGCAACGCG AGRAAGGATT CTGTCATGTC GGCCAATGGG AAGCCAGATC 780

	CTGACACTGT TCCGGACTCG TAGCCAGCCT GTTTAGCCAG CCCTGCCCAT AAATACACTC	840
	TGCGTTATTG GCTGTGCTCT CCTCAATGGG ACATGTGGAA GAACTTGGGG TCGGGGAGTG	900
5	TGTTTGTAC TGGTMTTCA CTAGTAATGA TATTGTCAGG TATAGGGCCA CITGGAGATG	960
	CAGAGGATTC CATTTTCAGAT GTCAGTCACC GGCTTCGTCC TTAGTMTTCC CAACTTGGGA	1020
10	CGTGATAGGA GCAAAGTCTC TCCATTCTCC AGGTCCAAGG CAGAGATCCT GAAAAGATAG	1080
	GGCTATTGTC COCTGCCTCC TTGGTCACTG CCTCTGCTG CACGGGCTCC TGAGCCCACC	1140
	CCCTTGGGGC ACAACCTGCC ACTGCCACAG TAGCTCAACC AAGCAGTTGT GCTGAGAATG	1200
15	GCACCTGGTG AGAGCCTGCT GTGTGCCAGG CTTTGTGCTG AGTGCTGTTA CATGTATTAG	1260
	TTCCTTTACT GCTGACCACA TTGTACCCAT TTCACAGAGA AGGAGCAGAG AAATTAAGTG	1320
20	GCTTGCTCAA GGTATGTCAG TTAGTAAGTG GCAGAACAGG GACTTGAACC AAGCCCTCTG	1380
	CTCTGAAGAC CGCGTCCTGA ATTTCTTCAC TAGAGCTTCC TCATCAGGTT ACCCAGAAGT	1440
	GGGTCCCATC CACCATCCAG GTGTGCTTGG ATGTTAGTTC TCCACCCTCG AGGTGTACGC	1500
25	TGTGAAAAGT TTGGGAGCAC TGCITTATAA TAAATGAAA TATATTCTAA AAAAAAAAAA	1560
	AAAAAAAAA	1569

30

(2) INFORMATION FOR SEQ ID NO: 46:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1924 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	GGGCCCCCCC WGWKTITTTT TTTTITTTTT TTTAATTAGG ATAATGCCTT TATTAACGAG	60
45	AATGAAACGT TCATTCTCTC TTCCACTCCT TCTCGTTGGT TTTCTGGACA CAGCTCACCT	120
	GATCCTGCTA GAAACGTTGT CAGTCTGCTT GTGGCTTCCC TCCTTGATTG ACTCACGCTG	180
	TGTGATGTCT TGAGAAGTAT CTATCCACTT CATGTGAATG AGCACTCCAA TATCAGCCAA	240
50	CATCAATCAT TCTTACCTAA AGAATAATAA GAAAAAGTTA ATATAAAGA CAAGGGTATA	300
	AAATAAAGGT TTGAAATGC TAGTCAACTT CAAAATTAA AGAGTAAAAA TCCAGAGATA	360
55	AAGATTGGGG GTAAGTTACA GCATAAAAAA ATAGGAAGAA ACTTCATGGT GGGGGGGAAA	420
	TCTAAAATTA TTCTTACATA AAATAAGTAG ACACCTGAAT TAGAATGAAA ACTGTATTTT	480
60	CTTTAAATG TAAAAGCCTG ACTCTCAGTT TCACCAGTCT GAGCACAAGT TTGACTGCAA	540

CCCCCAATAT ACTATCCCTT ATGTGAAGGT ATGTGACAAC GTTGACCTCA CCAAATGAGT 600
 TTTAACATCA GCTCTTTTTT CATATGAAAG CACATACCCT GCTCCCCATT CAAGTATGTC 660
 5 TTCCATTGTC AGGCAGGCTG ACCACCTTCA GCAGGAGTCC TCCAAGAGTG CCCAACTCCC 720
 CTTCCACAG TACACAACGC TGTAGTTGTT GTCCTGCAAT CCTTTGTATT TACCTCATTC 780
 10 TTTCCCATCT AAGTCCTCAC TGAGTTTAA AGTTAGGGCT GGAAAAGCTA TGCCTTACTG 840
 GGACAGCAAG GAACCAATTT TTTTCTGAGG GAGAAGACAT TCACCTTCAC TATATGCCTG 900
 GCAGGGCCAC AGTGCACAAA ACAAGATCA GCCTTCATTC AAGTTCAGG TTTTCTTCC 960
 15 TCCCTGAATG ATTACTGCAA AGGGTATATG AAGTAAGAGT TCCCTGTTGC ACATGTACCA 1020
 TCCATAAGGG ATACTATATC GTTTTGCATT CTCCCCCA TTCTCCACAT TGTCTATCT 1080
 TAAGTCCAAG CCCTTTTCAC TCTCAAAAAA AAAAAAAAAA TATTTTTC AGCACTGGTG 1140
 20 TTCAAAGCA ACGTTTAT GGTAAATGGT TTACCAGCAA CTGTTGAGAT TTCCAGTTGA 1200
 GTCTTAAAAA TTGCCAATCA TTATCTAGCA GCAATGACAG ATGATTAGGA GCAGTCAAAT 1260
 25 CCTCTGAATT CTTCCCTAA TAGGCAGCCA TTTGAGAACT GCACTAGCTG ACATCACTAA 1320
 AACATTATCA GCTAAAGCCA AAACCAATA AAGGCCAGA CCAACATCCT GGCTCTCTAA 1380
 AACCTGTCCA AAATCATTA GTGAAAGGCA GTAAATGCAG GACTGTGGAT CATGTCACTG 1440
 30 CAGCTGACAA TGATTAACAA TAGGAGACAT GCAACCCCA TTAAGGTTAA AAGTCCAAA 1500
 CTAGTCACAC GCATCTCTT ATTGGGAAA AGTGAGACTA TTATGCATTC TTGGTAGGTT 1560
 35 TGCAACCTTG CATGAAGAGC ACCCATGCA TTTCTTTCAT CTTTCAGAAA GCACCGGTAT 1620
 CTGTTCCAAG GGCCTAACAG TACGAAAATA CATTCTGGCA TCACACCTCT GAACCAAGA 1680
 CTGTTCTCAT TAAAAATAAT TTTGGTTGT AACAAAATA TGAAATACAA TGCAAGCACC 1740
 40 TCGGTATAGC ATTATTACTG AAACCACTTA ATTCCAGCT TTTGAGTTT TTTAAAAAA 1800
 CCCACTGCAC TAAGATTCAC AATTCATTC TACATACAAA TTAAAGCTAG TAAGAACACA 1860
 45 CTAACGTAC AAGTTTCTCA TTCTAAAGTG CAAAAGCCTA ATCATCTGAA AGTGAACAGG 1920
 GTAA 1924

50

(2) INFORMATION FOR SEQ ID NO: 47:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

5 TGGTGTGGGG CCCAGAAAMC AAGGGACCAG TGAAAACAMC CCCAGAGACT TGTATCCGCC 60
AGGAAAGCCA TTGCCAMTYC TGAGCCCTTG AAGGGCAAGG AGGGAAACAG TGTACCAGA 120
GCCCAGTAAG AACTGCTGTC ATGAAGGAGG GGCCACCTTG TAAGAGACAT CATTACTACC 180
AGAACTGTGG TGCCAAATIG CTGGTGTCTC TCTTTGGAGA AACCAACCAG ATACATCTGC 240
10 TGGAGACCCA GGTGGGCACA GAGAAGGGTG GAGAGAGAAT CTGGGAAGAG AAATGGAGAA 300
TAAGCAGCAC AGTGTATATC ATTTCTGTAA ATTCTATGT AGAAGGCTCA GTGTTAGAAA 360
TAAAGTTATT CTAAGTAGTG CAAGTTAAGT GTTCTGTGTT GTTCTGCTTT CCTGTTAGCA 420
15 TAAGTAAACT CCCTTTGGAA CTACACAGGT ATGTCTCTCC TTCAACATGT GTGAA 475

20

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

AAGGGACAGA GACCTGGATT CAGATCTCAT TTTACAATGA AGACCCCAAT GCAGAAAGTC 60
ATGTCTGAAA TTCTGAGCTT ACTCTTCTGC CTGCTGGGAC CTGCTCTGGA TGAGAGAAGG 120
35 GAGGAAAAGG ACTAATCAGA GGAGCCAATG AAGTCACTCC ATGAGTTTCC TGAACCCCTGC 180
CCAGCTAGAG ATTAACGIYT GACCWICAAC GTAGGACACT GTGCAGATGG CTACTTGCTG 240
GCGCATATGA AGACCAAAGC CAGGACCAAG CCCCMASCCT GCTWAACACG GCAGARTCTT 300
40 GCCCAGCCMA CYTCTGTGAR AATCTGCTTC CCTCCACAGC TGACCC 346

45

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 1366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TAGGTGTCAG CCGCCACCCC CCCCCATAT GCAGATTTAC TSGGCATGGT AGTGGCCAGC 60
TTCTAACACA GCTGGTATTT CAAGTCTCCT GGGACCTCAC TCAGGAATGA TACCCCTCA 120
60 GTAGAAGCAG CAGGTGATCT TAACTCCTTT CAAAGAGCAG GCCTGTCTGG GAAGCCATGT 180

	CCTCAGCAGG CACAGCAACC CCTCTGGAAA TGGATCACAA ACTCACTTCT CAGCCAGGCA	240
	GGCCAAGCTT CTATGTAAAC AGTAGGCACA GTATAGTCGG ATCATCACAT CAGCTGGGTT	300
5	TTTGGTTTAG TCATCTAGAG TCGTCTGGAC TAAAGGTCTT TCAGGTCTCC TTGCCCTGTG	360
	AGTGCCTGAA CCTCCCCACC CGAATTGCCT CAGTTGTCTT GAGCCTCATG TCTCTCTGG	420
10	TGGTGGGCCA GGCCCTAGCA TGGGAAGGGA GCCTGCTGCG GGGCAGGCCA GCTGGGGGTG	480
	CTCACCTATG CGCAATGANA GTTATTGAAG GACTGGTTGT TGATGTTGGT GAGCGTATCC	540
	TTCATGGCCA GCGCGAAGTC GGCCAGGTCA GCCAGGTGCT GCCAGCGCTC TCTCTCGAC	600
15	TTGTCTTCTT GTGCCAGGG ACCGTGGAGA AAGTGTCTAG GGGCGCTCAC TGCAGCAGCC	660
	TGCTCTGCTG CCTTCCCTGG CAGTGTCTTG GGGGTGGATT CCCTACAMCT AGATGTTCAA	720
20	GGCCTTACTT TTCCTCCAC AAAGGAGTCG CAGCCACGCT AGCTCTGACT TGCCACTGTG	780
	ACAAAGTTCA CGTAGCAGGT CTAGGCAAAG ACTGGGCAAT TGAGCAGAGG AGACGGACCT	840
	GTGAGTCTGA CCRYGAGSCG GRCCCTTCA CCTTGGCTGG GCTGGTCTG GTCCTTAGGT	900
25	TTTGTAGGT TGTCTTGTG TGGATCCCTC AACTAGGTGA TAAGCACTGG AGGGGGATGA	960
	CCCGCCTTGG ACGTGTCTT TTAACCTCAT CCATATAATA GGGCGTGGG ATGGTTGTAG	1020
30	AGGTAAAGCA GGATGATGGT GTTTTAAGAC CAGAGCTTGG GACCAGGGCT CCTACACCTA	1080
	ATTTTCTCTC CTGGTAGCTG AACAAAGTC TAAATTAGCT TAACAAAAGA ACAGGCTGCC	1140
	GTCAGCCAGA GTTCTGAAGG CCATGCTTTC AGTTTCCCTT GTTGACAATT GCTCTCCAGT	1200
35	TCCTATGAAA GCACAGAGCC TTAGGGGGCC TGGCCACAGA ACACAACCAT CTTAGGCCTG	1260
	AGCTGTGAAC AGCAGGGGGT TGTGTGCTG TTCTGTTTCT CTGCTTGCCG AACTTTCTCA	1320
40	ATAAACCTTA TTTCTTATTT ATAAAAAAA AAAAAAAA AAAAAA	1366

45 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55	GCAGTAATTC CTGTTAGCCA CTGCATCCAC CAAACTACT TTATTTTTC CCTCAAATTC	60
	ATGATTTTTA CGTCTGTAC AAAGGAATT TTGCTGATAG CTCTTTGGGT CCCACTGTTC	120
60	CATTTTATGC TAATAGATTC CATCTAGGG CCCAGCCGTC TCTTGACTGA TGGTGTTC	180

	TTTAACCCCTT GGCATGTATA ATAGAATTTT GGTGAATGAA AGAACCCAAA TAGGCCAGAT	240
	AGTCCCCCA GGCCTGATA TCCATAAAG GCTTGGGAAT GCATTATGTA ATTGTCCTTA	300
5	GTCTTTTGT TGTTTTAGAA AAAAAAACA AGATGGGCTC AGATGGATGC CTACGTAAAA	360
	ATGGTTCCTA GCTGTGTACT CATAACTTTT CTTTGAATTG AGTAGTGAAA GGAAGGAGGA	420
	GGAAAGGAAA TTAAATGTCC TTCTAGTATT CTCTGGACTC AAGTCTGACA TATGAGATAA	480
10	TAACCTATAT TGAATGCCA AGAATTGTAT CTGAAACAAG AGAACAGTTT GACACATTTA	540
	TCATGCCTTC ATATTACATA TTAACGTAAA CCAATTAATA AACATATGAA ATATCCATTG	600
15	CACAAGGCAA AGGCACCTAA ACCTTTTGT TCTTTTCTA CATAGCAGAA ATTGATTTTT	660
	TTTTTATTTT TTTAGGGGAA CCTATATAAT TATGACCCAG TGATGTCITT TGGTGACTTA	720
	AGCTTATGAA TTCAGGTAC AATTGAGTTG ATTCTAGATG GTTACTACCT TGAAAAGGAT	780
20	GTGTGTGCTT TATGTGACAC GAGCCAGAGC CTGCTGGGGA ATAAACAAAG CAGGTTTCAT	840
	GCCAACACCA ACTCGTAGCT TTAGTGGGCA GATGGGGAGT GGTTCACAGA CTTCCCAAAA	900
25	TGTGGGGGCT TTGGGATTTT CCACACCATC CCACGTGTGT TGTTCATTCT TCCTCTTTTC	960
	ACACTCTTGG ATGGATWATT TGRAAATGGT GRAAWYMMC YKRAATTG CCCAATAGCC	1020
	WTGRGCCACC ATTCTTWATG ACACCATAAC CAAATAGTTC CWTAAATGTTG AAATATTAGA	1080
30	AACCTGTTAC CAGCCYKSMA KTWACCCWNA WTTTCCCAT GTTGTGGAA TTGATATTGA	1140
	AATAGCAGGG CTAAGGAATT ACTGGCAAGT TTAGCCTGT GGGTAATACC TTAGGGTTAT	1200
35	TTAAATATTT GTAATTTTAT TTAAATGTTT ATGAATGTTT GAAAGGAACA AAATTATCAG	1260
	GGATGGCTCT TTGCCATGGG TCTTATTTTC ACCCTCTTTT CTGTAAGAAA AAAGAACAAT	1320
	GTCTTAATGT ATTTTAAAG TTTTGGTAT AGTTTCTAAT TCCAATTTTA ATAAAAGTTT	1380
40	TWRTAAAAA AAAAAAAAAA AAAAA	1405

45

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55

CGGATTTTCT AGGACCCCAA AAAAAAAAAA AGGGNAAAAA AAACCCNCAA AACCANCCAA	60
AACCCCAAAA AAAAAAAAAA TCCACAAAAA CAAAAAACT ATAAAAAGA AAGAATTAAA	120
AACCTTCAGA GAATTACTAT TTACTTTATT AACTTACGGA TTTATTATAT AAATATATAT	180

60

TCACCTAGCA ACATATCTCT GCCGTCCTC CTGCTCTCAT AATGAAGACA TAGCCGATTC 240
 TCTGCCCCGG CCCCTTGCTG ATGCTCCTCC GGGTCTGCGT CGGGCGTGGG TCTCTGGGGA 300
 5 CCCTCCAGAG GTGGAGGTGG GCTGATGGCC TGGCTGCCCTG GTGGTTGATG GTTTTGCTCC 360
 CCCTACCITT TTTTITGAG TTTATTCTGA TTGATTTTIT TTCTTGGTIT CTGGATAAAC 420
 10 CACCCTCTGG GGACAGGATA ATAAAACATG TAATATTTT AAGAAGGAAA AAAAAAAAAA 480
 AAAAAACTNG GGGGGGCCCC CGAA 504

15

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

NAAGTATCTT GGCCAGTTTA TTACAGAGGA CGATAAATGA TTCCATGTGG ATAGGGCATA 60
 ACATACAGAG AATGAGACTA TGCCAGAAAT GGGAGGAGGC ATTTGAAACA ACATGAGTAT 120
 30 CTCAGGGACA GATGGATTGA TTCTGCTATT GGTAGGCCTG GAAGCAANGG TCAGAAGTAG 180
 CAAAAAATGG ATACCAAAG CACTATTWGT CACCCAAGCT AAGTGAATA GCTGGCCCAG 240
 35 TAGGAGAAAT GCAGGTTTIG CTCTACACTA AGTCTCCTCA CTCTTGATAA GCCTCCAAAA 300
 ACAAATGTTA GGGGAAAAA ACGCAGCTGG TTATGAAAAG ATATATCTCA TTTCATTAAA 360
 AAATCAATGT CAATGCTGTT AATAGAATCC TTTTATCTTC AGGACAGAGG CAATGCCCTA 420
 40 AACAAACACC AGCTCAAGAG CCTCTGATGC CAACCTAGAG GGTACCCAAA CACAACTTA 480
 GCATAGAGGT AAGAATCTCT ATGTCITTTG GTGGAGGCAA AGCCATTTGG TTGGTACTTC 540
 45 ACAGGAACAT CTTTCTACCA AGTCTTCATC ATATGGTATG TGCCACGAGT CTCCAGTTGT 600
 TTGCACCACT GTGTCATAGC TGAGAATACG CTGAAAGGTT AGTTTGTATC CTGGAACCTT 660
 ATTTACAATT GCCAGCTGAT GTCCCTGCTG CCACTTAAAA AAGGCTTGGG TCTGGCATAG 720
 50 GCAGAMAGGC CTGTGGTCCC CTCGTGCCGA TTCTNGGCTC GAGGCCAATT NCCTTAT 777

55

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

5
ATGACTACAG TGTATATACCC TCCAATCTTT GCAGGTGGGC ATGGAACACT GCTTGATCA 60
CTCTGTGCAC GGTATAAATC CATATATCCA CAAAAACACA CATCCATCCA TCAACATATA 120
10 CATGGTTTGG GATGAGCAGG TCAATAGTTT TGAGAGGGAG TTTGTTCCCTT TTTTPTTTCT 180
CAITATACTC TTAAATTGTT GTCAGTTATC AAACAACAA ACAGAAAAAT TGTTTGGAAA 240
AACCTTGCAAT ACGCCTTTTC TATCAAGTGC TTAAAAATAT AGACTAAATA CACACATCCT 300
15 GCCAGTTTTT TCATTACAGT ACAGTATCCT TACCTGCCAT TTAATATTAG CCTCGTATTT 360
TTCTCACGTA TATTACCTG TGACTTGAT TTTTATTTA AACAGGAAAA AAAACATTCA 420
20 AAAAAAGAAA AATTAACTGT AGCGCTTCAT TATACTATTA TATTATTATT ATTATGTGA 480
CATTTTGAA TACTGTGAA GTTTTATCTC TTGCATATAC TTTATACGA AGTATTACGC 540
CTTAAAAATA CGAAAATAAA TTTTACAAGG TTCCGGTTTT GGTGGTGGAA AGAGTAAATT 600
25 GA 602

30
(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40
AGTCACTGAC TTGGAGCCGC TCGGGGAAG TCCCGCCCAG ACAGGCGGTG GGTGGGAATG 60
CCTCACTTCA GTTTGAAGAG GGTCCGATC CAAAGGGTT AAAACGAGCG AATCCCGATC 120
45 CCGGACCACA CTTCCCGCCT CCTAAAACG CACACCCGC TAGCCATGG CAGCCGCGAC 180
CACCTGTTCA AAGTGCTGGT GGTGGGGAC GCCGAGTGG GCAAGACGTC GCTGGTGCAG 240
GATTATTCCC AGGACAGCTT CAGCAAACAG TACAAGTCCA CGGTGGGACT GGATTTTGCT 300
50 CTGAAGGTC TCCAGTGGTC TGACTACGAG ATAGTCCGC TTCAGCTGTG GGATATTGCA 360
GGGAGGAGC GCTTCACCTC TATGACACGA TTGTATTATC GGGATGCCCTC TGCCTGTGTT 420
55 ATTATGTTTG ACGTTACCAA TGCCACTACC TTCAGCAACA GCCAGAGGTG GAAACAGGAC 480
CTAGACAGCA AGCTCACACT ACCCAATGGA GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC 540
AAGTGTGATC TGTCCCCTTG GGCAGTGAGC CGGGACCAGA TTGACCGGTT CAGTAAAGAG 600
60

	AACGGTTTCA CAGGTTGGAC AGAAACATCA GTCAAGGAGA AAAAAAATAT TAATGAGGCT	660
	ATGAGAGTCC TCATTGAAAA GATGATGAGA AATTCACAG AAGATATCAT GTCTTTGTCC	720
5	ACCCAAGGGG ACTACATCAA TCTACAAACC AAGTCCTCCA GCTGGTCCTG CTGCTAGTAG	780
	TGTTTGGCTT ATTTTCCATC CCAGTTCTGG GAGGTCTTPT AAGTCTCTTC CCTTTGGTTG	840
10	CCCACCTGAC CATTMTATTA AGTACATTG AATTGTCTCC TGACTACTGT CCAGTAAGGA	900
	GGGCCCATG TCACCTAGAA AAGACACCTG GAACCCATGT GCATTTCTGC ATCTCCTGGA	960
	TTAGCCTTTC ACATGTTGCT GRTCCACATT AGTGCCAGTT AGTGCCTTCG GTGTAAGATC	1020
15	TTCTCATCAG CCCTCAATTT GTGATCCGGA ATTTTGTGAG AAGGATTAGA AATCAGCACC	1080
	TGCGTTTTFAG AGATCATAAT TCTCACCTAC TTCTGAGCTT ATTTTCCAT TTGATATCA	1140
20	TTGATATCAT GACTTCCAAT TGAGAGGAAA ATGAGATCAA ATGTCATTTC CCAAATTTCT	1200
	TGTAGGCCGT TGTTCAGAT TCTTTCTGTC TTGGAATGTA AACATCTGAT TCTGGAATGC	1260
	AGAAGGAGGG GTCTGGGCAT CTGTGGATTT TTGGCTACTA GAAGTGTCCT AGAAGTCACT	1320
25	GTATTTTGA AACTTCTAAC GTCATAATTA AGTTTCTCTT GTCTTGGCAT CAAGAATAGT	1380
	CAAGTTTPTT GGCCGGGCAT GGTGGCTCAT GCCKGTAATC CCAGCACTTG GGGAGGCCAA	1440
30	GGCAGGCGGA TCACATGAGG CCAGGAATTC GAGACCAACC TGGTCAGCAT GGCAAAACCC	1500
	CGTCTCTACT AAAAGTACAA AAATTAGCCA GCGTGATGG CACGTGCTG TAATCCCAGC	1560
	TACTCTGGAG ACTGAGGTGG GAGAATCGCT TGAGACTGGG AGGCAGAGGT TGCAGTGAAC	1620
35	CGAGATCATG CCACCGCACT TCAGCCTGGG TGACAGAGAA GGACTCCGTC TCAAAAAAAA	1680
	AAAAAAAAA AAAACTCGAG GGGGGGCCG GTACCCAAAT CGCCSTGATA GTGATCGTAW	1740
40	ACAATCNAA	1749

(2) INFORMATION FOR SEQ ID NO: 55:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

55	AAAGAGATGG GCTCTTTATT TTCTCGAAAA ACCAATTTGG AGTTACTCAT TTTTCCATAA	60
	CATTAAATTT CTTACAGTGA ACTACATATT GTCCATAAGT GCTTCATCAG GACTCATCGC	120
	CCTCTGTCT ACTGGCTCCA AATAGACCAT GTCAGCTTCA CCCCCTGGCT TTGTGTCTAT	180
60	GGTGGCCTG TGGTATATGG AAAAGTAGCA GGGTGGTCAG GGTGGGAGAC ACAAGATGTT	240

	TTTATAGTCT AGAGCCTTTA AAAAACCAG CAGAATGTAA TTCAGTATTT GTTTATTGGC	300
5	TGTTTTTTGA CAGATTGTTG AAATTAAATG AATTGAAAGG GAAACTCAGA GTACTAGGAC	360
	GTTTATTAAA AGGAAAAAAA TGTCTTGCAA TGTGCTGTAA TCACAAGAGG AGAAAATAAC	420
	TTGTTTCCTT GATCTGTCAG AGGTCACAGT AACCTGGGCC GAGCTGTTAT TATTTATTAT	480
10	ATAATAGTAG TAGGAAGTGA ATAACGGTTT CTCTGTGTTT CAAGCACAAT ATTACAACCT	540
	CTTTTGAACC GTAAATATCA GAATGAATCC TCTTCCCAGG GGATTGAACA GAAGCTTAAT	600
15	GTTTACAAGT GTTTGAATTT GTGATCTGAA ATAACACAAA ATTAAAAACA TGATTTCTCT	660
	AATTTTCCAA CTAGAGGAAG AGAAACTTGT GGAAAAGTTC TTTTMTTTC TTTTMTTTC	720
	CTTAAAGAAG GGCAGCCAAG GTAGTAACCT AAAAATAGTG CCCAGGCATA TGAGAGTTGT	780
20	CCTACGAGGT TAAAGAACAC ACTGTTCCAC TGTATGGCTT TGGCCCTGAG TGGCCAGGGA	840
	GGTCAACTTG ACCCTGCCAT GTTGGTTTGA CTTACTAAGA CACAGGAATC ATGTGTTTCC	900
25	TTGACCAGGG TCTCACACCC TGGAGGAATG TTAAGTAAGA GAAAGAACCT CTTTCTGAA	960
	TATTGACATG TAAAGACCA AAGTAATTTT TCTGAATTC TGCAATTCTG AGAACTCTCC	1020
	AAGGAATTTA CAGTGATTTT AGTGCTTGTC AGCATTTTTC CATGAGGACT TTCATACATT	1080
30	TGACTCTTTA GTTCACAGGT TCCCATTGAT TGTGAGCAAG ATATTTATCT CTTTAGCCCT	1140
	TGGGGATCCA GCTGAGAGCA ATCTCTTGCA TTTTMTTACC CGTGTATGTA CAGATATCAT	1200
35	TTCTTGTTGA TGCCATGACT TGAAAAAGTT TGGGAAGCTC TTTAGCAATA TCAGCTAAAA	1260
	GGATATGAAA TCACAGGTGA TAGCAGTTGT CATTCACTAA TTTCTACAA GCAGCACCCC	1320
	AAAGGAAATA TAGTCCTAAT CTTTACTATC CACTTCTAAA TTTAATGTGA ATTTTCATACA	1380
40	TGTTATTAGT TGTTTTCTTT ATAATTTTAT AAAAATTATT CATCGGGAGT TTAACCTCCA	1440
	CTTCCATGCT ATCGGATGTG TTGGGCTCCA TGCAAGAACT TGGAAGAAAA ACAGGCAGGA	1500
45	ATGCATTTGC ATAATGACCC AGATCATCAT TTTCTGCAAC TGAGAATTAT ATTTTCATCAT	1560
	TGCTTCTAGA AGTCTGCAAT TCTTTACTTT TCTTTGGTGC ATTATTATCT AGGTGCCATC	1620
	ACTGGATAAT GTGGAGTGAC TAGAGAAGTC AYATATCACT GTAAGGTACA GTTAGGGGTA	1680
50	ACACTTTAGA GGTTTATTAT TTTTAAAAAA CTTTCTTGA ACTCCTGGGC CAACATGGGT	1740
	GAAACCCCGT CTTCTTACTT AAAAATACCC AAAATTAGGC CAGGGGCGTG GATGGGTGGG	1800
55	GTGCCCTGTTA ATCTTCAGCT ACTTNGGGGA GGGCTTGAAG CCAGGGAGGA ACTGCCCTGG	1860
	ANCCCCGGGG NGGGCCAGNA GGTGTGCCAG TTGAGT	1896
60		

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

10 TCTTTTAAAA ATAGACATTT GTGGGGCTCA CACAATATAT GAAATAGTAC CCTCTAAAAA 60
AGAGAAAAAA AAAATCAGGC GGTCAAACIT AGAGCAACAT TGTCTTATTA AAGCATAGTT 120
15 TATTTCACTA GAAAAAATTT AATATCAAGG ACTATTACAT ACTTCATTAC TAGGAAGTTC 180
TTTTTAAAT GACACTTAAA ACAATCACTG AAAACTTGAT CCACATCACA CCCTGTTTAT 240
TTTCCTTAAA CATCTTGGA GCCTAAGCIT CTGAGAATCA TGTGGCAAGT GTGATGGGCA 300
20 GTAAATACC AGAGAAGATG TTTAGTAGCA ATTAAAGGCT GTTTCACCT TTAAGGACCA 360
GCTGGGCTGT AGTGATTCTT GGGGCCAGAG TGGCATTATG TTTTACAAA ATAATGACAT 420
25 ATGTCACATG TTTGCATGTT TGTTCGCTG TTGAATTTT GAACAGCCAG TTGACCAATC 480
ATAGAAAGTA TTAATTTCTT TCATATGGTT TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG 540
AATATCTATG GCCACAGCAG CATACCAGTT TCCATCCTAA TAGGAATGAA ATTAATTTTG 600
30 TATCTACTGA TAACAGAATC TGGGTCACAT GAAAAAAAT CATTTTATCC GTCTTTTAAG 660
TATATGTTTA AAATAATAAT TTATGTGTCT GCATATGCA GAACAGCTCT GAGAGCAACA 720
35 GTTTCCTATT AACTCTTTCT GACCAATAGT GCTGGCACC GGTCTTCTC TTTGGGAAGA 780
GGAAAGGGTG TGTGAACATG GCTAACAATC TTCAAATACC CAAATTGTA TAGCATAAAT 840
AAAGTATTTA TTTTATGCCT CAGTATATTA TTATTTAATT TTTTAGGTAA TGCCTATCTC 900
40 TTGGTCTATT AAGGAAAGAA GCAATCAGTA GAGAATTCAG GATAGTTTGT TTTAAATTCT 960
TGCAGATTAC ATGTTTTTAC AGTGGCCTGC TATTGAGGAA AGGTATTCTT CYATACAACT 1020
45 TGTTTTAACC TTTGAGAACA TTGACAGAAA TTATGCAATG GTTTGTTGAG ATACGGACTT 1080
GATGGTGCTG TTTAATCAGT TTGCTTCCAA AGTGGCCTAC TCAAGAGGCC CTAAGACTGG 1140
TAGAAATTA AAGGATTTCA AAAACTTTCT ATTCTTTCT TAAACCTACC AGCAAACCTAG 1200
50 GATTGTGATA GCAATGAATG GTATGATGAA GAAAGTTTGA CCAAAATTTGT TTTTGTGTG 1260
TTGTGTGTGT TTTGAATTTG AAATCATCTT TATTCCCTTT AAGAATGTTT ATGTATGAGT 1320
55 GTGAAGATGC TAGCGAACCT ATGCTCAGAT ATTCATCGTA AGTCTCCCTT CACCTGTTAC 1380
AGAGTTTCAG ATCGGTCACG GATAGTATGT ATTTCTTTAG TAAGAATGTG TTAATAATTAC 1440
AATGATCTTT TAAAAAGATG ATGCAGTTCT GTATTTATGT TGCTGTGTCT GGTCCCTAAGT 1500
60

GGAGCCAATT AAACAAGTTT CATATGTATT TTTCCAGTGT TGAATCTCAC AACTGTACT 1560
TTGAAAATTT CCTTCCATCC TGAATAACGA ATAGAAGAGG CCATATATAT TGCCTCCTTA 1620
5 TCCTTGAGAT TTCCTACCT TTATGTTAAA AGTTGTGTAT AATTGTTAAA ATCTGTGAAA 1680
GAATAAAAAG TGGATTTAAA TTAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA 1740
AAAAAAAAAGG GGG 1753
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(2) INFORMATION FOR SEQ ID NO: 57:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGGAAGTTA CTGCAGCCGC GGTGTGTGTC TGTGGGAAG GGAGAAGGAT TTGTAAACCC 60
25 CGGAGCGAGG TTCTGCTTAC CCGAGGCCGC TGCTGTGCGG AGACCCCGG GTGAAGCCAC 120
CGTCATCATG TCTGACCAGG AGGCAAAACC TTCAACTGAG GACTTGGGGG ATAAGAAGGA 180
30 AGGTGAATAT ATTAACTCA AAGTCATTGG ACAGGATAGC AGTGAGATTC ACTTCAAAGT 240
GAAATGACA ACACATCTCA AGAACTCAA AGAATCATAC TGTCAAAGAC AGGGTGTTC 300
AATGAATTCA CTCAGGTTTC TCTTTGAGGG TCAGAGAATT GCTGATAATC ATACTCCAAA 360
35 AGAACTGGGA ATGGAGGAAG AAGATGTGAT TGAAGTTTAT CAGGAACAAA CGGGGGGTCA 420
TTCAACAGTT TAGATATTCT TTTTATTTT TTTCTTTCC CTCAATCCTT TTTTATTTT 480
40 AAAAATAGTT CTTTGTAAAT GTGGTGTTC AAACGGAATT GAAACTGGC ACCCATCTC 540
TTTGAAACAT CTGGTAATTT GAATCTAGT GCTCATTATT CATTATTGTT TGTTCATT 600
GTGCTGATT TTGGTGATCA AGCCTCAGTC CCCTTCATAT TACCTCTCC TTTTAAAAA 660
45 TTACGTGTGC ACAGAGAGGT CACCTTTTC AGGACATTGC ATTTTCAGGC TTGTGGTGAT 720
AAATAAGATC GACCAATGCA AGTGTTCATA ATGACTTTCC AATTGGCCCT GATGTTCTAG 780
50 CATGTGATTA CTTCACTCCT GACTGTGAC TTTCACTGGG AGATGGAAGT TTTTCAGAGA 840
ACTGAAGTGT GGAATAATGA CCTTCCTTA ACTTGAAGCT ACTTTTAAA TTTGAGGGTC 900
TGGACCAAAA GAAGAGGAAT ATCAGGTGTA AGTCAAGATG ACAGATAAGG TGAGAGTAAT 960
55 GACTAACTCC AAAGATGGCT TCACTGAAGA AAAGGCATTT TAAGATTTT TAAAAATCTT 1020
GTCAGAAGAT CCCAGAAAAG TTCTAATTTT CATTAGCAAT TAATAAGCT ATACATGCAG 1080
60 AAATGAATAC AACAGAACAC TGCTCTTTT GATTTTATTT GTACTTTTG GCCTGGGATA 1140

5 TGGGTTTTAA ATGGACATTG TCTGTACCAG CTTTCATTAAA ATAAACAATA TTTGTAAAAA 1200
TCAWAAAAAA AAAAAAAAAA 1220

10 (2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

20 TCGCGCCTGC AGACACAGCA TCTACTCAGC GTGGGTCACC TCTGTGAACA TCACTGACTG 60
CAAGCCTCCC TCAATTTCTG GTGCAGCCCC TCAGGGACCC ACAGCGCCTG GGAGGATGGT 120
GCGGATCTTG GCCAATGGGG AAATCGTGCA GGACGACGAC CCCCGAGTGA GGACCACTAC 180
25 CCAGCCACCA AGAGGTAGCA TTCCTCGACA GAGCTTCTTC AATAGGGGCC ATGGTGCTCC 240
CCCAGGGGGT CCTGGCCCCC GCCAGCAGCA GGCAGGTGCC AGGCTGGGTG CTGCTCAGTC 300
CCCTTTCAAT GACCTCAACC GGCAGCTGGT GAACATGGGC TTTCCGCAGT GGCATCTCGG 360
30 CAACCATGCT GTGGAGCCGG TGACCTCCAT CCTGCTCCTC TTCTGCTCA TGATGCTTGG 420
TGTTCGTGGC CTCCTCCTGG TTGGCCTTGT CTACCTGGTG TCCCACCTGA GTCAGCGGTG 480
35 ACCTCTGAGG GCTGATAGGG GTGGGTTTGT TGAGAGGGAC TTGCTGGGCC TTGGTGTGAG 540
AGCAGGCATA TTIGGAGGGG ATCTGGTGGT GCCTTGAAGG TATGATCAGA GAGGGGACCA 600
CAGGTGTGTG TTTCCCTTTT GTGTTAAGCG TGAGGCAGAG GGAGACGTTA GTCCCAGCAT 660
40 TTCCCAAAGT GTGGGTGGGT CCGTTGGTTC CCGAGATACT TTTAGGTGGT ATGGGGCCTG 720
CATTAAGTGG CACAAAATCA GAGCAAGAAA GCGATGCCCT TCCCAATTCT CTCAATCCTT 780
45 TTATGCCGAG AAGATCTCAG CTGGATGCCA ACATGTTCCG ATGCCTGTGG AAGACATGCC 840
GACGTCTCCT CTGCCTAGGG AGCAGGACTT GGGCTTAGGG CAGGTGGAAA AAATTCCAGA 900
CTTTTITAGC ACTGTTTTTG TTTTAATGGT ATATTTTAT TGGCTACTTT ATTGTTTAGG 960
50 ACAAGTGTA GTGGCATTCT ATTTATTGTG ACCTTTTCAA TAAATAGATT TAAGTAAAAA 1020
AAAAAAAAA AAAACTCGAG GGGGGGCCCC 1049

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(2) INFORMATION FOR SEQ ID NO: 59:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

	AAAGAGGATG TGMAGCTAGA GGTCCCCGAT GGCTGGTCGG ATGGGAAGCA CAAGGCTGAG	60
10	GGACTGGATT GTAAAGGCAC TAAGTCGTTC TCGGTGAGA ATCAGACATG GGGGACCTCT	120
	AGCTTCACAT CCTCTTTCCT TGCAGSTCTG GACATCCTGA GCCCAAGTCC CCCACACTCA	180
15	GTGCAGTGAT GAGTGCAGAA GTGAAGGTGA CAGGGCAGAA CCAGGAGCAA TTTCTGCTCC	240
	TAGCCAAGTC GGCCAAGGGG GCAGCGCTGG CCACACTCAT CCATCAGGTG CTGGAGGCCC	300
	CTGGTGCTTA CGTGTTTGGA GAACTGCTGG ACATGCCCAA TGTTAGAGAG CTGGCTGAGA	360
20	GTGACTTTGC CTCTACCTTC CGGCTGCTCA CAGTGTTCG TTTATGGACA TACGCTGACT	420
	ACTTAGCTGA AGCCCGGAAT CTTCTCCAC TAACAGAGGC TCAGAAGAAT AAGCTTCGAC	480
25	ACCTCTCAGT TGTCAACCCTG GCTGCTAAAG TAAAGTGTAT CCCATATGCA GTGTTGCTGG	540
	AGGCTCTTGC CCTGCGTAAT GTGCGGCAGC TGAAGACCT TGTGATTGAG GCTGTGTATG	600
	CTGACGTGCT TCGTGGCTCC CTGGACCAGC GCAACCAGCG GCTCGAGGTT GACTACAGCA	660
30	TCGGGCGGGA CATCCAGCGC CAGGACCTCA GTGCCATTGC CCGAACCCTK AANAAAAACC	720
	ATTAAAGTTA CGACGGCAGC AGCAGCCGCA GCCACATCTC AGGACCCTGA GCAACACCTG	780
35	ACTGAGCTGA GGAACCAGC TCCTGGCACC AACCAGCGCC ASCCAGCAAG AAAGCCTCAA	840
	AGGGCAAGGG GCTCCGAGGG ANCGCCAAGA TTTGGTCCAA GTCGAATTGA AAGRACTGTC	900
	GTTTCCTCCC TGGGATGTG GGGTCCCAGC TGCTGCTG CCTCTTAGGA GTCCTCAGAG	960
40	AGCCTTCTGT GCCCCTGGCC AGCTGATAAT CCTAGGTTCA TGACCCTTCA CCTCCCCTAA	1020
	CCCCAAACAT AGATCACACC TTCTCTAGGG AGGAGKCAA TGTAGGTCAT GTTTTGTGTG	1080
45	GTACTTTCTG TTTTGTGTGA CTTCATGTGT TCCATTGCTC CCCGCTGCCA TGCTCTCTCC	1140
	CTTGTTCCT TAAGAGCTCA GCATCTGTCC CTGTTCAITA CATGTCAITG AGTAGGTGGG	1200
	TAGCCCTGAT GGGGTCGCT CTGTCTGGAG CATAACCCAC AGGCGTTTTT TCTGCCACCC	1260
50	CATCCCTGCA TGCCTGATCC CCAGTTCCTA TACCCTACCC CTGACCTATT GAGCAGCCTC	1320
	TGAAGAGCCA TAGGGCCCCC ACCTTTACTC ACACCCTGAG AATTCTGGGA GCCAGTCTGC	1380
55	CATGCCAGGA GTCACGGAC ATGTTTCATC TAGAATCCTG TCACACTACA GTCATTTCTT	1440
	TTCTCTCTC TGGCCCTTGG GTCTGGGAA TGCTGTGCT TCAACCCAG AGCCTAAGAA	1500
	TGGCAGCCGT TTCTTAACAT GTGAGAGAT GATCTTTCT TGGCCCTGGC CATCTCGGGA	1560
60	AGCTTGATGG CAATCCTGGA AGGGTTAAT CTCCTTTTGT GAGTTTGGTG GGAAGGGAA	1620

GGGTATATAG ATGTATTAA AAAAAAAAAAG GTATATATGC ATATATCTAT ATATAATATG 1680
ACGCAGAAAT AAATCTATGA GAAATCTATC TACAAAMWAA AAAAAAAAAA AAAAAAAAAA 1740
5 AGGAATTCGA TATCAAGCTT ATCGATACCG TCNACC 1776

10

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACAGATAAAT AAATAAATAA TAAATTAAAT TAAATAAAAA ATCTGAGCTA ATCTGAATAA 60
ATTGAGAGAT TTCACATGAA AGCCAGGATT TCTGGCTTCC CAGGAACAGT CAGAAGAGCT 120
25 AGCTAGCAAC ACTGGTCTGC TTGGCTACCT TCTTTGGAAC AACATGAAAT CTAGCTCCCT 180
TTTTTTTTTT TTTTGGCCCC ACTTCATCCA TTCACATGAC CTGCCTGGCC TCTGCAGGTA 240
AGTGAGTATG CAACAAAAAT GTAGCACAGG TTTTGTGCGT GAACACGTG GTTTCAGGTC 300
30 CAGCTCTGCC ACTTGCTAGC ATGACCTCGT GCCGAATTCC NGCACGAAGT TTTTTTTTTT 360
TTTTTCAGTG CTCAGTCCC CCTATTGGAG AATCCTGCCC CCCCCTGGGA CAGAATGTTT 420
35 ACCCTGGCCC CGCGANTCCC TGA 443

40 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2888 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

50 TTAATGTTGT CAATAACCAC CAGGCCAAAC AGAATTATA TGACCTGGAT GAAGATGATG 60
ATGGTATAGC TTCCTTCCT ACTAAACAGA TGAAGTTTGC AGCCTCAGGC GNCTTTCTCC 120
ACCACATGGC TGGGCTAAGC AGTTCCAAGC TTTCCATGTC CAAGGCCCTC CCTCTACCA 180
55 AAGTGGTTCA GAATGATGCA TACACAGCTC CTGCTCTCCC TTCCTCTATT CGAACAAAAG 240
CCTTGACCAA CATGTCCCGG AACTGGTGA ACAAGGAAGA ACCCCCCAAA GAGCTGCCAG 300
60 CTGCTGAGCC TGTCTCAGC CCATTGGAAG GCACCAAGAT GACTGTGAAT AATCTGCACC 360

	CTCGAGTCAC TGAGGAGGAC ATTGTTGAGC TTTCTGTGT GTGTGGGGCC CTCAAGCGAG	420
5	CTCGACTGGT CCATCCTGGG GTAGCGGAGG TGGTGTGTGT GAAAAAGGAC GATGCCATCA	480
	CCGCATATAA GAAGTACAAC AACCGGTGTC TGGACGGGCA GCCGATGAAG TGCAACCTTC	540
	ACATGAATGG GAATGTTATC ACCTCAGACC AGCCCATCCT GCTGCGGCTG AGTGACAGCC	600
10	CATCAATGAA AAAGGAGAGC GAGCTGCCTC GCAGGGTGAA CTCTGCCTCC TCCTCCAACC	660
	CCCCTGCTGA AGTGGACCCT GACACCATCC TGAAGGCACT CTTCAAGTCC TCAGGGGCTT	720
15	CTKTGACCAC GCAGCCACCA GAATTCAAAA TCAAGCTTTG AGCAGGGGAG TGAGGCAGCC	780
	AGAAGTGGGG GCAGAGGAGG GTGGCTCTGT TTCCCAAGG CAAAGCTTAT GACCAATGGG	840
	CCATCGGACT GGAGACCCCT GATTGTGGGA AGGGTTGCCA GGGATAAAGA GCTTCCTCAC	900
20	TGGATGGGAC CCGCCTTTCT GTGTGTGTGT CTGCCCTGTG CTCTTCTCTC TACGTTAACG	960
	TTTCCTGTAG TATGTTTCTT CATCTCATCG CCAAGGTAGG CTTGTGTMTT TCAGTGTGTG	1020
25	CCTCCCGGAG CCTCAGCCCC AAGCTGATTT CTTATCTGGA AATGGTACAC TGAATTCTCT	1080
	GGGTGGCTTT CTTGTGGCCC CATGGGATGC AGCGTGGGG CTGTCTGAAG GACCCTGCTT	1140
	TTTCCAGGGG CCGAGGGGCT GCCTTTCCCT TGTGTGTATT AAGCTTTTCA AACAATGGAG	1200
30	GGGATGGAGA GCCCTGGTGT CCTGACGGGA GCCAGGTCGG CCTGAGAGCT GTGCCGCTCC	1260
	TCTGTCTTGT CAGTGGAGGT GCCTGGGTGG GGAGCAGGTC TCAGGCCTCT TGTCTCTCTC	1320
35	CCAGTGGCTC CAGGCCTCAC TAGTGGCAAG GGCAGGATGA GGCTGCACCG CTGGGAAGAG	1380
	TCTATCTAAG YTCITGGCTT GGAGTCCCGT GTCGTCTCCR CCCAGAGGAA GTTCTCCAGA	1440
	GTTCACCTTT CCCTTTTCCT TGAGTGTGTC TGAATGCCCC ACCCCAGCTC TCTTTCCCTT	1500
40	CTGGGTGTCT TTGCTGGGAG GGGCTGTGT TGTGAGCCCT CCCGGTCTC ACCTCGCCTG	1560
	GCACTTAACC ACACCTGGT TTTGTGTAGC CGCCAGCTCT CTTCTGGTTG GGCTTTTGAA	1620
45	AGGCTCAGCC TCCCATTTGT CAGTGCTTGG GTTTGGAGCT TATTTGAATG GAAGAGGTCA	1680
	GTTTGTTCCT GGCTCTCCAT TTCTGGCTC AGTTGTCTAC AGGACAGTGG TCAGGGATGC	1740
	CTGGAGGCAT ATATCCAGCT GCCACCAAGG GGCAGTGTTC GTTCCCACTT ATGTGAGTGA	1800
50	CCCCATCCAT CCATGACCAG AGGATTAATT TCCTGCCTTG GCAGAGGAGG AGGAGTCAAG	1860
	GGAGCAGGGC AGCTCTACCA GGCAAGGTGT TTCCCCASCA TAGGCGCAGA CAGTTGGGAC	1920
55	GAAACTTCAG AGCCCAGGCA GTCCCTGAAT GACCAGGCCA GTGTGTGCAC TGAGTGGTCC	1980
	CCTGCTGGTT GGGAGTGAAG AGAATCCAGG CTGGCAGAGC TGGAGCCAGT TGGGGAGCAC	2040
	GGTCTGGGA GCTCTGAAA ATCAGTAGCA AGTGCTGGAA AAGGCACATG CCGAAGATAC	2100
60	TCAAGAGCTC CCAAGATTG CTTGAGGCTA GCCCAGTGAA RAAAACCAGA GACTCATGTT	2160

TCCAGGGGTC AGTCTGTGAG GCAGGAAGGA CCCAGGATTT GAACCCAGCT TCAGTGTGCA 2220
 GGCTCTGAGG CTGCCCAGGA CGGGAAAGTC CAAGGAAGGG GCCTGGTGGT GCTCCACTTG 2280
 5 CAGTTCTTTA AAGAATGCTG CTTTMTATTC TCCTAACCCT TTCAAGTGGG TGCAGACTTC 2340
 TCGTTAGCAG CTGGAAGACA TTCCTCCAC ACTTTTCCCT TCCTGGCCCA AGAGAGCATC 2400
 10 CAGAAGGCAG TAGGACCTGG TTTTTCAGGT ACTGGGAGCC GGGGGCTCAC TGCTTGCACT 2460
 GTGCTTAGGG TAGGGATGGT AAATATCCTC CCTGCATGGC TTTATCCTCC CTCTCATCCC 2520
 AAAGCAGGTA TCTTCTGGTT GTCACAGAGT TTCATTGAGT CCAGCTGCAG CCACGTGGCC 2580
 15 ATCTGGAGCT GGTGCTATAG GTGACCATCT GGTACATTGA GGGGACCTGT TTGCTCCTC 2640
 CACTCTATAA GCAGTCATCT TGGGAGACCG GGAGGAGAAG GTGGTGGGCT AGTCCTGTGT 2700
 20 CCTCCTCCAC TTCCCATGCC TCTATGTTAC CCATCTGTGT CTCCTGTGCA GAAGGAGAGG 2760
 AAGGGGCATT AAGAGATGAA GGGTGATTAT GTATTACTTA TCCATTTCGT AATAAACATT 2820
 TGTATTCCCT AAAAAAAAAA AAAAAAACT CGAGGGGGGG CCCGGWACCC AWATCGCCSK 2880
 25 AAAGTGAG 2888

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(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1851 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

40 CACTAGTATA ATTTATAATT ATAACTATT CTGATTCTT TTCAAATATT AGGTGTCCTA 60
 GTTGCTATG AAGGTTTGCC ACTTCATCTT GCACTGTTCC CCAAACCTTG GACTGAGCTA 120
 45 TGCCAGACTC AGTCTGCTAT GTCAAAAAAC TGCATCAAGC TTTTGTGTGA AGATCCTGTT 180
 TTCGCAGAAT ATATTAAATG TATCCTAATG GATGAAAGAA CTTTTTTAAA CAACAACATT 240
 GTCTACACGT TCATGACACA TTTCTTCTA AAGGTTCAA GTCAAGTGT TTCTGAAGCA 300
 50 AACTGTGCCA ATTTGATCAG CACTCTTATT ACAAACCTGA TAAGCCAGTA TCAGAACCTA 360
 CAGTCTGATT TCTCCAACCG AGTTGAAATT TCCAAAGCAA GTGCTTCTTT AAATGGGGAC 420
 55 CTGAGGGCAC TCGCTTTGCT CCTGTCAGTA CACTCCTCA AACAGTTAAA CCCAGCTCTA 480
 ATTCCAACCT TGCAAGAGCT TTTAAGCAAA TGCAGGACTT GTCTGCAACA GAGAACTCA 540
 CTCCAAGAGC AAGAAGCCAA AGAAAGAAAA ACTAAAGATG ATGAAGGAGC AACTCCCAT 600
 60

	AAAAGGCGGC GTGTTAGCAG TGATGAGGAG CACACTGTAG ACAGCTGCAT CAGTGACATG	660
	AAAACAGAAA CCAGGGAGGT CCTGACCCCA ACGAGCACTT CTGACAATGA GACCAGAGAC	720
5	TCCTCAATTA TTGATCCAGG AACTGAGCAA GATCTTCCTT CCCCTGAAAA TAGTTCTGTT	780
	AAAGAATACC GAATGGAAGT TCCATCTTCG TTTTCAGAAG ACATGTCAAA TATCAGGTCA	840
10	CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG ATTGTAAAGA ATTTAAAGAC	900
	CTCCACTGTT CCAAGGATTC TACCCTAGCC GAGGAAGAAT CTGAGTTCCC TTCTACTTCT	960
	ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT GTGATGGCCA AGCTTTGCCC	1020
15	TCCCAGGACC CTGAGGTGTC TTTATCTCTC AGTTGTGGCC ATTCCAGAGG ACTCTTTAGT	1080
	CATATGCAGC AACATGACAT TTTAGATACC CTGTGTAGGA CCATTGAATC TACAATCCAT	1140
20	GTCGTCACAA GGATATCTGG CAAAGGAAAC CAAGCTGCTT CTTGACATTA GGTGTAGCAT	1200
	GTCTACTTTT AAGTCCCTCA CCCCCAACC CCATGCTGTT TGTATAAGTT TTGCTTATTT	1260
	GTTTTGTGTC TTCAGTTTGT CCAGTGCTCT CTGCTTGAAT GGCAAGATAG ATTTATAGGC	1320
25	TTAATCTCTG GTCAGGCAGA ACTCCAGATG AAAAAAAGCT GCATCTTCAG TATACTTCCT	1380
	AAAGGGCAAT CAGATAATGG ATATGTTTTA TGTAATTAAG AGTTCACITT AGTGGCTTTC	1440
30	ATTTAATATG GCTGTCTGGG AAGAACAGGG TTGCCTAGCC CTGTACAATG TAATTTAAAC	1500
	TTACAGCATT TTTACTGTGT ATGATATGGT GTCCTCTGTG CCAGTTTGTG ACCTTATAGA	1560
	GGCAGATTGC CTCGATCGC TGTGGTTCTT ATTATCAAAA TTAAGTTTAC TTGTATACGG	1620
35	AACAACCACA AGAAATTGTA TTCTGTAAAG AATCCTCTTT AGCTGTGGCC TGGCAGTATA	1680
	TAAATGGTGC TTTATTTAAC AGAATACCTG TGGAGGAAAT AAAGCACACT TGATGTAAAA	1740
40	ATAATGTGTT TATTTTATT GACATGACTG ATTGATTGCT ATTCTGTGCA CTTAATTAAA	1800
	CTGATTGTGA TGACTTWWAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1851

45

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 3542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

55

TCCAATGCTG ATGAGCGTCT TCGCTGGCAG GCCAGCTCCT TGCCTGCTGA TGACCTTTGC	60
ACAGAAAATG CCATCATGCT GAAACGATTC AATAGGTATC CGCTGATCAT TGACCCCTCT	120
GGACAGGCCA CAGAATTCAT TATGAATGAA TATAAGGWTG GTAAGATCAC ACGGACCAGC	180

60

	TTCCTGGATG ACGCCTTCAG AAAGAACTTA GAGAGTGCAC TGAGATTTCGG TAACCCCTTT	240
5	CTGGTCCAGG ATGTGGAAAG CTACGATCCA GTTTTGAACC CGGTGCTGAA CCGTGAAGTG	300
	CGGCGAACAG GGGGGAGAGT GCTGATCACT CTCGGGGACC AGGACATAGA CCTGTGCGCA	360
	TCGTTTGTCA TCTTCCTGTC CACCCGGGAT CCAACTGTCTG AGTTCCCACT AGATCTCTGT	420
10	TCCCGGGTTA CTMTTGTAAG CTTCACAGTT ACCCGTAGCA GTTTACAAAG CCAGTGTCTA	480
	AATGAAGTAC TTAAAGCAGA AAGACCTGAT GTGGACGAGA AACGATCTGA TCTTCTTAAA	540
15	CTTCAAGGGG AATTTTCAGCT CCGTTTGGCT CAGCTGGAAA AATCTCTACT ACAAGCTCTG	600
	AACGAGGTGA AAGGGCGCAT TTTGGATGAC GACACGATCA TAACCACTCT GGAGAACCTG	660
	AAGAGAGAGG CTGCAGAGGT CACCAGGAAA GTTGAGGAGA CGGACATGTG CATGCAGGAG	720
20	GTGGAGACCG TGTCACAGCA GTACCTCCCG CTCTCCACCG CCTGCAGCAG CATCTACTTC	780
	ACCATGGAGT CCCTCAAGCA GATACACTTC TTGTACCACT ACTCCCTCCA GTTTTTCCTG	840
25	GACATTTATC ACAACGTCTT ATACGAGAAC CCGAACCTGA AGGGTGTGAC CGACCACACA	900
	CAGCGCTGT CCATTATAAC AAAGGACCTC TTCCAGGTGG CGTTTAACCG AGTGGCTCGA	960
	GGCATGCTGC ATCAGGACCA CATTACCTTT GCCATGCTGC TGGCAAGAAT CAAACTGAAG	1020
30	GGCACCGTGG GGGAGCCAC CTACGATGCA GAATTCCAGC ACTTCTTGAG AGGAAATGAG	1080
	ATTGTCCTGA GTGCTGGCTC CACCCCAAGG ATCCAGGGCC TGACTGTGGA GCAGGCGGAG	1140
35	GCGTGGTGA GGCTGAGCTG CCTTCCCGCG TTAAAGGACT TGATTGCAA GGTTGAGGCA	1200
	GACGAGCAAT TTGGCATCTG GCTGGACAGC AGCTCCCGG AGCAGACTGT GCCCTACCTC	1260
	TGGAGTGAAG AAACACCTGC AACACCCATT GCCCAGGCCA TCCACCGCTT GCTCCTGATC	1320
40	CAGGCTTTCC GGCCCGATCG CCTGTTGGCC ATGGCCACA TGTTTGTTTC AACAAACCTT	1380
	GGGAGTCTT TCATGTCCAT CATGGAGCAG CCGCTCGACC TGACCCACAT TGTGGSCACA	1440
45	GAGGTGAAGC CCAACACTCC TGTCTTAATG TGCTCTGTGC CTGGTTATGA TGCCAGTGGA	1500
	CATGTGAGG ACCTTGACAG CGAGCAGAAC ACGCAGATCA CTTCAATTGC AATCGGCTCT	1560
	GCAGAAGGCT TTAACCAAGC AGATAAGGCA ATAAACACCG CTGTAAAGTC GGGCAGGTGG	1620
50	GTGATGCTGA AGAATGTGCA TCTGGCCCCA GGGTGGCTGA TGCAGCTGGA GAAGAAGTTG	1680
	CATTCCCTGC AGCCGATGCT CTGCTTCCGA CTCTTCCTCA CCATGGAGAT CAACCCCAAG	1740
55	GTGCTGTGA ATCTGCTCCG TCGGGGCCG ATCTTTGTGT TCGAGCCACC GCCAGGGKTG	1800
	AAGGCCAACA TGCTGAGGAC GTTCAGCAGC ATTCCCGTCT CACGGATATG CAAGTCTCCC	1860
	AACGAGCGTG CCCGCTGTGA CTTCTGCTG GCCTGGTTTC ATGOGATCAT CCAAGAACGC	1920
60	TTACGATACG CACCACTGGG GTGGTCAAAG AAGTATGAAT TTGGAGAGTC TGACCTGCGG	1980

	TCANYTTGCG ATACGGTGGA CACGTGGCTG GATGACACGG CCAAGGGCAG GCAGAACATC	2040
	TCACCGGATA AGATCCCGTG GTCTGCACTA AAGACCTTAA TGGCCAGTC CATTATATGGC	2100
5	GGGCGCGTGG ACAACGAGTT TGACCAGCGT CTGCTCAACA CCTTCCTGGA GCGCCTGTTC	2160
	ACAACCAGGA GTTTCGACAG TGAGTTTAAAG CTGGCATGCA AGGTCGACGG ACATAAAGAC	2220
10	ATTCAAATGC CAGATGGCAT GCAGGCGAGA GGAGTTTGTG CAGTGGGTGG AGTTGCTCCC	2280
	CGACACCCAG ACGCCCTCCT GGCTGGGCTT GCCCAACAAC GCCGAGAGAG TCCTCCTTAC	2340
15	CACACAGGGT GTGGACATGA TCAGTAAAT GCTGAAGATG CAGATGTTGG AGGATGAGGA	2400
	CGACCTGGCC TACGCAGAGA CTGAGAAGAA GACGAGGACA GACTCCAGT CCGACGGGCG	2460
	CCCTGCCTGG ATGCGGACAC TGCACACCAC CGCGTCCAAC TGGCTGCACC TCATCCCCCA	2520
20	GACGCTGAGC CACCTCAAGC GCACCGTGGA GAATATCAAG GATCCTTTGT TCAGGTTCTT	2580
	TGAGAGAGAA GTGAAGATGG GCGCAAAGCT GCTTCAGGAC GTTGGCCAGG ACCTTCGAGA	2640
25	TGTCGTCCAG GTGTGCGAAG GAAAGAAGAA GCAGACCAAC TACTTGCGCA CGCTGATCAA	2700
	CGAGCTAGTG AAAGGGATCT TGCCTCGGAG CTGGTCCAC TACACGTGC CTGCCGGCAT	2760
	GACCGTCATC CAGTGGGTGT CCGACTTCAG CGAGAGGATC AAACAGCTGC AGAACATCTC	2820
30	ACTGGCAGCT GCATCTGGTG GCGCCAAGGA GCTAAAGAAC ATCCACGTGT GCCTGGGTGG	2880
	CCTGTTCTGT CCTGAGGCGT ACATCACTGC CACCAGGCAG TATGTGGCCC AGGCCAACAG	2940
35	CTGGTCCCTG GAGGAGCTCT GCCTGGAAGT CAACGTCACC ACCTCAGAG GCGCCACCCT	3000
	TGACGCTTGC AGCTTCGGAG TCACGGGTTT GAAACTTCAA GGGGCCACGT GCAACAACAA	3060
	CAAGCTGTCA CTGTCCAATG CCATCTCAAC CGCCCTTCCC CTGACGCAGC TCGCTGGGT	3120
40	CAAGCAGACA AACACCGAGA AGAAGGCCAG TGTGGTAACC TTACCTGTCT ACCTGAACTT	3180
	CACCCGTGCA GACCTCATCT TCACCGTGGA CTTCGAAATT GCTACAAAGG AGGATCCTCG	3240
45	CAGCTTCTAC GAGCGGGGTG TCGCAGTCTT GTGCACAGAG TAAACTTTTC TAGCTGCCCC	3300
	TTTCTGTAAT AGTGAAAGTT GGTATTTAAC ATTTATTCAT TTTTAAATA TTTGGAAGGT	3360
	CTGAGCTTGT GAAAAGAAAG TGGTTGGTCT GAGGTTGGAG GAAGCTGAAT GGAATCTGAC	3420
50	GGTTGGGAGT GGTGGAAATT GGAAGGATAC CAGGAGGTAT TTGGGAAGGC CAATGGCGTG	3480
	GCTCCTTTGA GGAAATAAAA CACTAAGCAT GAAAAAAAAA AAAAACTTA CAANCCNCAA	3540
55	GG	3542

(2) INFORMATION FOR SEQ ID NO: 64:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

10 AGGTGATTTT AATGATAGGT GTCATATATA GGACGGATAA TCTGTTTACA TTCTGTTCTT 60
 CTCGATGCAC TCACAAGCGG GTAAC TAGGT GACAAGAAAA CAAAGATCTT ATTCAAAAGA 120
 GGTCTTACAG CAACCCAACG TCTCATCTTC CCATAGTAAA GATGACGGCG CCTTGAGGTA 180
 15 AGCTACAGGC AACACCACTT CCGCGTTTCT CTGCGCCCT GGTCCAAGAT GGCGGATGAA 240
 GCCACGCGAC GTCTTGTC TGAGATCCCG GTGCTGAAGA CTAACGCCGG ACCCCGAGAT 300
 CGTGAGTTGT GGGTGCAGCG ACTGAAGGAG GAATATCAGT CCCTTATCCG GTATGTGGAG 360
 20 AACAACAAGA ATGCTGACAA CGATGCTTC GACTGGAGT CCAACAAGGA AGGAACTCGG 420
 TGGTTTGGAA AATGCTGGTA TATCCATGAC CTCCTGAAAT ATGAGTTTGA CATCGAGTTT 480
 25 GACATTCCTA TCACATATCC TACTACTGCC CCAGAAATTG CAGTTCCTGA GCTGGATGGA 540
 AAGACAGCAA AGATGTACAG GGGTGGCAA ATATGCCTGA CGGATCATTT CAAACCTTTG 600
 TGGGGCCAGG AATGTGCCA AATTGGACT AGCTCATCTC ATGGCTCTGG GGCTGGGTCC 660
 30 ATGGSTGGCA GTGAAATCC CTGATCTGAT TCAGAAGGGC GTCATCCAAC ACAAGAGAA 720
 ATGCAACCAA TGAAGAATCA AGCCACTGAG GCAGGGCAGA GGGACCTTTG ATAGGCTACG 780
 35 ATACTAWTTT CCTGTGCATC AACTTAACT CATCTAACTG TTCCCCGGAC ANCCTCCACT 840
 CTAGTTGTTA CTAAGTANTG CAGTAGCATT NTGGGAAGA ACA 883

40

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

50

GGCAGGAGGT GGCTCTACC CTGGGCTCAT CTGGCTACAC AGGGACTCTA AACGCTTCCA 60
 GATTCCCTGG AAACATGCCA CCCGGCATAG CCCTCAACAA GAAGAGGAAA ATACCATTTT 120
 55 TAAGGCCTGG GCTGTAGAGA CAGGAAGTA CCAGGAAGGG GTGGATGACC CTGACCCAGC 180
 TAAATGGAAG GCCCAGCTGC GCTGTGCTCT CAATAAGAGC AGAGAATTCA ACCTGATGTA 240
 60 TGATGGCACC AAGGAGGTGC CCATGAACCC AGTGAAGATA TATCAAGTGT GTGACATCCC 300

TCAGCCCCAG GGCTCGATCA TTAACCCAGG ATCCACAGGG TCTGCTCCCT GGGATGAGAA 360
 5 GGATAATGAT GTGGATGAAG AAGATGAGGA AGATGAGCTG GATCAGTCGC AGCACCATGT 420
 TCCCATCCAG GACACCTTCC CCTTCCTGAA CATCAATGGT TCTCCCATGG CGCCAGCCAG 480
 TGTGGGCAAT TGCAGTGTGG GCAACTGCAG CCCGGAGGCA GTGTGGCCCA AAACCTGAACC 540
 10 CCTGGAGATG GAAGTACCCC AGGCACCTAT ACAGCCCTTC TATAGCTCTC CAGAACTGTG 600
 GATCAGCTCT CTCCCAATGA CTGACCTGGA CATCAAGTTT CAGTACCGTG GGAAGGAGTA 660
 CGGGCAGACC ATGACCGTGA GCAACCTCA GGGCTGCCGA CTCTTCTATG GGGACCTGGG 720
 15 TCCCATGCCT GACCAGGAGG AGCTCTTTGG TCCCGTCAGN CTGGAGCAGG TCAAATTCCT 780
 AGGTCCTGAG CATATTACCA ATGAGAAGCA GAAGCTGTTC ACTAGCAAGC TGCTGGACGT 840
 20 CATGGACAGA GGAATGATCC TGGAGGTCAG CGGTCAATGCC ATTTATGCCA TCAGGCTGTG 900
 CCAGTGCAAG GTGTACTGGT CTGGGCCATG TGCCCCATCA CTGTGTGCTC CCAACCTGAT 960
 TGAGAGACAA AAGAAGGTCA AGCTATTTTG TCTGGAAACA TTCCTTAGCG ATCTCATTGC 1020
 25 CCACCAGAAA GGACAGATAG AGAAGCAGCC ACCGTTTGAG ATCTACTTAT GCTTTGGGGA 1080
 AGAATGGCCA GATGGGAAAC CATTTGGAAAG GAAACTCATC TTGGTTTCAGG TCATTCCAGT 1140
 30 AGTGGCTCGG ATGATCTACG AGATGTTTTC TGGTGATTTC ACACGATCCT TTGATAGTGG 1200
 CAGTGTCCTG CTGCAGATCT CAACCCAGGA CATCAAGGAT AACATCGTTG CTCAGCTGAA 1260
 GCAGCTGTAC CGCATCCTTC AAACCCAGGA GAGCTGGCAG CCCATGCAGC CCACCCCCAG 1320
 35 CATGCAACTG CCCCTGCCG TGCTCCCTCA GTAATTGTGA ATGCCATCTT CTTCCTTCTC 1380
 TTTTATATAA TATTGTACAT ATGGATTTT TTATGTGTTA GATTTAACCA GCTTTTAAAT 1440
 40 CTCTGTTTTC TGTGACAGTG TTAGAAGTTT GTGATCTCC AAATATGCCT AGATTTAAAG 1500
 CTGATTTAAT TTATGGAAAA AAAAAAAAAA AAAAAAAAAA A 1541

45

(2) INFORMATION FOR SEQ ID NO: 66:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAAAAATGAA TGTTAGAAGG TGCCTGCCGA GCGGGACAG AGTGTTCGCT CGCGCTGGAG 60
 AAGGCTCTGC TCAGCCCTGA GAGTCCCTTC CTGCCCCACC GATACTGGCA CTTTAAAAAG 120
 60

GAAGCTGACC GCACAGTGTC CAGACGAATT GGGCCCCAGA AGATGGGGAG TTCTGTCTCTG 180
CCCTTCTGTG TCTGCGTGAC CTCACCCAGC CTAGGAGGGA GGTGCATTCA GGGTAGATTT 240
5 GCCTCTCATT CAAAGTTCTG GGGCTTTGGG CGGAAAACAG CCAGCTTTGG CGCTGTGGG 300
GAGACTCCTC CAGACCAGGA ACCCCAGAAG GAGACAGAGC CTGCCACATC CTCCCACGCC 360
10 AGGCCCTGGG CCAGGGTGAT TGGACTGAGA ATTTGGCCAC AACCAAATTG ATGCTGGCTG 420
GAACCAGAGG CCAGAAAGCC TGGCCTTGTC CCCATGTGGG AGCCCTGTCC TCAGCCCTCT 480
TGTCCCTTG AGCTCAGTGA ATTCCACCA GGTGCCACA GCTCCTGGAC TTCAAATTCT 540
15 ATATATTGAG AGAGTTGGAG AGTATATCAG AGATATTTT GGAAAGGAGT TGGTCTATGC 600
AATGTCAGTT TGAATCTTC TTGAAAGTTT AATGTTTTTA TTAGGAGATT TAAAGAAAAT 660
AAAGGTCTAC AATATCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
20 AAAAAAAAAA AA 732

25

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTAAGGAATT CGGCMCGATC CCGCAAGTA ACATGACTAA AAAGAAGCGG GAGAATCTGG 60
GCGTCGCTCT AGAGATCGAT GGGCTAGAGG AGAAGCTGTC CCAGTGTCCG AGAGACCTGG 120
40 AGGCCGTGAA CTCCAGACTC CACAGCCGGG AGCTGAGCCC AGAGGCCAGG AGGTCCCTGG 180
AGAAGGAGAA AAACAGCCTA ATGAACAAAG CCTCCAATA CGAGAAGGAA CTGAAGTTTC 240
TTCGGCAAGA GAACCGGAAG AACATGCTGC TCTCTGTGGC CATCTTTATC CTCCTGACGC 300
45 TCGTCTATGC CTA CTGAGACC ATGTGAGCCT GGCCTTCCC CACAACCAGC ACAGGCTTCC 360
ACTTGGCCCC TTGGTCAGGA TCAAGCAGGC ACTTCAAGCC TCAATAGGAC CAAGGTGCTG 420
50 GGGTGTTCCT CTCCTAACCT AGTGTTCAG CATGGCTTCC TGGCGGCCCA GGCCTTGCTT 480
CCCTGGCCTG CTGGGGGGTT CCGGGTCTCC AGAAGGACAT GGTGCTGGTC CCTCCCTTAG 540
CCCAAGGGAG AGGCAATAAA GAACACAAAG CTGAAAAAA AAAAAAAAAA AACTCGTAGG 600
55 GGGGGCCCGT ACCCAATCGC CCTNCTGTG 629

60

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

10 CTGCTAGCCG GCCGGCGCAG GCTGCCGAGC GGGTGAGCGC GCAGGCCAGG CCAAAGCCCT 60
GGTACCCGCG CGGTGCGGGC CTCAGTCTGC GGCCATGGGG GCGTCCGCGC GGCTGCTGCG 120
15 AGCGGTGATC ATGGGGGCCC CGGGCTCGGG CAAGGGCACC GTGTCGTGCG GCATCACTAC 180
ACACTTCGAG CTGAAGCACC TCTCCAGCGG GGACCTGCTC CGGACAACA TGCTGCGGGG 240
CACAGAAATT GCGGTGTTAG CCAAGGCTTT CATTGACCAA GGGAACTCA TCCCAGATGA 300
20 TGTCACTACT CGGCTGGCCC TTCATGAGCT GAAAAATCTC ACCCAGTATA GCTGGCTGTT 360
GGATGGTTTT CCAAGGACAC TTCCACAGGC AGAAGCCCTA GATAGAGCTT ATCAGATCGA 420
25 CACAGTGATT AACCTGAATG TGCCCTTTGA GGTCACTAAA CAACGCCTTA CTGCTCGCTG 480
GATTCATCCC GCCAGTGGCC GAGTCTATAA CATTGAATTC AACCCCTCCA AAATGTGGG 540
CATTGATGAC CTGACTGGGG AGCCTCTCAT TCAGCGTGAG GATGATAAAC CAGAGACGGT 600
30 TATCAAGAGA CTAAAGGCTT ATGAAGACCA AACAAAGCCA GTCTTGAAT ATTACCAGAA 660
AAAAGGGTG CTGAAACAT TCTCCGGAAC AGAAACCAAC AAGATTGGC CCTATGTATA 720
35 TGCTTTCTTA CAACTAAAG TTCCACAAAG AAGCCAGAAA GCTTCAGTTA CTCCATGAGG 780
AGAAATGTGT GTAACATTA ATAGTAAGAT GGGCAAACCT CCTAGTCCTT GCATTTAGAA 840
GCTGCTTTTC CTAAGACTTC TAGTATGTAT GAATTCCTTG AAAATTATAT TACTTTTATT 900
40 TCTACTGATT TTATTTTGA TACTAAGGAT GTGCCAAATG ATTCGGATAC TAAGATGCAT 960
CGTTTGAAAT CATCTAGTGT GTTGATGCA GTTATCCTCA AAAACATCAG CGATGTCTGA 1020
45 ACCTTTAAAA CATCTGTTAG AGCAAAATTA AAAGAGCATT TGGTAGTAAT CTAACCTTTT 1080
GTTTCAGTTA TAAGTGGTTG ATAAAGTTTC CATATTTTTC TGGAAAAGTT AAAAAAGTT 1140
ACATGTCATT TGGAGAAAAT ACGTAATCAG AAATTTGTGC ATAGATTGAT GCCAAAAAG 1200
50 ACATTTCCAG CATGTGGAA CATGGTGAGA CACTATATAA AATTCAGAA AGAAAGCAAC 1260
TGGATTIACA GATTTATTGT GAGACACAAA TTCACTGCTG CCTTTACACT AAGAAATGTA 1320
55 TATGTTAACC ATATATGCTG TATTTATTTT GTCGTTAAGC ATACTTTCAG TTTACTCAGA 1380
ATTTTCAATT TGCTATAAAG ATGTATCAAT TAGCATATAG AAAAATATTA CTTTAAGATG 1440
ACTTGTTTCC TTGAAAATA CCTGTGACT GAGGGTTATG ATTTGTGTCA AAAATTGACA 1500
60

TAAGTGCCTT TACAAGCACC AAAGTTGAAT GAATTTTCAA CAAAATGTAA TTAAAGTCTA 1560
TGTTTTTCAGT TATGACTCAG GTTAAGAAAT GTGTTTTAGG ATCTACTTGC TGGTTTTTCT 1620
5 TTTTGATCCA AATGTGTGAT CTGCCCTGAT AAATAACAAG TTATNGTACC ATCTCCCCCG 1680
CCAATAAAAA AAAAAAAAAA AAAAAAAAAAC TCGAGGGGGG GCCCGGTACC CAATTCTCCG 1740
NAATAGGNAG T 1751
10

(2) INFORMATION FOR SEQ ID NO: 69:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGCACGAGAT TATGTATTAA AATGTTTTTG AATTGTGAAA TATTAGAATA TTGTTACTAT 60
25 TTGACCCAAC TCAAAATCTC CATGGGAAAA TACCTGTCGA TACCCACAGT ATTGTTGAAA 120
ATAATCAGAT GCAGTATCAC AGCTGTGTCA GACTCTAGTA CCAGTTGGGC AATCAAGGCA 180
30 CAGCTAAAAA TTGAAAACAA AGATCTGGAC AACAAAACAG CCAAAGGTGG GGGTCAAGAA 240
GCTCTGACGT GTACCTAGCT GTAGAATGCT ATGCACACGT GCCAGGTGTA GTGTGCATAT 300
CCAGGAAAAA CTGCAGAGAG CCCCAGTCTT CACCTCTGGT TGACCATGAG CTCTGTGTAA 360
35 GCAGGAAGTG AAGGCTAAGG CAGATTTAAG CTCTGAAAGC ATTCCACAAC ATACACACAA 420
ATCGTGCAAA GCATTAAGGA AATCTTGTTA CTGCTAAGTG TTGCTGACCC AGGAACAACT 480
40 CCTACTCAGC TGGACTTAAA AATAAAAA 508

45 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

55 TACATAGAGC AAAGAGAAAT TTCCAGAATT TCTARAATTC TGGAAAGAGA ATTTTCCTGA 60
GATTGCAGAT TTGCTGTGT CCTCAGGTGA TGATGAGGGC TGTTTTCCCC TGTGTCTCTT 120
TCCTCACACT CATGCTTCCT CTCCTAGAGT GTCTGGTTGG CATGATCATG TGCTACCTAG 180
60

GCATTTCTTT CACTGATACA AGGAAAAC TG CAGGGTTAAA AAAAAAAAAA AAAAAAAAAA 240
NCNCG 245

5

(2) INFORMATION FOR SEQ ID NO: 71:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATGTTCTCTCA TGAGGATGCA CTGTGCTTC TGCAAGTATT GCTGCAGCTT CATAGTGACT 60
20 CCCACCAGCA CCAGCAATAC AGCTAGCTAC CTGTGGCCTT GGATCTCAGC CAGCATGGCT 120
GGGAGAGGGA GCAGCTGGGC ATGTACCCTA AATGCTGTTA CCAGGGAAGG ACTCCCAGAG 180
TGAAGACAAG TAGGGACTTC CTGCAGAGGT GGTACATGTG CTCTCTGTAT CCATACTTTT 240
25 TTTTTTTTTT TTTTGAGATA GAGTTTCACC CTGTGTGCCC TGGCTGGAGT GCAATGGTGC 300
GATCTCAGCT CACTGCAACC TCTCTGCCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC 360
30 T 361

35

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

45 AGGATCACAC AATAGAGAAC ACTGTAGTAA CATTCGGTC TGCTCACAAG ACCCAGAACA 60
TTGATCAGTT TTTGTGTGTG GTTATTATT TTTCTGTAA AAAATTGTGA AAAGTTTGT 120
TTAGCTAGAT GATATTTTAA TAGCTGCGAG TGCTTTGGAA CTATAAGAT GTCACTACTT 180
50 AACACACATA CCTTATGTTT TGTMTTGT TTGTTTACAC TCAGTATAAA TCAGGAGAAG 240
TTAGCCAACC ATCTAGCATT TAGAATCCTC TTTTTTATIG TCTTCTAAGG ATATGGATGT 300
55 TCCCATAACA GCAACAAAAC AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT 360
AAGCACCTGC TTAACTTTGT GTCCCAAATA TTTAGTGTGT ATATATATAT ATATATATAT 420
ACACACACAC ACATATATAT TCAACAAATA AAGCAAAATA TAACATGCAT TTCACATTTT 480
60

GTCTTTCCTT GTTACGATTT TAATAGCAGA ACTGTATGAC AAGTTTAGGT GATCCTAGCA 540
TATGTTAAAT TCAAATTAAT GTAAAACAGA TTAACAACAA CAAAGAACT GTCTATTGTA 600
5 GTGAAGTCAT GCTTCTATT ATAATAACTT GGCTTCGGTT ATCCATCAAA TGCACACTTA 660
TACTGTTATC TGATTGTTTA TAATAAGAA TACTGTACTT ATAAAAAAAA AAA 713

10

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAAAGTCAGA GCTGTCCAAT CCCTCAGCAC CTTTGTAGATT TGCTCCAAAT TAGAAACGTG 60
GGGACTATGT GTTCTGGGCA ATCACAGGTC TGGAAATGG CTCTGCAGGC TCTTGATAGT 120
25 GAGACAGTGG TCATCTTACC AGACATGCAT CTGATTTTAA GCCTCAGGCT AATCCACAAT 180
GCTCGCCCAT GCCTATGATT AACAAACAAA AGCAAATCT GCTTTTATAG TTTAGGAAAC 240
30 CTGGATAGAA CAGTATTTTT CAGCATTCCTT GGATAAGCA GTTCTGCATT TTTAAATTGG 300
GACTGCAGAA GTGACTGTCT ATAGTTGTGA AATACAAAA ATGGTATGTT TGATCAGAAA 360
AGGAAGCCCG TGCCTGGCAC TTGGAAAGAT ACTGAGCATC ATAACCCTAA TGAGAAAATG 420
35 TAGGCTCTGT GAATGTTAAC TACAAATCAG GTTAGGAAAG CATATGACAC CCTTTGTCAA 480
ACTAAGCTTC ACTAGGAGGA CCTGTGCTCA TAGAAGAATA TGCTTTAAAA GTATCAATTT 540
40 TCCACAGTCG ATGATGGAGA AAAGTTCATT TGCACCAGAA TGCTGATAGT CACAATACAC 600
AGCCTGACAT ATATACAAT ACAGTTTTCT GTAAACAGAA GTTCTTCCTC TTCCAATTCA 660
GGAGTCAGTC AGAGCATAAA TATTGCATGT TTCACTTTAG AAAGTGATTC ATTTTAGAAA 720
45 GCAGATCTGG ATTATTTTGC AGGGTAGAAA TGAAGGCTAT TTCTGGCATT CTTGCTCAAA 780
AAGTCAATAT ATGTACATTA AGTATAAAAA AGGGTCTCTT TCACCTCTTT TGTTCGTTAG 840
50 CATTTGGCTAC ATAACCTCGT CC 862

55 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4602 base pairs
60 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

5	GCGAGGGGGC GKGGGAGCA GCGCCGARGC CGCCGCTCC GCCTCCGCCG CCTAGGACTA	60
	GGGGGTGGGG GACGGACAAG CCCCATGCC GGGGAKACG GAAGAGCCGA GACCCCGGA	120
	GCAGCAGGAC CAGGAAGGGG GAGAGGCGC CAAGGCGCT CCGAGGACC CGCAACAACG	180
10	GCCCCCTGAG GCGGTCGCGG CGGCGCTGC AGGGACCACT AGCAGCCGCG TGCTGAGGGG	240
	AGGTGCGGAC CGAGGCCGG CCGCTGCGRC CGCCGCGCMG CAGCTGTGTC CCGCCGGAGA	300
15	AGGCCGAGTA TCCCCGCCG CGAGGAGCAG CCCAGCGCC AGGCCTCCCG ACGTCCCCGG	360
	GCAGCAGCCC AGGCCGCGAA GTCCCCGTCT CCAGTTCAGG GCAAGAAGAG TCCGCGACTC	420
	CTATGCATAG AAAAAGTAAC AACTGATAAA GATCCCAAGG AAGAAAAGA GGAAGAAGAC	480
20	GATTCTGCCC TCCCTCAGGA AGTTTCCA'TT GCTGCATCTA GACCTAGCCG GGGCTGGCGT	540
	AGTAGTAGGA CATCTGTTTC TCGCCATCGT GATACAGAGA ACACCCGAAG CTCTCGGTCC	600
25	AAGACCGGTT CATTGCAGCT CATTGCAAG TCAGAACCA ATACAGACCA ACTTGATTAT	660
	GATGTTGGAG AAGAGCATCA GTCTCCAGGT GGCATTAGTA GTGAAGAGGA AGAGGAGGAG	720
	GAAGAAGAGA TGTTAATCAG TGAAGAGGAG ATACCATCA AAGATGATCC AAGAGATGAG	780
30	ACCTACAAAC CCCACTTAGA AAGGAAACC CAAAGCCAC GGAGAAAATC AGGGAAGGTA	840
	AAAGAAGAGA AGGAGAAGAA GGAAATTAAG GTGGAAGTAG AGGTGGAGGT GAAAGAAGAG	900
35	GAGAATGAAA TTAGAGAGGA TGAGGAACCT CCAAGGAAGA GAGGAAGAAG ACGAAAAGAT	960
	GACAAAAGTC CACGTTTACC CAAAAGGAGA AAAAAGCCTC CAATCCAGTA TGTCCGTTGT	1020
	GAGATGGAAG GATGTGGAAC TGTCTTGCC CATCTCGCT ATTTGCAGCA CCACATTAAG	1080
40	TACCAGCATT TGCTGAAGAA GAAATATGTA TGTCCCCATC CCTCCTGTGG ACGACTCTTC	1140
	AGGCTTCAGA AGCAACTTCT GCGACATGCC AAACATCATA CAGATCAAAG GGATTATATC	1200
45	TGTGAATATT GTGCTCGGC CTTCAAGAGT TCCCAATC TGGCAGTGCA CCGGATGATT	1260
	CACACTGGCG AGAAGCATTA CAATGTGAGA TCTGTGGATT TACTTGTGCA CAAAAGGCAT	1320
	CTCTTAATTG GCACATGAAG AAACATGATG CAGACTCCTT CTACCAGTTT TCTTGCAATA	1380
50	TCTGTGGCAA AAAATTTGAG AAGAAGGACA GCGTAGTGGC ACACAAGGCA AAAAGCCACC	1440
	CTGAGGTGCT GATTGCAGAA GCTCTGGCTG CCAATGCAGG CGCCCTCATC ACCAGCACAG	1500
55	ATATCTTGGG CACTAACCCA GAGTCCCTGA CGCAGCCTTC AGATGGTCAG GGTCTTCCTC	1560
	TTCTTCCTGA GCCCTTGGGA AACTCAACCT CTGGAGAGTG CTTACTGTTA GAAGCTGAAG	1620
60	GGATGTCAAA GTCATACTGC AGTGGGACGG AACGGGTGAG CCTGATGGCT GATGGGAAGA	1680

	TCTTTGTGGG AAGCGGCAGC AGTGGAGGCA CTGAAGGGCT GGTATGAAC TCAGATATAC	1740
	TCGGTGCTAC CACAGAGGTT CTGATTGAAG ATTCAGACTC TGCCGGACCT TAGTGGACAG	1800
5	GAAGACTTGG GGCATGGGAC AGCTCAGACT TTGTATTTAA AAGTTAAAAA GGACAAAAAA	1860
	AAAATCTAAA GCATTTAAAA TCTAGTGAAA TAACTGAAGG GCCTGCTCTT TCCATTGTGG	1920
	ATCAGAGCAC ACACATACAT ACACCCCTCCA CCTCCCCATC CCCTGTTCTC CCTCTGTTGC	1980
10	TCCCCTTATA AAATTGATGT TGTCTTTACC AGAAAGGTAG ACAAAAAAGA AGCAGCAGCA	2040
	GCTCTTAAAG TGAGGGTTAT TCTCATACTC GGTTCAGCC ATCAGCAGAC TTCCTGCTCA	2100
15	TCGGCAGATC CCCCTTTCCA ACCTGTAACCT CTGATGTGCT CTGGATCAGC TTTTAACTTT	2160
	TAATCATATA TTACTGTCTT CTAAATCCCT TCTCCTCCTC TACTGCTGCC CTATGGTTCT	2220
	GGCTCCTACC CCCTGCGGCA CACTTATCTT CAAATACCAT AGAATTCTAA TCTCTGAAAT	2280
20	CATAGCTCTC CAGTGGCTTT TAAAGAAAGC TGGTCTCAG CACTAACAAA ATCACTACAA	2340
	TAGCCTAGTG CTTTTTTGGA AGCCTTTTGA GGAAGAATG TTAGGTTCAT GGTAAGTAGT	2400
25	ATGCTCTTTG AGATTTTTAC AGTGTGAAA CTTAAGAATT TTGAGAGGGT GAGGAGGGTT	2460
	GTTCAGAATC TAAATTACAG ATAGATGATT GTTCTGTG AATTGTGTTT TTTTCTTTT	2520
	TTTTGTGCCC TACCATTTCC TTACATTTCC CTGGGGCCC ATCTCTGGCT CCTTGCTTTT	2580
30	TGTTCTTGC TTTGCTTTAT CAGTTCATTC CAGCTCCCTG TTAGTGAAGG ACCTGCTGT	2640
	TAGTGAAGGA ACAAAGTCTA TGAGTCCTAA AATTTTAAGT CAAAGAAAAC TGCTCTGTTT	2700
35	CCCCTTTAGT AACACTTCTG AAGAGGAAAA ACTTCAATAG CCAAAGTTAA TAATCCTATA	2760
	TAATAAATGC TTTGGCTTTC ACCTAAAATT CTGGGCATCA CAATTTCTCT GGGATAGAGG	2820
	TTGTGTGGG GAATAGATTG CTTATGCTG TTCACTGGAG AGAAAAGGTA GTGTTTTGT	2880
40	ACAAGGTCAT ACCGCCAGAA GCCCCAAATC CTATTTTGGC TCATCTTCAG GTAAAGAGTA	2940
	ATTCCTATCC TGTGTGCCTC AGAAGCTAGA ATCGAAGGCT TACCCTATTC ATTGTTTATT	3000
45	GTCAGAAATG CATGATGGCT CTGGAAAGA ATGACGTTTT GCTGGAAAAA AAAAAAARAA	3060
	CMGTTTGTGT TTCACAAACA TGGCTTATCA ATTTTTTCAA AGAATTCCTT TTTCCCAAAA	3120
	AGAGGAGTAA CAAAATGTCA TTTCTGAAAG AGGCTTACTT TATACCAACT AGTGTACGCA	3180
50	TTTGGGATGC CAGGGAACAG AGAGTGAGAC ACCTACAATC ACCAGTCTCA AATGCGCTAT	3240
	TGTTTCTTTT CAGAGTGTG CAGATTTGCC ATTTCTCCAT AATATGGGGA TAGAAAATGG	3300
55	AATAAAGATA GAAGGGATGT AGAATATGCT TTCCTGCCAA CATGGTTTGG AGTCGACTTT	3360
	GGTATATTGA CTAGATTGA AAATACAAGA TTGATTAGAT GAATCTACAA AAAAGTTGTC	3420
60	CTCCTCTCAG GTCCCTTTTA CACTTTTGA CTAAGTAGCA TCTATATTCC ACCTTAGCT	3480

TTTTGTGTCAC ACTTATCCTT TGTCTCCGTA AATTTTCATTT GCAGTGGTTA GTCATCAGAT 3540
 ATTTTAGCCA CCTACACAAA AGCAAACGTC ATTTTAAAA ATCTTTCTGA GATGGGAGAA 3600
 5 AATGTATTCT CCTTTCCTAT ACCGCTCTCC CAACAAAAA ACAACTAGTT AGTTCTACTA 3660
 ATTAGAAACT TGCTGTACTT TTTCTTTTCT TTTAGGGGTC AAGGACCCTC TTTATAGCTA 3720
 CCATTTGCCT ACAATAAAT ATTGCAGCAG TTTGCAATAC TAAAAATTT TTTATAGACT 3780
 10 TTATATTTT CCTTTTGATA AAGGGATGCT GCATAGTAGA GTTGGTGTA TAAACTATC 3840
 TCAGCCGTTT CCCTGCTTTC CCTTCTGCTC CATATGCCTC ATTGTCCTC CAGGGAGCTC 3900
 15 TTTTAATCTT AAAGTCTAC ATTTCATGCT CTTAGTCAA TTCTGTTACC TTTTAATAA 3960
 CTCCTCCAC TGCATATTT CATCTGAAT TGGTGGTTCT AAATCTGAA ACTGTAGTTG 4020
 AGATACAGCT ATTTAATATT TCTGGGAGAT GTGCATCCCT CTTCTTTGTG GTTGCCCAAG 4080
 20 GTTGTTTTGC GTAACGAGA CTCCTTGATA TGCTTCAGAG AATTTAGGCA AACACTGGCC 4140
 ATGGCCGTGG GAGTACTGGG AGTAAATAA AAATATCGAG GTATAGACTA GCATCCACAT 4200
 25 AGAGCACTTG AACCTCCTTT GTACCTGTTT GGGGAAAAAG TATAATGAGT GTACTACCAA 4260
 TCTAACTAAG ATTATTATAG TCTGGTTGTT TGAAATACCA TTTTCTCTC CTTTGTGTT 4320
 TTTCCCACTT TCCAATGTAC TCAAGAAAAT TGAACAAATG TAATGGATCA ATTTAAAATA 4380
 30 TTTTATTCT TAAAGCCTT TTTGCTGTG TGTAATGTG AGGACCCTC TCCTTTCATG 4440
 GGAGAGACAG GTAGTTACCT GAATATAGGT TGAAAAGGT ATGTAAAAG AAATTATAAT 4500
 35 AAAAGGGATA CTTGCTTTT CAAATCTTG TTTCTCTTA TTCTAGGTAA GGCATATTAA 4560
 AAATAATAT GTAAAGAAGA AAAATAAAG TTGTCTTCAT GG 4602

40

(2) INFORMATION FOR SEQ ID NO: 75:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGCGCCCCGG GCCGGCGGGT TTCTCTAACA AATAACAGA ACCCGCACTG CCCAGGCGAG 60
 CGTTGCCACT TTCAAAGTGG TCCCCTGGGG GAGCTCAGCC TCATCCTGAT GATGCTGCCA 120
 55 AGGCGCACTT TTTATTTTAA TTTTATTTTT ATTTTTTTTT TAGCATCCTT TTGGGGCTTC 180
 ACTCTCAGAG CCAGTTTTTA AGGGACACCA GAGCCGCAGC CTGCTCTGAT TCTATGGCTT 240
 60 GGTGTGTTACT ATAAGAGTAA TTGCCTAACT TGATTTTTCA TCTCTTTAAC CAAACTGTG 300

GCCAAAAGAT ATTTGACCGT TTCCAAAATT CAGATTCTGC CTCTGCCGAT AAATATTTGC 360
 CACGAATGAG TAACTCCTGT CACCACTCTG AAGGTCCAGA CAGAAGGTTT TGACACATTC 420
 5 TTAGCACTGA ACTCCTCTGT GATCTAGGAT GATCTGTTCC CCTCTGGAT GAACATCCTC 480
 TGATGATCAA GGCTCCAGC AGGCTACTTT GAAGGGAACA ATCAGATGCA AAAGCTCTTG 540
 10 GGTGTTTATT TAAAATACTA GTGTCACTTT CTGAGTACCC GCCGCTTCAC AGGCTGAGTC 600
 CAGGCCTGTG TGCTTTGTAG AGCCAGCTGC TTGCTCACAG CCACATTTCC ATTTGCATCA 660
 TTACTGCCCTT CACCTGCATA GTCACCTCTT TGATGCTGGG GAACCAAAAT GGTGATGATA 720
 15 TATAGACTTT ATGTATAGCC ACAGTTCATC CCCAACCTA GTCTTCGAAA TGTTAATATT 780
 TGATAAATCT AGAAAATGCA TTCATACAAT TACAGAATTC AAATATTGCA AAAGGATGTG 840
 20 TGTCTTTCTC CCCGAGCTCC CCGTTCCCC TTCATTGAAA ACCACCACGG TGCCATCTCT 900
 TGTGTATGCA GGGCTATGCA CCTGCAGGCA CGTGTGTATG CACTCCCCGC TTGTGTTTAC 960
 ACAAGCTGTG GGGTGTACG CATGCCTGCT TTTTCACTT AATAATACAG CTGGAGAGA 1020
 25 TTTTGTATC ACATTATAAA TCCCCTCGC TCTTTTGTAT GGCCACATAA TAACTACTGC 1080
 ATAATATGGA TACGCCTTAT TTGATTTAAC TAGTCCCTA ATGATGGACT TTTAAGTTGT 1140
 30 TTCTTTTCTT TTCTTTTCTT GCTACTGCAA ACGATGCTAT AATAAATGTC CTTATCAAAA 1200
 AAAAAAAAAA AAAAAAAAAA AAAAAANCCC NGGGGGGGGG CCCCAGGAAC NCAAT 1255

35

(2) INFORMATION FOR SEQ ID NO: 76:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGCACGAGAG AAATGTTTGA TTCTCTTTCC TATTTTAAGG GATCTTCTCT CTTGTTGATG 60
 TTGAAAACCTT ACCTTAGTGA AGATGTGTTT CAACATGCTG TTGTCCTTTA CCTGCATAAT 120
 50 CACAGCTATG CATCTATTCA AAGTGATGAT CTGTGGGATA GTTTAATGA GGTCACAAAC 180
 CAAACACTAG ATGTAAAGAG AATGATGAAA ACCTGGACCC TGCAGAAAGG ATTTCTTTTA 240
 55 GTGACTGTTT AAAAGAAAGG AAAGGAACCT TTTATACAAC AAGAGAGATT CTTTTTAAAT 300
 ATGAAGCCTG AAATTCAGCC TTCAGATACA AGGTACATGC CCTCTTCTTT TTCATGCCAT 360
 CTCTTTTGCA CTCTCAGGTG GAAATATTTT GAAGTGTMTT ATAATCATAA GTTCTTGTGA 420
 60

AACCTAACAA GATTATCCCT TCCTAAGAAT ACTTAACCTT CCTACCAAAT TAAAA

475

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(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

15

TTCTCTCTGC TCTTCGACTG CACCGCACTC GCGCGTGACC CTGACTCCCC CTAGTCAGCT 60

CAGCGGTGCT GCCATGGCGT GCGGCGGCG CGAACCRGCG TCGGGGCTCG CGGCGTGTG 120

20

GCTCTGGCGT TGCTCGCCCT GGCCCTGTGC GTGCCCGGG CCCGGGGCCG GGCTCTCGAG 180

TGGTCTCGG CGTGGTAAA CATCGAGTAC GTGGACCCGC AGACCAACCT GACGGTGTG 240

25

AGCGTCTCGG AGAGTGGCCG CTTGCGGAC AGCTCGCCA AGGAGGGCGC GCATGGCCTG 300

GTGGCGTCC CGTGGGCGCC CGGCGGAGAM CTCGARGGCT KCGCGCCCGA CACGCGCTTC 360

TTCGTGCCCC AGCCCCGCGG CCGAGGGGCC GCGCCCTGGG TCGCCCTGGT GGTCTGGGG 420

30

GCTGCACCTT TCAAGGACAA AGTGCTGGTG GCGGCGCNGA ANGAA 465

35

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 1907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45

ACATGCAGCC CAACTACAGA TTCTTATGGA ATTCTCAAG GTTGCAAGAA GAAATAAGAG 60

AGAGCAACTG GAACAGATCC AGAAGGAGCT AAGTGTTTG GAAGAGGATA TTAAGAGAGT 120

50

GGAAGAAATG AGTGGCTTAT ACTCTCCTGT CAGTGAGGAT AGCACAGTGC CTCAATTGA 180

AGCTCCTTCT CCATCACACA GTAGTATTAT TGATTCCACA GAATACAGCC AACCTCCAGG 240

TTTCAGTGGC AGTTCCTAGA CAAAGAAACA GCCTTGGTAT AATAGCACGT TAGCATCAAG 300

55

ACGAAAACGA CTTACTGCTC ATTTTGAAGA CTGGAGCAG TGTACTTTT CTACAAGGAT 360

GTCTCGTATC TCAGATGACA GTCGAACTGC AAGCCAGTTG GATGAATTC AGGAATGCTT 420

60

GTCCAAGTTT ACTCGATATA ATTCAGTACG ACCTTTAGCC ACATTGTCAT ATGCTAGTGA 480

TCTCTATAAT GGTTCAGTA TAGTCTCTAG TATGAATTT GACCGGGATT GTGACTATTT 540
 TCGGATTGCT GGAGTTACAA AGAAGATTAA AGTCTATGAA TATGACACTG TCATCCAGGA 600
 5 TGCAGTGGAT ATTCATTACC CTGAGAATGA AATGACCTGC AATTCGAAAA TCAGCTGTAT 660
 CAGTTGGAGT AGTTACCATA AGAACCTGTT AGCTAGCAGT GATTATGAAG GCACTGTTAT 720
 TTTATGGGAT GGATTCACAG GACAGAGGTC AAAGGTCTAT CAGGAGCATG AGAAGAGGTG 780
 10 TTGGAGTGTT GACTTTAATT TGATGGATCC TAAACTCTTG GCTTCAGGTT CTGATGATGC 840
 AAAAGTGAAG CTGTGGTCTA CCAATCTAGA CAACTCAGTG GCAAGCATTG AGGCAAAGGC 900
 15 TAATGTGTGC TGTGTTAAAT TCAGCCCCCTC TTCCAGATAC CATTTGCTT TCGGCTGTGC 960
 AGATCACTGT GTCCACTACT ATGATCTTCG TAACACTAAA CAGCCAATCA TGGTATTCAA 1020
 AGGACACCGT AAAGCAGTCT CTTATGCAAA GTTTGTGAGT GGTGAGGAAA TTGTCTCTGC 1080
 20 CTCAACAGAC AGTCAGCTAA AACTGTGGAA TGTAGGGAAA CCATACTGCC TACGTTCCCTT 1140
 CAAGGGTCAT ATCAATGAAA AAAACTTTGT AGGCCTGGCT TCCAATGGAG ATTATATAGC 1200
 25 TTGTGGAAGT GAAAATAACT CTCTCTACCT GTACTATAAA GGACTTTCTA AGACTTTGCT 1260
 AACTTTTAAG TTTGATACAG TCAAAAGTGT TCTCGACAAA GACCGAAAAG AAGATGATAC 1320
 AAATGAATTT GTTAGTGCTG TGTGCTGGAG GGCCTACCA GATGGGGAGT CCAATGTGCT 1380
 30 GATTGCTGCT AACAGTCAGG GTACAATTAA GGTGCTAGAA TTGGTATGAA GGGTTAACTC 1440
 AAGTCAAATT GTACTTGATC CTGCTGAAAT ACATCTGCAG CTGACAATGA GAGAAGAAAC 1500
 35 AGAAAATGTC ATGTGATGTC TCTCCCCAAA GTCATCATGG GTTTTGGATT TGTTTTGAAT 1560
 ATTTTCTTCT TTTTCTCTTT TCCCTCCTTT ATGACCTTTG GGACATTGGG AATACCCAGC 1620
 CAACTCTCCA CCATCAATGT AACTCCATGG ACATTGCTGC TCTTGSTGGT GTTATCTAAT 1680
 40 TTTTGTGATA GGGAAACAAA TTCTTTTGAA TAAAAATAA TAACAAAACA ATAAAAGTTT 1740
 ATTGAGCCAC AGTTGAGCTT GGAAAGTTT TGTCAAATGC NGCAAGAGAT AACTCTTTT 1800
 45 ANGAAGTAGC ATATGTGAAC TATAATGTAA CAGTGAATAA TTTGTAAAGT TCGTATTTCC 1860
 CAACCTCTTT GGAATTACA CATATCAATA TAAACAAAAT ATAAAGT 1907

50

(2) INFORMATION FOR SEQ ID NO: 79:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

5 GCTGGGGTGT CCCCKCSGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA 60
CCCATGACTG ATGCTTATAA ATTTGTCAA GGCAAACGAC CAATTATCTC CCCAAACCTT 120
AACTTCATGG GGCAGTTGCT AGAGTTCGAG GAAGACCTAA ACAACGGTGT GACACCGAGA 180
ATCCTTACAC CAAAGCTGAT GGGCGTGGAG ACGGTTGTGT GACAATGGTC TGGATGGAAA 240
10 GGATTGCTGC TCTCCATTAG GAGACAATGA GGAAGGAGGA TGGATTCTGG TTTTTTTTCT 300
TTCTTTTTTT TTTGTAGTT GGGAGTAAGT TTGTGAATGG AACAAACTT GTTTAAACAC 360
TTTATTTTAA ACAAGTGTA GAAGACTATA ACTTTTGATG CCATTGAGAT TCACCTCCCA 420
15 CAAACTGACA AATTAAGGAG GTTAAAGAAG TAATTTTTTT AAGCCAACAA TAAAAATATA 480
ATACAACCTG TTTCTCCCC TTTCTCTTTT AAGCTATTG TAGAGTTTAT GACTAAATAG 540
20 TCTGTGCAGG TTCATAGACC GAAGATACTA CACACTTTAA ACCAATTAAA AAGAACCAAA 600
AGTAAATAGA AAAGACATTG AATCACCAG GCCTGGGATC AACCTGGGCT GTCCACACAG 660
AAAACAAAAA CCCAACCAA CCAAGCCCTG TTGTGCTCAC TGGTGCAAAG AGAAGATCAG 720
25 GGCAGCTTAA GTGGTCTAAG RATCCTTCAG GCATTCTTTA AGGAGAAAAA OGATACCTTT 780
GATTTTGCTG GTTTCATGCT CTGGATTTTT TTTTTTTTCT CTCTCTGGG TTAAAGAGAT 840
30 TTTTTTTGAA ATAGTGAGGA ACTGACCATT ATATGCCCTC ACTGGCTTCT TGTGCAATAA 900
TATGATGTTT TAAGTGTGCA AACAAGTTAG AGCTGGCAGC TGAATGATAG ACAAATAGTG 960
CAAATTTGCC AGCTTGAGGA TAGAAAGGAA TTCAACAATA TATCAAATAC TTTCCTTCCC 1020
35 ACCTTTTCC TTTTTTTTTT TTTTTTCTGA TTTGATTCTG GTTACAGTGC CATAAACCTT 1080
GTTACATATG TATATCAGAA TGAAGAAAA AAAAATTTAT TTAATAATAT TTTTCGCAAA 1140
40 AAAAAAANNA AAAAATCGA GGGGGGCC 1168

45 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

55 AGAAAATCAC ATCCTAACAA AGAAGTCTGT CTAAGACAGT ACATCTCCTG TTGAACTTGC 60
ATCTTTCCAC AGGACTTTCT GTTTTAGGG ATGAGACTAT TCTCTGCTTC ATCAAGGAAA 120
GAGAAATGTT CAGGGTTGTA GGGATGGCAC ACTTATTAGT TCTGCCTGTC TGAAAGGTTT 180
60

	CTGCAGGACA GTTTGGTCAG AGCTGCAATT CTTAGTCCAT GGTCTAATGC TTGAGTATCT	240
	CTTCTTTCCC TTTCCTGTCT CAGGAATCAG CTGAGAATTC ATTGATTGT CATGCCTCTA	300
5	GCCCCTTACT GTGATTGTGT GGTGCACTT TCATTTGCTT TAGTTCTAGA ATCACCTGTT	360
	GACTCCTCAG ACTTCACCTA ACTTTGGAAA CTCTCTTTTG GAGGCTTCTC ATTTCCCCCT	420
10	AATTCTGTGC TGCTGAGCC CTAGAATTTT CCCACCAACG AATTATTCCA GGTAGATCCT	480
	AAGTTGCTGG ATCTAGTTGA TATTTAAACA ATATCTAGTT GATATTTCTC ATTCACTTGG	540
	ATCCAGAAAC CAGTATCTCT NAAAAACAAC CTCTCATACC TTGTGGACCT AATTTTGTGT	600
15	GCGTGTGTGT GTGCGCGCAT ATGTATATAG ACAGGCACAT CTTTTTACT TTTGTAAAAG	660
	CTTATGCCCTC TTGGTATCT ATATCTGTGA AAGTTTAAAT GATCTGCCAT AATGTCTTGG	720
	GGACCTTTGT CTCTGTGTA AATGGTACTA GAGAAAACAC CTATATTATG AGTCAATCTA	780
20	GTGGTTTTTA TTCGACATGA AGGAAATTTC CAGATAACAA CACTAACAAA CTCTCCCTTG	840
	ACTAGGGGGA CAAAGAAAAG CAAAACTGAC CATAAAAAAC AATTACCTGG TGAGAAGTTG	900
25	CATAACAGA ATTAGGTAGT ATATTGAAGA CAGCATCATT AAACAGTTAT GTTGTCTCC	960
	TTGCAAAAAA CATGTACTGA CTCCCGTTG AGTAATGCCA AGTTGTTTTT TTTATTATAA	1020
	AACTTGCCCT TCATTACATG TTTCAAAGTG GTGTGGTGGG CCAAAATATT GAAATGATGG	1080
30	AACTGACTGA TAAAGCTGTA CAAATAAGCA GTGTGCCTAA CAAGCAACAC AGTAATGTTG	1140
	ACATGCTTAA TTCACAAATG CTAATTTTAT TATAAATTGT TTGCTAAAA TACACTTTGA	1200
35	AACTATTTT CTGTATTCCA AGAGCTGAGA TCTTAGATTT TATGTAGTAT TAAGTGAAAA	1260
	AATACGAAAA TAATAAACAT TGAAG	1285

40

(2) INFORMATION FOR SEQ ID NO: 81:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	TCTCCAGCCC CAATTTCTAC GCGCACCGBA AGACGGAGGT CCTCTTCTCT TGCCTAACGC	60
	AGCCATGGCT CGTGTCCCA AGAAGCATCT GAAGCGGGTG GCAGCTCCAA AGCATTGGAT	120
55	GCTGGATAAA TTGACCGGTG TGTTTGCTCC TCGTCCATCC ACCGGTCCCC ACAAGTTGAG	180
	AGAGTGTCTC CCCCTCATCA TTTTCTGAG GAACAGACTT AAGTATGCCC TGACAGGAGA	240
60	TGAAGTAAAG AAGATTGCA TGCAGCGGTT CATTAAAATC GATGGCAAGG TCCGAACTGA	300

	TATAACCTAC CCTGCTGGAT TCATGGATGT CATCAGCATT GACAAGACGG GAGAGAATTT	360
	CCGTCTGATC TATGACACCA AGGGTCGCTT TGCTGTACAT CGTATTACAC CTGAGGAGGC	420
5	CAAGTACAAG TTGTGCAAAG TGAGAAAGAT CTTTGTGGGC ACAAAGGAA TCCCTCATCT	480
	GGTGACTCAT GATGCCCCGA CCATCCGCTA CCCCATCCC CTCATCAAGG TGAATGATAC	540
10	CATTCAGATT GATTTAGAGA CTGGCAAGAT TACTGATTTC ATCAAGTTCC ATTCACCCAG	600
	CCAGGTGGTC TCGTCACCTC AGAGGCTCCG CAGACTCCTG CCCAGGCCAG GACTGAGGCA	660
	AGCCTCAAGG CACTTCTAGG ACCTGCCTCT TCTCACCAAG ATGAACTCAC TGGTTTCTTG	720
15	GCAGCTACTG CTTTCTCTCT GTGCCACCCA CTTTGGGAG CCATTAGAAA AGGTGGCCTC	780
	TGTGGGAAT TCTAGACCCA CAGGCCAGCA GCTAGAATCC CTGGGCCTCC TGGCCCCSGG	840
20	GGAGCAGAGC CTGCCGTGCA CCGAGAGGAA GCCAGCTGCT ACTGCCAGGC TGAGCCGTCG	900
	GGGGACCTCG CTGTCCCCGC CCCCCGAGAG CTCCGGGAGC CCCAGCAGC CGGGCCTGTC	960
	CGCCCCCAC AGCCGCCAGA TCCCCGCACC CCAGGGCGCG GTGCTGGTGC AGCGGGAGAA	1020
25	GGACCTGCCG AACTACAAC TGAACCTCTT CGGCTGCGC TTCGGCAAGC GGGAGGCGGC	1080
	ACCAGGAAC CACGGCAGAA GCGCTGGCG GGGCTGAGG CGCAGGTGCG GGCAGTGAA	1140
30	CTTCAGACCC CAAAGGAGTC AGAGCATGCG GGGCGGGGGC GGGGGCGGG GACGTAGGGC	1200
	TAAGGGAGGG GCGCTGGAG CTTCCAACCC GAGGCAATAA AAGAAATGTT GCGTAACTCA	1260
35	AAAAAAAAA AAAAAAAAAA TCGGGGGGGG	1290

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	TTTATTGTAT TCTGTAACTA TAGAACTTCT ATTTWATTCT TTTTGGACT TGCTAAGTTG	60
50	TCTTTWATGG TTTTWAGTTC CATGCTGAAG TTTCAGTAT TGAATTATCC CCTTGAACAT	120
	GAGTTGTTTT ATAGACTCTR ATGATTCAAA AATCTTACAT CTTTGGTAG TCTCTTTCAT	180
55	TTGTYCACTG TTTCTGTGA TTCTWACTCA TGGTATTTTA ATTCTTCGTT WTTTTTTTC	240
	TGTTWAGAWA CATTCTTTGA AAAATAATTT GGAGGAATAT TTGATTCTTA TGAACAAGGC	300
60	ATTACTCACC AGAGAAGATT TTTTGTITYT ACCARGTGCC TARGAATGCT AACAGTCTGG	360

5 GAMCACATAG AMCACCAGGT GATGAGACAA TCCTGGGART CCTGTMTTAC TTTGGSCCAT 420
 CTTTCTCCCC AACCTGTGG GAATARTCAT YCATATCCTA RCTGCAGGCT ARAAGGTGGT 480
 10 TTATCAGAGC CCAACTTCGA GGGCTCTGGG CTTTAGCTAC TGTCACCCCA TCATAACTGA 540
 GCTTCATGGA TTGATCTCT TTTTATCTTT CAGATTTTCT TTTAAAAATC TTTGTTTTTT 600
 TTTTCTTCC GAAAGATTCC CCCAACATTA CCATCCCCA CCTTCCGTTG AATTTTTTTG 660
 15 GCTCTCATTT TGAATTTTTT AAGA 684

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 2024 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

25 CTGCAGGAAT TGGCACAGC TGGCTGGAG GCTTCATCTT TGCCGCCGCT GCCGTCGCCT 60
 TCCTGGGATT GGAGTCTCGA GCTTCTTCG TTCGTTGCGC GCGGGGTTG CGCCCTTCTC 120
 30 GCGCCTCGGG GCTCGAGGC TGGGAAGGG GTTGAGGGG GCTGTTGATC GCCGCGTTTA 180
 AGTTGCGCTC GGGCGGCCA TGTCGGCCG CGAGGTCGAG CGCCTAGTGT CGGAGCTGAG 240
 CGCGGGGACC GGAGGGGATG AGGAGGAAGA GTGGCTCTAT GGCGATGAAA ATGAAGTTGA 300
 35 AAGGCCAGAA GAAGAAAATG CCAGTGCTAA TCCTCCATCT GGAATTGAAG ATGAAACTGC 360
 TGAAAATGGT GTACAAAAC CGAAAGTGAC TGAGACCGAA GATGATAGTG ATAGTGACAG 420
 40 CGATGATGAT GAAGATGATG TTCATGTAC TATAGGAGAC ATTAAAACGG GAGCACCACA 480
 GTATGGGAGT TATGGTACAG CACCTGTAAA TCTTAACATC AAGACAGGGG GAAGAGTTTA 540
 TGGAACTACA GGGACAAAAG TCAAAGGAGT AGACCTTGAT GCACCTGGAA GCATTAAATGG 600
 45 AGTTCCACTC TTAGAGGTAG ATTTGGATTC TTTTGAAGAT AAACCATGGC GTAAACCTGG 660
 TGCTGATCTT TCTGATTATT TTAATTATGG GTTTAATGAA GATACCTGGA AAGCTTACTG 720
 50 TGAAAACAA AAGAGGATAC GAATGGGACT TGAAGTTATA CCACTAACCT CTAATACAAA 780
 TAAATTAACG GTACAGCAGG GAAGAACTGG AACTCAGAG AAAGAACTG CCCTTCCATC 840
 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 900
 55 GAGATTACCT GGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 960
 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 1020
 60 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 1080

CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 1140
 TCCACCACCG GGTTTTCCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 1200
 5 AGAAAGTGGA CATTCCTCTG GTTATGATAG TCGTTCTGCA CGTGCAATTC CATATGGCAA 1260
 TGTGCGCTTT CCCCATCTTC CTGGTCTGTC TCCTTCGTGG CCTAGTCTTG TGGACACCAG 1320
 10 CAAGCAGTGG GACTATTATG CCAGAAGAGA GAAAGACCGA GATAGAGAGA GAGACAGAGA 1380
 CAGAGAGCGA GACCGTGATC GGGACAGAGA AAGAGAACGC ACCAGAGAGA GAGAGAGGGA 1440
 GCGTGATCAC AGTCCTACAC CAAGTGTTTT CAACAGCGAT GAAGAACGAT ACAGATACAG 1500
 15 GGAATATGCA GAAAGAGGTT ATGAGCGTCA CAGAGCAAGT CGAGAAAAG AAGAACGACA 1560
 TAGAGAAAGA CGACACAGGG AGAAAGAGGA AACCAGACAT AAGTCTTCTC GAAGTAATAG 1620
 20 TAGACGTCGC CATGAAAGTG AAGAAGGAGA TAGTCACAGG AGACACAAAC ACAAAAAATC 1680
 TAAAAGAAGC AAAGAAGGAA AAGAAGCGGG CAGTGAGCCT GCCCCTGAAC AGGAGAGCAC 1740
 CGAAGCTACA CCTGCAGAAT AGGCATGGTT TTGGCCTTTT GTGTATATTA GTACCAGAAG 1800
 25 TAGATACTAT AAATCTTGTT ATTTTCTGCG ATAATGTTA AGAAATTTAC CTAAATCTT 1860
 GTTCTGTTTG TTAGTATGAA AAGTTAACTT TTTTCCAAA ATAAAAGAGT GAATTTTTC 1920
 30 TGTTAAGTTA AAAATCTTTG TCTTGTAATA TTTCAAAAAT AAAAAGACAG CAATGACTTT 1980
 ATATCCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCC 2024

35

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 931 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CGCGCCMATA GCCGGACGGG GATCTGAGCT GGCAGGATGA ATGTGGGGGT GGCACACAGC 60
 GAAGTAAACC CCAACACCCG AGTGATGAAT AGCCGAGGCA TCTGGCTGGC CTACATCATC 120
 50 TTGGTAGGAT TGCTGCATAT GGTCTACTC AGCATCCCCT TCTTCAGCAT TCCTGTTGTC 180
 TGGACCTGA CCAACGTCAT CCATAACCTG GCTACGTATG TCTTCCTTCA TACGGTGAAA 240
 55 GGGACACCCT TTGAGACTCC TGACCAAGGA AAGGCTCGGC TACTGACACA CTGGGAGCAA 300
 ATGGACTATG GGCTCCAGTT TACCTCTTCC CGCAAGTTCC TCAGCATCTC TCCTATTGTG 360
 CTCTATCTCC TGGCCAGCTT CTATACCAAG TATGATGCTG CGCACTTCCT CATCAACACA 420
 60

GCCTCATTGC TAAGTGACT GCTGCCAAG TTGCCCCAGT TCCATGGGGT TCGTGCTTT 480
GGCATCAACA AATACTGAGG GATGGGTTT GGCACAGCTC CATGGGCATG GGAAGGCAC 540
5 TGAAACAGAG GACTATAAAA CATCCTTCTC TTATTCTCCA TACTGTCTTC TACACCTTTA 600
AAGCCTGAGA ACTATACAAC CTTTCCCAGA CTCCAAGAA GAGAAGAGAT TGGCAAATGG 660
10 GGCTCCTGGG CCCAGTCTG CTAGTGGCAA GTTCTTTTGA ATCAGGAAGG CAGGTGAGGT 720
AAGGGCCAAA TCACTCTCCT CCATAGCAGG AAGCCATTG GGCAGCTCCT TTGGTGATTA 780
CATCTTTCCA TATCTTTTAC ACTTACCACC TTCCAGCTCT GTTTTGCTGT GTATTTTCT 840
15 TACAATAAT TTTTTCAGCT ATAGCTGCAG TTAATCAGG ATGGGTAGAG AGCTGTCCTC 900
ATAAGGCTGG GGGTGGGAAG ATGAATACT G 931

20

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CGGGGCCGGC GGGGTCTTCA GGTACCGGG CTGGTTACAG CAGCTCTACC CCTCACGAG 60
CAAACATGGC AGCGCAGAAG GACCAGCAGA AAGATGCCGA GCGGAAGGG CTGAGCGGCA 120
35 CGACCCTGCT GCCGAAGCTG ATTCCCTCCG GTGCAGGCCG GGAGTGGCTG GAGCGGCGCC 180
GCGCGACCAT CCGGCCCTGG AGCACCTCG TGGACCAGCA GCGCTTCTCA CGGCCCCGCA 240
40 ACCTGGGAGA GCTGTGCCAG CGCTCTGTAC GCAACGTGGA GTACTACCAG AGCAACTATG 300
TGTTCTGTGT CCTGGGCTC ATCCTGTACT GTGTGGTGAC GTCCCCTATG TTGCTGGTGG 360
CTCTGGCTGT CTTTTTCGGC GCCTGTTACA TTCTCTATCT GCGCACCTTG GAGTCCAAGC 420
45 TTGTGCTCTT TGGCCGAGAG GTGAGCCCAG CGCATCAGTA TGCTCTGGCT GGAGGCATCT 480
CCTTCCCCTT CTCTCTGGTG GCTGGTGGG GCTCGGCCGT CTCTGGGTG CTGGGAGCCA 540
50 CCCTGGTGGT CATCGGCTCC CACGCTGCCT TCCACCAGAT TGAGGCTGTG GACGGGGAGG 600
AGCTGCAGAT GGAACCGTG TGAGGTGTCT TCTGGGACCT GCGGGCCTCC CGGGCCAGCT 660
GCCCCACCCC TGCCCATGCC TGTCTGCAC GGCTCTGCTG CTCGGGCCCA CAGCGCCGTC 720
55 CCATCACAAG CCCGGGGAGG GATCCCGCT TTGAAAATAA AGCTGTTATG GGTGTCATTC 780
AGGAAAAAAA AAAAAAAGG GGGGCCCTC TAGGGGTCAA AGTTA 825

60

(2) INFORMATION FOR SEQ ID NO: 86:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATGTAAAAG GATGAAATGT GACTTCTGGT GTTTTTTAT TTCTATGGAG GGACTTTCTG 60
15 GGGACGGTTT CTGGCTCTCA GGCTCTGAGA AGCTGCAGTT TATGAGTGGC TCTGTGTGTG 120
CTGCCACCTA CTGGAGAAGC CATAAGCTGC AGCTTTAGGA AAAGGGAACC CGGGGCAGAG 180
TGTTGGGAAG TGGGATGCCA GCATGGCAGG GCTTTGGAAA ATGAGAGGTG AGAGTKTKTC 240
20 CAGGAAGGGT GTAAGGAGAG GATGGATCCT GATACATGGA TTCAGGATCA TTAGGGTCCT 300
GTCTGGGACA CTGGCCCTTC TGCTTACCTG CTCTTTCCTT CCTCCTTGGT CGGAGGAGGG 360
25 GCTGGCTCAC TGCTCTGGCT TCATTTTCCA GAGCTGCCTG CTGCAGTCAC ACTTAGGTCA 420
TCTTCTCTCA CTMTTCTCCT TTTGCCGATT AGTGGACGTG ACAGAGATGT GAATGGGGCA 480
GGGATGTCCT TTGATGGCAT CAAGACTTTA GCTTCTGGTG CGCTGTGTCC CAGCTCTGAT 540
30 TTCAGTTGCA GCCGTGATGG AMAGTTNGCA TGGAGCTGA GACTCTCACT GACAGTGAAA 600
CCCTCAAATG AACACAATCC CTGCTTTCCT GCCAAGGATC CTGTAGGGT NCCCCAGCT 660
35 TCCCCACTTT TTTTCTGTGT CCTGACAAAG AAACACAGAG TAACTTGATT GCCCTGTGAC 720
CTGGCCAGTT GCATTTCCCC TGCAGGCTTG AGCCCAAGCC AGAGCCTGA AAAGGTATTC 780
AGGTTGTTGC CCAAAACACT GAAAAAACT GCCCTGGCCC TGAACCAAAT ACCTTGAACC 840
40 CTCGTAAACT CCATACCCTG ACCCCCTTGT TTTGGATATA CCCAGGTAGA ACAACTCTCT 900
CTCACTGTCT GTTGTGAGGA TACGCTGTAG CCCACTCATT AAGTACATTC TCCTAATAAA 960
45 TGCTTTGGAC TGATCACCTT GCCAGTCTTT TGTCTPGGC AATCTATACT TTTNCTCAGA 1020
GGTTCCAAG GCCTACTGAA GGGACTTAAC ATACTCTTAA TGGCTTTCCT CTCTCTTGTT 1080
TTACCTTATG CCCTCACTTC CTGAGTTAAC CTCCCAAATA CAGGATTCAC CTGTACCCAA 1140
50 GCCCTTAGCT TCAAGAATAC AGGATCACCT GTACCCAAGC CCTTAGCTCA AGCTCTGCTT 1200
TGGAAGAACC CAACTAAGA CAGTGCTCCT GGTGCCCT 1238

55

(2) INFORMATION FOR SEQ ID NO: 87:

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

	ATTGCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA TCCCGGAGA GCATTCTTGG	60
10	CTGCTCCTCC TGACCCGGGG CTTGGTGGGG GTCGGGGAGG CCAGTTATTC CACCATCGCG	120
	CCCCTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGCG ACCGGATGCT CAGCATCTTC	180
15	TACTTTGCCA TTCCGGTGGG CAGTGGTCTG GGCTACATTG CAGGCTCCAA AGTGAAGGAT	240
	ATGGCTGGAG ACTGGCACTG GGCTCTGAGG GTGACACCG GTCTAGGAGT GGTGGCCGTT	300
	CTGTGCTGT TCCTGGTAGT GCGGGAGCCG CCAAGGGGAG CCGTGGAGCG CCACTCAGAT	360
20	TTGCCACCCC TGAACCCAC CTCGTGGTGG GCAGATCTGA GGGCTCTGGC AAGAAATCCT	420
	AGTTTCGTCC TGTCTTCCCT GGGCTTCACT GCTGTGGCCT TTGTACGGG CTCCTTGGCT	480
25	CTGTGGGCTC CGGCATTCTT GCTGCGTTCC CGCGTGGTCC TTGGGGAGAC CCCACCCTGC	540
	CTTCCCGGAG ACTCCTGCTC TTCCTCTGAC AGTCTCATCT TTGGACTCAT CACCTGCCTG	600
	ACCGGAGTCC TGGGTGTGGG CTTGGGTGTG GAGATCAGCC GCCGGCTCCG CCACTCCAAC	660
30	CCCCGGGCTG ATCCCCTGGT CTGTGCCACT GGCCTCCTGG GCTCTGCACC CTTCCTCTTC	720
	CTGTCCCTTG CTTGCGCCCG TGGTAGCATC GTGGCCACTT ATATTTTCAT CTTTATTGGA	780
35	GAGACCCTCC TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC	840
	CCTACCCGAC GCTCCACCGC CGAGGCCTTC CAGATCGTGC TGTCCACCT GCTGGGTGAT	900
	GCTGGGAGCC CTTACCTCAT TGGCCTGATC TCTGACCGCC TGCGCCGAA CTGGCCCCC	960
40	TCCTTCTTGT CCGAGTCCG GGCTCTGCAG TTCTCGCTCA TGCTCTGCGC GTTGTGTGGG	1020
	GCACTGGGCG GCGCACTTCC TGGGCACCG CATCTTCATT GAGGCCGACC GCCGGCGGGC	1080
45	ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC ACAGACGACC GGATTGTGGT	1140
	GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT GTGCTCATCT GGAGAGGCTG	1200
	CCGCTCACCT ACCTGCACAT CTGCCACAGC TGGCCCTGGG CCCACCCAC GAAGGGCCTG	1260
50	GGCCTAAACC CCTTGGCCTG GCCCAGCTTC CAGAGGGACC CTGGGCCGTG TGCCAGCTCC	1320
	CAGACACTAC ATGGGTAGCT CAGGGGAGGA GGTGGGGGTC CAGGAGGGG ATCCCTCTCC	1380
55	AACAGGGGCA GCCCAAGGG CTCGGTGCTA TTTGTAACGG GATTAAAATT TGTAGCCAGA	1440
	AAAAAAAAA AAAAAAAAAA	1460

60

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 CAGGTGCAAA GTGGGAAGTG TGAGTCCTCA GTCTTGGGCT ATTCGGCCAC GTGCCTGCCG 60
GACATGGGAC GCTGGAGGGT CAGCAGCGTG GAGTCCTGGC CTTTTCGCTC CACGGGTGGG 120
15 AAATTGCCCA TTGCCACGGC GGGAACTGGG ACTCAGGCTG CCCCCGGCC GTTCTCATC 180
CGTCCACCGG AYTCTGGGGC GCTCGCACTG GCGCTGATGT AGTTTCCTGA CCTCTGACCC 240
GTATTGTCTC CAGATTAAAG GTACGACATT TGGAGGCCCC AGCGAGAAAC GTCACCGGGA 300
20 GAAACGTCAC CGGGCGAGAG CGGKCCCGCT GTGTGCTCCC CCGGAAGGAC AGCCAGCTTG 360
TAGGGGGGAG TGCCACCTGA AAAAAAATT TCCAGGTCCC CAAAGGTGA CCGTCTTCCG 420
25 GAGACACGG ATCGACTACC ATGTGGGTGC CCACAAAAAT TYCACCTYTG AGTCCTCAAC 480
TGCTGACCCC GGGGTCAGTT CCAGAGAGAA GGAATCCCTC CTGCTTGGA GAGACCTCAC 540
ACCGTCATCA CGATGCCAAC GGCTCTGAAG GTGGATGGCA TTCCTGCGTG GATTCATCAC 600
30 TCCCGCATCA AAAAGGCCAA CRGAGCCCAA CTAGAAACAT GGGTCCCCAG GGCTGGGTCA 660
GGCCCCCTAA AACTGCACCT AAGTTGGGTG AAGCCATTAG ATTAATCTTT TTTCTTAATT 720
35 TTGTAAACA ATGCATAGCT TCTGTCAACT TATGTATCTT AAGACTCAAT ATAACCCCTT 780
TGTTATAACT GAGGGAATCA ATGATTTGAT TCCCCAAAA CACAAGTGGG GAATGTAGTG 840
TCCAACCTGG TTTTACTAA CCCTGTTTTT AGACTYTCCC TTTCCTTTAA TCACTCAGCC 900
40 TTGTTTCCAC CTGAATTGAC TCTCCCTTAG CTAAGAGCGC CAGATGGACT CCATCTTGGC 960
TCTTTCNACT GGCAGCCGCT TCCTYCAAGG ACTTAACTTG TGCAAGCTGA CTCCAGCAC 1020
45 ATCCAAGAAT GCAATTAACT GATAAGATAC TGTGGCAAGC TATATCCGCA GTTCCCAGGA 1080
ATTCGTCCAA TTGATTACAC CMAAAGCCC CGCGTCTATC ACCTTGTAAT AATCTTAAAG 1140
CCCCTGACCC TGGAATATT AACGTTCTG TAACCATTTA TCCTTTTAAC TTTTTCCTT 1200
50 ACTTATTTT TGTAAATTTG TTTTAACTAG ACCCCCCCTC TCCTTTCTAA ACCAAAGTAT 1260
AAAAGCAAAT CTAGCCCCTT CTTCAAGGCC AGAGAATTTG GAGCGTTAGC CGTCTCTTGG 1320
55 CCACCAGCTA AATAAACGGA TTCTTCATGT GTAAAAAAA AAAAAAAA CTCCGAGGGG 1380
GGGCCCGGTA CCCAA 1395

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GGCACGAGCC GGCAGCCGA GCTAGGGTGA AAAGTGGGG CGCACCAGGA TGTNNGACAG 60
AAAAGCAGAA GATGAGACTC TGTTCATTCA CTTTTCCTAG GCCCATCCTG TGGTCATCTT 120
15 TCCCCCTCCC ATCATACCTC CTCCTTCCTG GAGCCTCTGC CGGCTTGGCT GTAATGGTGG 180
CACTTACCTG GATATTTTCTG TGGGAGGATG AAAGGCGAGA CTCACCCTAC GCGGTGGGAC 240
20 AGATGGGGAG AGGAAAAAGG CAGAGATGGC CAGGAGAGGG GTGCAGGACA AACCAGAGAG 300
GTTGGGTCTG GGGAAAAGGG TGGGAGAGAA GAGGGGTGCA GGCCCTGCAG GCCGGTTAGC 360
CAGCAGCTGC GGCCTCCCGG GGCCCTTGGC ATCCAACCTC GCAGACAGGG TACCAGCCTC 420
25 CTGGTGTGTA TCATAGGATT TGTTCACATA GTGTTATGCA TGATCTTCGT AAGGTTAAGA 480
AGCCGTGGTG GTGCACCATG ACATCCAACC CGTATATATA AAGATAAATA TATATATATA 540
30 TGTATGTAAA TTATGGCAGC AGAAATTATA GCACTGAGGG CCCTGCTGCC CTGCTGGACC 600
AAGCAAAACT AAGCCTTTTG GTTGGGTAT TATGTTTCGT TTTGTTATTT GTTTGTTTTT 660
GTGGCTGTG TTAGTCTGTG ATAGCACAAG TGCCAGTCGG ATTGCTCTGT ATTACAGAAT 720
35 AGTGTTTTTA ATTATCAAT GTTCTAGTTA ATGCTACCT CAGCACCTCC TCTTAGCCTA 780
ATTTTAGGAG GTTGCCCAAT TTTGTTCTT CAATTTTACT GGTACTTTT TTGTACAAAT 840
40 CAATCTCTT CTCTCTTCT CTCCTCCCCA CCTCTCACC TTGCCCTCTC CATCTCCCTC 900
TCCCGCCCTC CCTCCTCCC TCTGGCTCCC CGTCTCATTT CTGTCCACTC CATCTCTCT 960
CCCTCTCTCC TGCTCTCTGC TGCCCCCTCC CCAGCCCACT TCCCGAGTT GTGCTTGCCG 1020
45 CTCCTTATCT GTTCTAGTTC CGAAGCAGTT TCACTCGAAG TTGTGCAGTC CTGGTTGCAG 1080
CTTCCGCAT CTGCCTTCGT TTCGTGTAGA TTGACGCGTT TCTTTGTAAT TTCAGTGTTT 1140
50 CTGACAAGAT TTAACAAAAA AAAAGGAAA AAAAAAAA AAAAAA 1186

55 (2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

5	AAAACATGCT TTCAGGGCGT CCCCTATGTA TTCGGGGGGC CCACGGACAC TCAGGCTGGA	60
	KATCGTCCT CACTGCGCTC AAGATGGCCT CAGCAGACAC CAGTTACCCA GCTGAAAGTC	120
	ACAATCCCTC CCAGAAGTCT CCCAACACTA GTGCTGACCA GAGGTGGGGC TCTCAGGCTA	180
10	GGAGTTTCAC ACACAATGAC AGGCTGCTGG GGGACATTGC AGGACCCCTT TTCCTYTCTT	240
	CTCCATGCTA GAAGCCAGCC CTAGGMAGCT GCAGTTACTC CCTGTGACTC AGCAGCAGGC	300
15	TGATTCAACA CAGCTGCCCA CACAAAGCCA GTGGTAATAC ATCTGTTTAC CTTCCTCTAT	360
	CACCCAGACA CAAGCCCTT TCCCAGGTCA AACCACAGGC CGATGCATCT CCAGTTTGAC	420
	AGTCAAATCA CTACTTCCAT TGCTACTTTA GATCAGCCAA AGTGGTGACT GCTGCAGTGT	480
20	GTGGCTATCC CTACAAGGCC CACCAAGGG ATGCCCAAAG CCAACCTTC TCCAGGGCTG	540
	CAGCAGNAGC AACCCACCA GCCTAAGTCC AGCAGAGGAC CTCCCACCCA ATGTCTTGTT	600
25	CTAATTAGAA GGGGAAGTTA GCCACAGAAA ATCAACTTAT CTATAATTAC AAAATTCTCT	660
	TGACTCACCT TAAAGTTCCT ATGACATCT ACTGCTTTTA AACCTATTTG AAAACTCTGA	720
	TACTAAAACA AATGACACTC TAAGAAAGTT TGGGAGCCCC ATGCTGAGAA CCATTCTCTG	780
30	GCAGTGAGGA TGTTTCCAGA AGCTACTTAC CTACATGTGA ATGTGCCATT TTCTTTCTCT	840
	TTGTAGAGAA AATCCCTTT ACTTTTGGGA ACAGTAATGG CAGCTTCTAG TACAGCCATT	900
35	ACAGTTTCAT ATGAGAAAAA TTAAGAATAA CTATAAAATT GTTAAATAT CCAATAATGG	960
	ATAATGATGG CCAGAAGATT TAACATACAA AGTAATTCTC AATGTAAAGC TATTCAGCTC	1020
	TTCCAGGTG AATGCCCTGT AACCCACCT GACCTTCCAC ATCATCTTCA AAAAGCAGTT	1080
40	TCTCTGTTCC CCATGATTCT CCTATAAGGT AACTCTTTAG TCCTCCATT AGCACATTTT	1140
	AAATCCTCCA AAGAATAAGT ATCATGTGAT TATTTTAGCT TTACAAAAAA AAAGTTGAAT	1200
45	GGCGTTTTAT TTTTCATGGCC TATAAGCAGG TACCTTAGTA GGCAGATAT AGGAAAAACA	1260
	AATTAGAGCA AAACAAATCC TCTACAAATC CAAGGCAGGA AAAGTGGTGG CAGAGTGAAT	1320
	CATTCTCTG TCCCTCCCAT CAGGTCAAAT CAGGAGGCTG CAGTGAATGC CTGTTCTTTG	1380
50	AATGTGTAGC AGTTGTCTCT GTAACCTCTT AAAACTTGGC TATAGGCTGT TTAGCACAGT	1440
	ACAGATTAAA GATACAGTTA CGTAAACAGC AAAGTAATTT TATAGTGCTT CATCCATTTA	1500
55	TCATGCTTTG GTTGTCTAAT TTTTCACAT ACCTTTTCT ATCAGCTCT GTTGCTTTTG	1560
	TACACATTTT TCATATTGGG GTTCGACAGG TAAACACAAA CTGCTATTTT AGTAGAAAAA	1620
60	GTTATTTGTTA TGGAATATTA AACCCAATAA ATGTATATAA GGTAAAAAA AAAAAAAAAA	1680

AAAAAAAAA AAAAAAAAAA AAAAAAATTC CTGCGGGCCG CANGCTTTT CCCTTTGGGT 1740
GAGGGGTAT TTTNGCCTG GGCACCTGGC CCTCGTTT TACAACGTCG TGANGGGGG 1800
5 AACCCGGGGG GGGTTTCCCC C 1821

10 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

20 TGCCCTTTT CCCACGATT CGGGGCTGG TGAAGGTGG AGATGTGAAC TCCAATTAAG 60
GGACTGGAGA GAGGTGAAGA ATTTGTCAGG TGGGAGATT GGATTGAAT GTGGACTTGT 120
AAATGACTTG ACCTTCCCAT CTGTGTCAA GGTACGGTT TGCTGTGGG TTCCTGGAG 180
25 AGCTTACTCA CCCCAGAGTC TTTCTTTCT CTTGCTCAA GAAGAGCCCT GTTGGTGCTT 240
TACCACCGCT TGGAGTCTCC CGAGGACACA AACAGGCAGA GAGGACGTG TAGGGAGAGT 300
30 TCTTTCCTGT TTTCTGTGCT TTCCTTTTA CAGGACTCCC GGAAGGCCAC TCATGGCCAT 360
GCCAGGAGCT TTCTCAGAAA CAGTCATAAA CGATCTCTTG AGTCTCTTTC TTGTCCTCCC 420
AGCTGAGCTT TCTTATCCA CCCTTTCTGG TGTCTATAGG AATGCATGAG AAGACCCTGG 480
35 GACGTTTTTC TGCTCTCTC TGGCCCTCCA TGGAGCCATG GGCTCGGCC TCGGCGGCTC 540
CTCACCTCA CAATTTATTT CCTCCTCCG TCCAGCCCT TCTTTTGTGT CTGAAACCG 600
40 TTTTAAATG TGACTCTCCC AGAGAAGAAG CCGCTGGCTG TATGAAACTT GACGGCGCTT 660
TTGTAAGGTG CCACCCCAA ACTTAAGGT AGCTAAACCA ATTTTAAAA GATTCAATGG 720
CTTGTTCATC CTCAGATGT AGCTATTGAT GTACACTTCG CAACGGAGTG TCTGAAATTG 780
45 TGGTGGTCCT GATTATAGG ATTTCATAAT TAAATGTCT GCTGAATAA AAAAAAAAAA 840
AAAAACTCGA GGGGGGCCG GT 862

50

(2) INFORMATION FOR SEQ ID NO: 92:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTGAGGCGAG TGAAGTGGAC TCTGAGGGCT ACCGCTACCG CCACTGCTGC GGCAGGGGCG 60
 5 TGGAGGGCAG AGGGCCGCGG AGGCCGCAGT TGCAAACATG GCTCAGAGCA GAGACGGCGG 120
 AAACCCGTTT GCCGAGCCCA GCGAGCTTGA CAACCCCTTT CAGGACCCAG CTGTGATCCA 180
 GCACCGACCC AGCCGGCAGT ATGCCACGCT TGACGTCTAC AACCCCTTTG AGACCCGGGA 240
 10 GCCACCACCA GCCTATGAGC CTCCAGCCCC TGCCCCATTG CCTCCACCTT CAGCTCCCTC 300
 CTTGCAGCCC TCGAGAAAGC TCAGCCCCAC AGAACCTAAG AACTATGGCT CATAAGCAC 360
 15 TCAGGCCTCA GCTGCAGCAG CCACAGCTGA GCTGCTGAAG AACAGGAGG AGCTCAACCG 420
 GAAGGCAGAG GAGTTGGACC GAAGGAGCGA GAGCTGCAGC ATGCTGCCCT GGGRGGCACA 480
 GCTACTCGAC AGAACAATTG GCCCCCTCTA CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT 540
 20 TTCCAGGACA TCTCCATGGA GATCCCCAA GAATTTTCTA AGACTGTATC CACCATGTAC 600
 TACCTCTGGA TGTGCAGCAC GSTGGNTCTT CTCCTGAAYT TCMTCGSCTG CCTGGCCAGT 660
 25 TCTGTGTGGA AACCAACAAT GCGAGGGCTT TGGGT 696

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1886 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

40 CAGGCCACTG ACGCTTCTTT GCGAGGGATG CAGGAGGTCC TACAGAGAAA GGCGCTTCTT 60
 GCATKTCAGA GGGCCCACAG CCTGTCACCC ACAGATCACC AAGCAGCTTT CTACCTGGCT 120
 CTGCAGCTTG CCATCTCCAG ACAGATCCCA GAGGCTCTGG GGTATGTCCG CCAAGCTCTT 180
 45 CAGCTTCAAG GTGACGATGC CAACTCCCTG CACCTCCTTG CCTCCTGCT GTCAGCACAG 240
 AAGCATTACC ATGACGCTCT GAACATCATC GACATGGCCC TGAGTGAATA CCCAGAAAAT 300
 50 TTCATACTAC TGTTTTCCAA AGTGAAGTTG CAGTCACTCT GCCGAGGCCC GGACGARGCA 360
 CTGCTGACTT GTAAGCACAT GCTGCAGATA TGGAAATCCT GCTACAACCT CACCAACCCC 420
 AGTGATTCTG GACGTGGGAG CAGCCTCTTA GATAGAACCA TTGCTGACAG ACGACAGCTT 480
 55 AATACAATTA CTTTGCCAGA CTTGAGCGAT CCCGAGACAG GCTCCGTCCA TGCCACATCG 540
 GTAGCAGCCT CAAGAGTGA GCAGGCACTG TCGGAAGTGG CTTCTGTCTT GCAGAGCATG 600
 60 CCCCTAAGCA GGGCCCGCTG CACCCCTGGA TGACGCTGCG ACAGATCTGG CTCCATGCAG 660

CTGAAGTCTA TATCGGCATC GGAAGCCTG CAGAAGCCAC AGCCTGTACC CAAGAAGCTG 720
 CCAACCTCTT CCCAATGTCC CACAATGTCC TCTACATGCG CGGCCAGATT GCTGAGCTCC 780
 5 GGGGAAGCAT GGACGAGGCG CGGCGGTGGT ATGAAGAGGC CTTAGCCANT CAGCCCCACC 840
 CACGTGAAGA GCATGCAGCG ACTTGGCCCT GATCCTTCAC CAGYTAGGCC GYTACAGTCT 900
 10 GCGGAGAAG ATCCTCCGGG ACGCGGTGCA GTGAAGTCTG ACAGCCCACG AGGTCTGGAA 960
 CGGGCTGGGC GAGGTCTCTC AAGCTCAGGG CAACGATGCG GCGGCTACGG AGTGCTTCCT 1020
 GACAGCCTTG GAGCTGGAGG CCAGCAGCCC CGCCGTGCCC TTCACCATCA TCCCCCGGT 1080
 15 GCTCTGAGCA GCGCCCTGCC AGCCTCACCT GCCGCTCAGC CTNCAGAGGC CCTGCCGGGC 1140
 ACCAGGCTT GTGCCATGCG CCCAAGGGGA TGAATCTGCC GCACTGAGGC CAGGGACGAG 1200
 20 TGTTCAGTGG GCCACAGTGA ACCAACCAAA CCAACCCCGA ATCATCGCTC TCGCCATGTG 1260
 CGTTTCTCTT GTTTTTTTTG CCAGCCCAAT GGTAGTTTCT GAACCTATTG ACATTGTTC 1320
 AAATGGATCA TGTGCCATAT TTTGTTAGTT GACATCTGAG TTTTCAGTAA AATGATTATG 1380
 25 GAATTAATCA GCAAAATGTAG AAGAATATAT TCAAAGTTAA AATTCAGTGG CAGCACAGAT 1440
 TATTTTATC AGAGCTGTAA AGAAAACAAC TGTCCITTTT TCCCCACCAC CCCTCCTGCC 1500
 30 CCACTTTGGC CCAGAAACCA AATGTGAAT TCTGTCTCC CACCTCAGCA CTAGTCCATG 1560
 CCAGGACACC AGCTGACAAT TTCTTGTTT TACTGTCAAT AATTGTACCA TGTGATCAAT 1620
 TACTGTCTC ACTTAGAACA AAGCCTGAGT CCGAGAATAT TTATATTTTA CCAATATATG 1680
 35 CCTGTTACAA GAGAAGGAAA TATGAGTTAT TTAAGTTTAA CTTTTTTATG TGAATTCAGA 1740
 GTTTATTTAT CGAGGGAAAT ATGTACAAAG AAGCTTCAA TGAATATTT ACCGACATC 1800
 40 CTTATACATG ACAGACACTT GGCTACATGG GAAGATGATG TTAATAATAA AATGATTTT 1860
 AAATGGAAAA AAAAAAAAAA AAAAAN 1886

45

(2) INFORMATION FOR SEQ ID NO: 94:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CTCAGCTACC GTATACAGTA GGACATAACC CCATTTTACA TGCACTACAC TGAGACTTGC 60
 CTCCTCTCCC CCCACATTGA AGATGTTCTT TTTTCATAAC TATATACTAT TCCATTGCAT 120
 60

	GAATATTCTG TAATTTATTT AATCCCCTAT GGATTGATAA TTAGGTTTCAT TATAGATAGA	180
	AGTGTAATTA ACATTCCCTGT ACATGTATTT TGCTACTTGT GTGGGTATTT CTGTAGGATG	240
5	AATAACTAGA AATTTATTGG ATCAGGTTTC ACATTTGCAG TTTTGAAAAC TACTACCAA	300
	AAGATTTTAC CAATTTACAA CTCCATCATT AGTAAGAATG CCTGTTTGCC TATAGTCTGC	360
10	CAACCCTGAA TCCTTAAAAA TTTTGCCAA TCTGGTAGGC AAAATTTCTT TCTTTCTTT	420
	GAATATTAAT GAGGAGGAAC ATCTTTTCAT GTTCTTGCC CATTGTCATT TCCTATTATG	480
	AATTGCTTTT GCCCATTTTC CTTTTTAA TTATGAAAGT CTAATGACTA CCTTCTCATT	540
15	GTATAAAAAA CACAGTTCTT TGAATAGAGA GACCCTTTTC TCCAATGCTA CCAATCACAT	600
	TCCACTTACC ACAGTTTAA ACATACCTCT TAGTCACCTT TCCGTACGAA TATACATACA	660
20	CATAAAACA CTTTTTACAT AAATAGGATC TCATATCTG TAGCTTTTAA AAATTTTGGT	720
	CTCAAAAAA GATAACAGGT CTTTAAATTT CTTTAATGGT TGAATATGAT TAAATACTAT	780
	GAAAATGCCA TTATTTATTC CCTTAATTTT TTTCTCTCG CTATTACATT GCCAAAGTAA	840
25	ACATCCTATT CAGATGTCTT TGTGCATGTG TGTGAATATT TCTTTAGTCT GGAGTCCAGT	900
	AAGGTGGATT TTTGGATCAA AGGGTTTGT CTCTGTCCAC CTTCAGTCTT CCCAAAGGCC	960
30	TTTATACTG TATTTTCACC AAGTGTATGG AGAATGTTCA TTTCCCATTA TAACCATACC	1020
	TACACTTGAT AGTTTTTATC TGTGGGCGA AAAAGAACCT TTTCTTATTT TGCATTTCCC	1080
	TGATTATAAA AAAAAATGGT GAGATTGGGG TTATTTTCAT GTTTATTGGC CATTTATAGT	1140
35	TTACTGTGGA TTGTTTGTAT CCCITACCTG CTTTCTATG GGTATGTGT GGATATATTG	1200
	TTTTTATTTG TTCAGCATCT CCTCCCCAT CTTCTGTAA CACAACCTTT ATTTATTGT	1260
40	GGGGAACCTA TTCCCTGTGG CTTAGGTGAG CATGTGACCA GGCCTGGCCT CCTGAGTCCC	1320
	ACAGCTTCCT AGCCACAGTG ATAAAAGAAT GGGTATATAA CTTAAGCCAG GCTAAGGAAA	1380
	GCCCTTAACA GAACCTCTGC TGGAACACT GGAAAGAAG CTTTATGGAG ATCCCAGGAA	1440
45	CCAAGGACCA TGTAGCCTG AATTTGTGCC ATGTGGAGAG AGTCTGTCTG AGGAGAAACT	1500
	CGGATGCTAG CAGAAATGGA AAGAGAACTA AGTTCGTATG TCATTTTCTT GGAGGCCCTA	1560
50	GATCCAGCTG TGCCTAAAGC CTGCCCTACT CCGGACTTTA AAGTTTTGTG AGCCAATAAA	1620
	GTCCCTTTCT TGTTAAGAT AATTGAATG AGTTTCTGTT CTGATTAATA TAGGTTATTT	1680
	GTATTTTCTT ATTGATTGT AGAAAACCTT TGTAAATTTA AATTCTAGAC TTTATGCACT	1740
55	ATATAAGTTA ATAAAATTAG CATGGCCTTC CATG	1774

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

10	GGCACGAGCG AAGGCAAGGG GGCACCAGCT CAGGACTGCA TCTGCCTGCC ATTTCCCTTC	60
	CACTCCTCCT TTCTGGAGTC TGACATTAGA AAGCCAGCGA GAAGGAAGAT TCAAACAACC	120
	AACCCTGATT TCTGCTTCT CCTTTTCATG AGTGTTCCTG TGGTCTCTGC ACCTCCTTTC	180
15	TGTCCCCCGG CAGAGGGCAG TAGAGATGGC CGGCCCAAGG CCTCRGTGGC GCGACCAGCT	240
	GCTGTTTCATG AGCATCATAG TCCTCGTGAT TGTGGTCATC TGCTTGATGT TATACGCTCT	300
20	TCTCTGGGAG GCTGGCAACC TCACTGACCT GCCCAACCTG AGAATCGGCT TCTATAACTT	360
	CTGCCTGTGG AATGAGGACA CCAGCACCTT ACAGTGTAC CAGTTCCCTG AGCTGGAAGC	420
	CCTGGGGGTG CCTCGGGTTG GCCTGGGCCT GCCCAGGCTT GCGGTGTACG GGTCCCTGGT	480
25	CCTCACCTTC TTGCCCCC AGCCTCTCCT CCTAGCCCAG TGCAACAKTG ATGAGAGAGC	540
	GTGGCGSCTG GCAGTGGGCT TCCTGGCTGT KTCCTCTGTG CTGCTGGCAG GCGGCCTGGG	600
30	CCTCTTCTTC TCCTATGTGT GGAATGGGTC ARGCTCTCCC TCCCGGGGCC TGGGTTTCTA	660
	GCTCTGGGCA GCGCCAGSC CTTACTCATC CTCTTGCTTA TAGCCATGGC TGTGTTCCCT	720
	CTGAGGGCTG AGAGGGCTGA GAGCAAGCTT GAGAGCTGCT AAAGGCTTAC GTGATTGCAA	780
35	GGGTTCAGTT CCAACCATGG TCAGAGGTGG CACATCTGCT CAGCCATCTC ATTTTACAGC	840
	TAACGCTGAT CTCCAGCTCC AGCGATGGAA CCCACTACAG AGGAGGTGGG GCCCCTGTGT	900
40	CAAAGAGGCC GAGGGGCAGC AAGGGCAGMC AGGGCACCTG TGACTTCTTA GTACAAGATT	960
	GTCTGTCTTT CAGGACTTCC AAGGCTCCCA AAGACTCCCT AAACCATGCA GCTCATTGTC	1020
	ACACCAATTC CTGCTTTAAT TAATGGATCT GAGCAAATCT TCCTCTAGCT TCAGGAGGGT	1080
45	GGGGAGGGAG TGATTGCTGT CATGGGGCCA GACTTCCAGG CTGATTTGCC AAATGCCAAA	1140
	ATGAAACCTA GCAAAGAACT TACGGCAACA AACGAGGACA TTAAAAGAGC GAGCACCTCA	1200
50	GTGTCTCTGG GGACATGGTT AAGGAGCTTC CACTCAGCCC ACCATAGTGA GTGGGCCGCC	1260
	ATAAGCCATC ACTGGAATC CAACCCAGA GGTCCAGGAG TGATCTCTGA GTGACTCAAC	1320
	AAAGACAGGA CACATGGGGT ACAAGACAA GGCTTGACTG CTTCAAAGCT TCCCTGGACC	1380
55	TGAAGCCAGA CAGGGCAGAG GCGTCCGCTG ACAAATCACT CCCATGATGA GACCCTGGAG	1440
	GACTCCAAAT CCTCGCTGTG AACAGGACTG GACGGTTGCG CACAAACAAA CGCTGCCACC	1500
60	CTCCACTTCC CAACCCAGAA CTTGGAAAGA CATTAGCACA ACTTACGCAT TGGGGAATTG	1560

	TGTGTATTTT CTAGCACTTG TGTATTGGAA AACCTGTATG GCAGTGATTT ATTCATATAT	1620
5	TCCTGTCCAA AGCCACACTG AAAACAGAGG CAGAGACATG TACTCTGGTG TGATCTCTTG	1680
	TCCTCAGTGT CTCTTCTGGG CTCCTGTCCC TCTTGCTTTA TAGCTAGCTG CCCGGGGACC	1740
	AAGGTACAGG TGAAAGCAAG GTAGCAGCTT GCGGGAGGAG GCCTGTCTGG CTTACCAGTC	1800
10	TATACACTGT GGCCTCAACC TCCCAGACAG GGCAGAGAAC TGTGGGCAGC TCGTTTGCTT	1860
	TCTAGGCTGG CTGGAGAGGT GGGAGCTCAT TGATAGACTC ATGATGGAAA CTATTTTGTGA	1920
15	AACAGGCTTC CTCCTTCAGG AGAGATCATG CGGACTAAAC TGTAGCAATT CCAGTGCACC	1980
	TGGCAGTGAT CCTTTTCTTT GCAAAGTACT GTCTCTTTGG TTCCAGTAAG TTGGACCACC	2040
	ACATGACATY ATTTTCCCTG GAACCTGGTC ACTGACTAAC ACAGACAATT GGGACTCCAG	2100
20	AGCCTCAAGA GCCAGGAGAG GGCACAGTAC ATACAGAGGG AGTCAAATGG GATCTCATTT	2160
	TGAGTCCTGC CTTCGACACA CTCAGAACGG CANCCCCAAG GCCCGGAGTG TCCAGGGCTT	2220
25	CTGGCCTGAG GTGAATCTGC CAGGCCCAAG AAGGCACAAA GGTAGGAGCA CAGAGAGCCC	2280
	CATTCCCACA GCGGKOGGC CCAGCAGCAC CAGTGAAGC TCAGCTGTCC TCCAGCTGCT	2340
	CTCGGCAGAC AGTTCAGTGC ACAGTTTATG CCCTAGCTGA AAAAGATCTC CCGGACGTAT	2400
30	TTACAGCAT CTCTTCTC CTCCTCTCA GGGCTCTGC TACAGGCAGA GCTGGAACCC	2460
	CCCCGCCTCT GGAAGGGCT GAGGCCTGGA GYCAGTGCCT GTC	2503

35

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 2801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

	CTGGAAGCC GAGGGTAGCC GAGCGGGCG GCGCTCTGG AGCGCGGGT GTCGGGCTG	60
	CCGTCCGCTC CGCCAGAAGC ACCGAGCAGC CGAGCCGGG CCCGCCGCC TCCTCCTCCA	120
50	TGAGGCCCGA GTGAGGCGG GCGGCTATAG CCGACCGCG GCGCCTTCCC CCCGGTCTT	180
	ATCGCGAGCG CACGACMAGC GSCCCTTGA GGAGGAGCG GAGGAGGAGG AGCATGTCCG	240
55	ACGGTTTCGA TCGGGCCCCA GGTGCTGGT GGGGCCGAR CCGGGCCTG GGCCGCGAG	300
	GGGGCGGGC TRAGGCGGC GGTTTYCCGA AMGGARCGR GCCTGCTGAG CGGRCGGC	360
60	ACCAGCCGCC GCAACCCAAA GCCCCGGCT TYCTGCARCC AMCGCCGCTG CGCCARCCCA	420

	GGACGACCCC GCCGCCAGGG GCCCAGTGGC AGGTCCCCGC CAGCCCCCAG CGGCCTTCCC	480
	GGCCCGGGGC GCTCCCAGAG CAAACGAGGC CCCTGAGAGC TCCACCTAGT TCACAGGATA	540
5	AAATCCCACA GCAGAACTCG GAGTCAGCAA TGGCTAAGCC CCAGGTGGTT GTAGCTCCTG	600
	TATTAATGTC TAAGCTGTCT GTGAATGCCC CTGAATTTTA CCCTTCAGGT TATTCCTCCA	660
10	GTTACACAGA ATCCTATGAG GATGGTTGTG AGGATTATCC TACTCTATCA GAATATGTTT	720
	AGGATTTTTT GAATCATCTT ACAGAGCAGC CTGGCAGTTT TGAAACTGAA ATGAACAGT	780
	TTGCAGAGAC CCTGAATGGT TGTGTTACAA CAGATGATGC TTTGCAAGAA CTTGTGGAAC	840
15	TCATCTATCA ACAGGCCACA TCTATCCCAA ATTTCTCTTA TATGGGAGCT CGCCTGTGTA	900
	ATTACCTGTC CCATCATCTG ACAATTAGCC CACAGAGTGG CAACTTCCGC CAATTGCTAC	960
20	TTCAAAGATG TCGGACTGAA TATGAAGTTA AAGATCAAGC TGCAAAAGGG GATGAAGTTA	1020
	CTCGAAAACG ATTTTCATGCA TTTGTACTCT TTCTGGGAGA ACTTTATCTT AACCTGGAGA	1080
	TCAAGGGAAC AAATGGACAG GTTACAAGAG CAGATATTCT TCAGGTTGGT CTTGAGAAAT	1140
25	TGCTGAATGC CCTGTTTTCT AATCCTATGG ATGACAATTT AATTTGTGCA GTAAAATTGT	1200
	TAAAGTTGAC AGGATCAGTT TTGGAAGATG CTTGGAAGGA AAAAGGAAAG ATGGATATGG	1260
30	AAGAAATTAT TCAGAGAATT GAAAACGTTG TCCTAGATGC AAAGTGCAGT AGAGATGTAA	1320
	AACAGATGCT CTTGAAGCTT GTAGAATCC GGTCAAGTAA CTGGGGCAGA GTCCATGCAA	1380
	CTTCAACATA TAGAGAAGCA ACACCAGAAA ATGATCCTAA CTACTTTATG AATGAACCAA	1440
35	CATTTTATAC ATCTGATGGT GTTCCTTTCA CTGCAGCTGA TCCAGATTAC CAAGAGAAAT	1500
	ACCAAGAATT ACTTGAAAGA GAGGACTTTT TTCCAGATTA TGAAGAAAAT GGAACAGATT	1560
40	TATCCGGGGC TGGTGATCCA TACTTGGATG ATATTGATGA TGAGATGGAC CCAGAGATAG	1620
	AAGAAGCTTA TGAAAAGTTT TGTTTGAAT CAGAGCGTAA GCGAAAACAG TAAAGTTAAA	1680
	TTTCAGCATA TCAGTTTTAT AAAGCAGTTT AGGTATGGTG ATTTAGCAGA ACACAAGAGA	1740
45	GCAAGAAAAT GTGTCACATC TATACCAAAT TRAGGATGTT GAGTTATGTT ACTAATGTAT	1800
	GCAACTTTAA TTTTGTAA CACTATCTGC CAAAATAAAC TTTATTCCTT ATAACCTAAA	1860
50	ATGTGATAT ATATATAATA GTTTATTATG TACAGTTAAT TCTACTGTTT TGGCTGCAAT	1920
	AAAATCGATT TTGAAATAA TGAAATGTTG AAAATTTTGC TAGTTGGTTA GATGCTTATC	1980
	CTTTAAATTC TACTTTTCTT GAGGGGAAAA AGTCTTCGTC TGGAAATACA TATTAAGTCA	2040
55	AAAATGTAGC ATCCTTTTTT AGGTAGGAGT ATTATAGCTT YCATTTTAGT TKGACATTTA	2100
	GTGTCCCAAT GAATTGAATT TCAAATATGA ATCATAATCT TGAAATCTT TAGCACTAAA	2160
60	GTCMTGGGAA TATATCAACA ACTGATTTAC ATATGCAGAT GCTATTGNA TACCAAGGGC	2220

TTTTAAATG TCATGGGGG GAAAAACCCA ACTTGGTGA ACTCCAGCT AAACAACCAA 2280
 GACTCACTG GAAGATTAT TCCAATTCTA GGAATTGTC TTTTATTTT TTATTTTTC 2340
 5 AACTGRCTAA CTTCAITACC TTAAAGCCTA GAACATTATT CTGCTTTATT TATATGGCTT 2400
 TCTCACTTTT ATTTTGTAGC AKGGGTGCA TCGACTTTT TACTAGAGAA TTTTACTAGA 2460
 TATTGTTCAT TCAAGTTTTC ATCTGCTTTA TAATTGATAC ACCTTGAGGG TCACTTTTCT 2520
 10 AATACTTTTA CTATAATGTG GTACCACCTC AGCCCTAATA AATAATATTT TTACCTAATG 2580
 TCAAATCTTT TTCCAGCTAA CTAAAACTG TGTACAAAAG GATTGCTTGT AAATATGCAT 2640
 15 GTAAATAGTT CTGTTAATAA CCCACTGTTT TACATTTGGT ACATCTGTGT CTGCTAATAC 2700
 AGTTAGCTTT CTCACCTTTC TGCTTGTGTTG TTCAGTCTGA ATTAAATTA GACTTTGAAA 2760
 ATAAAGCTTA AAAAAAAAAA AAAAAAAAAA AAAAAGCTGA G 2801
 20

(2) INFORMATION FOR SEQ ID NO: 97:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

ATGGAGCCAA AGACAATCAC TGATGCTTTG GCTTCTAGTA TAATTAAGAG TGTGCTGCCT 60
 35 AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC CAGTGAGTGA ACTGTCCCTC 120
 GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG AACAGGGACA CACGAGGCAG 180
 40 TGGCTGAAGG GGCTGGTGG AGCGTGGACT GTGACCGCG GATACTTGCT GGATCTTCAT 240
 TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAACAGTG CAAATCAACA AGTTAACAAT 300
 AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG GAGAAGGCCT TCATGCAGCC 360
 45 CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGYTTTC AGCYTTACCG CCGACCTTTA 420
 AATTTTCCAC TCAGGATATT TCTGTGATT GTCTTCATGT GTATAACATT ACTGATGCCC 480
 50 AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT GGTTAATGTC GTTTTGGACG 540
 GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTC GTCTCTATGT TTGCTGGCTA 600
 ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCTC AGGGACGCAG AGTGATCTTC 660
 55 CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT TGATAGTTGC GGTGCTGTTG 720
 GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC TGGTCATTGT GGCTCCCTTG 780
 60 AGGGTTCCTT TGGATCAGAC TCCTCTTTT TATCCATGGC AGGACTGGGC ACTTGGAGTC 840

CTGCATGCCA AAATCATGTC AGCTATAACA TTGATGGGTC CTCAGTGGTG GTTGAAAACT 900
 5 GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG ACCTTCACTA TATTGTTTCGT 960
 AAACCTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC TGTGTGTACC TTATGTCATA 1020
 GCTTCTGGTG TTGTTCCITT ACTAGGTGTT ACTGCGGAAA TGCAAAACTT AGTCCATCGG 1080
 10 CGGATTTATC CATTTTACT GATGGTCGTG GTATTGATGG CAATTTGTG CTTCCAAGTC 1140
 CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA AGTACCTTGT GGGTCAACGA 1200
 CTCGTGAACT ACGAACGGAA ATCTGGCAAA CAAGGCTCAT CTCCACCACC TCCACAGTCA 1260
 15 TCCCAAGAAT AAAGTAGTTG TCTCAACAAC TTGACCTTCC CCTTTACATG TCCTTTTMTG 1320
 TGGACTTCTC TCTTTGGAGA TTTTCCAG TGATCTCTCA GCGTTGTTTT TAAGTTAAAT 1380
 20 GTATTTGACT TGTGTTCTCA GCATTCAGAG AGCAGCGGTG TAAGATCTG CTGTTCTCCC 1440
 TGGATCTTCT GACATTACTG CTGTCTGAGA TTTGTATATG TGTAAATACA AGTTCCCTGA 1500
 TACCCTAAAA CCTTGGATTA AACAGAATGT GCATTGTACA TCTTTAAACA AAATGTATAT 1560
 25 TAATTTATTA AATCTAGTTG TCACTTTAAA AAAAAAAAAA AAAAACTCG AGGGGGGCCC 1620
 GGTACCCAAA T 1631

30

(2) INFORMATION FOR SEQ ID NO: 98:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAGCTGGG CGAGAAGTAG GGGAGGGCAC GAGCCGCCGC GGTGGCGGTT GCTATCGCTT 60
 45 CGCAGAACCT ACTCAGGCAG CCAGCTGAGA AGAGTTGAGG GAAAGTGCTG CTGCTGGGTC 120
 TGCAGACGCG ATGGATAACG TGCAGCCGAA AATAAAACAT CGCCCTTCT GCTTCAGTGT 180
 GAAAGGCCAC GTGAAGATGC TCCGGCTGGA TATTATCAAC TCACTGGTAA CAACAGTATT 240
 50 CATGCTCATC GTATCTGTGT TGGCACTGAT ACCAGAAACC ACAACATTGA CAGTTGGTGG 300
 AGGGGTGTTT GCACTTGTGA CAGCAGTATG CTGTCTTGCC GACGGGGCCC TTATTTACCG 360
 55 GAAGCTTCTG TTCAATCCCA GCGGTCCTTA CCAGAAAAAG CCTGTGCATG AAAAAAAGA 420
 AGTTTGTAA TTTTATATTA CTTTTAGTT TGATACTAAG TATTAAACAT ATTTCTGTAT 480
 TCTTCCAAAA AAAAAAAAAA AAAA 504
 60

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	GGCACGAGGG AGGGAGCCCT CTCCGTTGGG TGA	60
10	CTCTCTGT GTGCCCTTGA GACAGGCTGG	
15	CCTGCCGTT CCACAGGTA CAGTTAGGAC TTGAGTCTTT	120
	CTTTTCTGT TTTGAGTTGG	
	TGAGTGAGTG ATAGGGTAAC ATGGGCCTTC AGGATGACCC	180
20	CTTGGAACTG TGCCGAGTTC	
	CTTAAATCTC AGCTGGGATC CTGGACCTGG GAGGCCCTG	240
	TGAGGGCCAG CTCTGGAAAA	
	ACCTGGGAGT TGATGCCGA GCTGTGAAG AACTCTGCTC	300
	GAGGGCAGGG TGCCCTGGAA	
25	CACTGGTAGT TCTGGGCTG GGAGGGAGAG GGGCTCCGGC	360
	TTTCTCTGAA ATGAACACTG	
	CTCTTCAGCA GTTCAAGTAC TGTCTCTCAA AACATTTTCT	420
	AATGATTTGG TAGGTTTTC	
	TAAGCATTGT TTTTAAAG CATGGAAGG GAAGAATGCT	480
	CAAGCAAGTC ATGTTTGT	
30	TTT TCACTGCT GGGGGCTTCC CCTTCATGTG	540
	GCACCTTTGT	
	GCAGGGGCCA CCAGGCAGAC TCTTCCCACC TTCTCCCACT	600
	GAAGCACCAA GGGGCTTGA	
35	ACCGTAATTT GGCTAATCAG AGGCATTTTT TTTGTCTAG	660
	TATCTTTCAC ACTTGTCCAA	
	CCGTCTTATT TTTTAAAG TTCTGTGCT TGTATTAACA	720
	CGAACTAGA GAGAAATAGT	
	TTCTGAAGCC AGTTTATTGT GAAGATCCCC AAGGGAGGT	780
	TCGGTAGAGA AAAATAGTAA	
40	GCTGTTTAG AAATGACGA GGGCAAACAG CCAGGACGCA	840
	TTGGAGAGGA ATTTGCCAAA	
	GATCTACCTT GAGATAACGC CTGTCCAGTG TCTTCACCAC	900
	GTGAATAACC AGCGCTCCAA	
45	AGTGTTTTTC TGCTTTGAAA AAAAAATTC CACAAGCTTT	960
	TAAAGGTGCA TTTAAGAATC	
	CATGTGACTT TAGAATGGAA CTGCCGGCCC TGGCAACTGT	1020
	CACGTGTGCT AGAAGGTTCG	
	ATGCCTCTGG AATGCATGTG ATACTCATCT CCATTTTGT	1080
	TCCTTGATG CATTTTGT	
50	CTTTTAGCAG ATCTGTCCCT GTGGTGGTG TCTAAGAAGT	1140
	CGGACACCTT GGTTTTGTG	
	TTAGATTGAG CTGGGAGCT GCAATCAGCT TCTTTATATG	1200
	CAATTAGGC ACGACCCATC	
55	TGTGGTTTCT GGTGGTGGC TAATGAAGTG AGGGGAGGGA	1260
	GGGATGTCAC CCCAAAAGTA	
	GGCCCTCCCA TTGGCTTTGG CCAGGCCAGA CACTTCACAT	1320
	CGTTTACATG GTTCTGTGTA	
	ATTTTAAAGT TTATGTGTAT AAAGCGAAGC TGTCTGTG	1380
	AAACTGTATA TTTGTAAAT	
60	AAATATATTG CTAATTGAAA AAAAAAAAAA AAAAAA	1416

5 (2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

15 GGCTAGGACA ATTTTGGTGC TTTACCTATC TCTGCAAAGA CTGGAGAATT TGGCATACCA 60
TTAATTACAA CCACCAATCA TATCCAACAA AAGTACCCTA AAAGAAGGAC CAGTGGCCAC 120
TCTCGAAAAA ATTTAAGTAT CAGAAGATTA AAAAGATTTT AGGATTGGA AGCTTGATT 180
20 GTCTTCCCC AATAATCATT GTTGTATCTC CAAATAGTAG CCTTATATTA GCAATRGACA 240
GATCATTGGT TCTCCATATC TGATCATATG TTAATACTTT GGAATCAGTA TTTGGGCAAA 300
25 TTCAAGCATT TATGCAGTGG ATATAAATGG AAATATAAAA ATATTGCCA ACCTGTCTCA 360
GTAACCTATC ATATCTCTGT GNATCCTCAA GGAAAGCACT TTTGCTTTTA CTTAGAAAGC 420
GTTTCAGATT TGCTTTATAG ACTCCTGCTG TCTTCAGTAC CTGATAAAAC TTTAACCAGG 480
30 GAAGCATTAA ACACAGTGCA GCAGCTTTTG CCCAGGCTTC TAAGTTCCTG CCGGCAGCAT 540
TTATCAATGT AAGAACTAGG ATGCTTCCTG CAGTGGCACT ACCTTCCCCT AGAGCTGGAG 600
35 CATGCTGCTT GGCCTTAAGC CCCAGCATGA TGAGGCTTCC CTCCTGCCAG GTCAGTAAAA 660
GTTAGAGAGC TCAGAATTGG GTCTTGCTTG GGTGCAGGTG GCAGGGTTTG CTGAAACCCC 720
TAAAGAGAAG TCACCAAGGG AGGCAGGTAA TGAATGTTTC CAGAATCAGT CKGATACTCA 780
40 TAGCAATTTT TGGCTATCTT TCAATGTTG AATTTCTGGA TGCTGAGAGG GACTTTGATT 840
TGATATCATT AAATCCAGGA CAGTCCCAAG AAGTGCTTGG AGTCTCGGCT CTGACAGCCC 900
45 AAGAAGGGAA ATAACTTGTA TTAAGGAACA ACTATGAGCC AGGCCCTGAG CTGTCTCTTA 960
GATAATAAAA CAGATGGGGA GTGGAAGAGT CATTTGCTTC AAGTTATACA GCTAGGAAAT 1020
ACTCAAGCCA AATCTTGAAC GCAGCTCCCC CTAATTCTGT GGACAGGCAC TTTGTACCAC 1080
50 ACACCATGGT CCACCTAAAA ACAGAAGGAT AAAAAGACTT CAGGTTTTCC CACTGTGTGC 1140
TGACCATCCC AATTTATGAA TCTTCTTCAA AATGACATTT CACAGTTATA GTTAGGGCTC 1200
55 AGAAATGGCA TTGAGGTAGC CTTATTTCTC CCCTTTAGCA GATGCTTTAA GTACACATTG 1260
CTGACTTGAG CCCACCCCA GGAGTTAGGA GAACATTTCC TTTTTCATGC CATCTTCCAT 1320
60 AAATAAGGTG TTTCTTGGCC TTCAAAGATA TAGAACTTTG CAGCAGTAGT AAAAGTGAAG 1380

	GGTGTCTGCG TCTCTACTCA ACTTTATTTG AAAATGTCCTG CAGCTTCACT CCTGTAGAAA	1440
	AGGAAATCTT CATATTTTAG TAAACTTAGC CGCCAGTGTA CTCTGTGAGG ATGTGGCAAT	1500
5	TCAAAGTCCA GTGAATCTGG CTCCTTACT GATTCCTGGT TTTAGTGTGT GTGTCGGGGG	1560
	AGTGTGTACC TATATATAAA GGACAAGTGT GATATGTGTG TATATGTATA TACATACATA	1620
10	CATGTCCACA CACACACACA CAATATTTGA GAGCTAAGGA AAACCTCAAAG CAGCCCCCTC	1680
	ATTATCTTGC GTACTACTTC AAAGATTTCT GTCAGCCCTA ATTACAAGTG TCACCATATA	1740
	GTGCGGCTT AGGTACTTGC TTACAGGAAG AGCAATTCCT TAGCAAAGGT CATTAGCTCC	1800
15	TAAGGCACTG AGTCAAAGTG ACAGCCCTGA AGGAAATTGC ACTCCAGCCC TCCTCCAGGA	1860
	TGTCTAATAA GATGGGAAAC TTGGATGCCC AGCCATTTTG GTGACCTGAG AGTCTAACTA	1920
20	CTCCAGTTAG ACCTAAGGGC ACAAATGCAG AATTCATGAC CTTGTAGTTG TGGCAGGGTC	1980
	TAGGAAGTCC TCTCTCCCA AGTAGAAAT ATTCTCTTGC CATTCCTGAA ATTCCACATT	2040
	CATATAATGG CTGTGCAATA CATGCTTCTC AATAAGAAAA TTAAGTGCAT GTTTACTGTG	2100
25	TGCTGATCAC ATCAGATTTT TATGTTTAAA AAAATCTCAT TATGGNTTGA GTCCAGCCCA	2160
	GCTCTAAGAG AAAAAGAAGG CCCATATGGG AGACTTCAGT CTCATTATTA TTGCCTTTAT	2220
30	CCAGCAGTGC TTATRAAGCC CCCTACCCCTG TCCCATTCOA GAAACCATAA GACTCAGGCA	2280
	GTTCITGATT CTGGAGGCCT GCCTGGTAAG ATAAGATAGT ATAATTTGGA ACTGAGAACA	2340
	TACCAGAAAC AGCAGAACGA GGGCCAGAGC AGAAAAATGA AAATAAGTGG AGACACTTAT	2400
35	GGATACATTG GTGCAAAAAA AGCCACGGGS CCCATACTGG GCTTGATATG ACTTTGAGGG	2460
	GACAGCAGAT TAATACTTAA TGAGGGTTAA ACCTGACCAG TCTTTCTACA GTGACAGGCC	2520
40	ACACTGCATG AATGGGGAGA ACCAATGAAT CCATTGTCTT CTGCCTATTT TCCTGTGCAC	2580
	AGTCACATTC CCTCCTTAGG AATCTTCCCC TTCCACCCTT TACATTAAAC AAGGGAACAC	2640
	TGAATCTTTC AAGGGAATTA CACGTTTGGG TTAATGTTTC AGTATATCAT TTTCATACTG	2700
45	TAAATTATTT TGTAAGAGAG ATTTACTGCT ATCCCAGGAT GTTCGGACTT GGTGCCCTCG	2760
	TGCATTGGA AATCAATAAA CTATTACTGG AAATGCCAAA AAAAAAAAAA AAAAAAAAAAN	2820
50	NAAAAAATC GAGGGGGGCC CGTACCC	2847

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

5	GAGATTGGTG GAGGAGAGTA AATAATCTAG AGGCAAGAGT TCAGTGAGGG CCAAGGGGGA	60
	CCCCCAGAAA AAGGTATGGA GCTAACTCAT CTCTTTTACA AGGGGTGGCC ATGACTTACT	120
	GTTCGAAAGT ACTCAGTGTA TATTTAATGT TGATTGTGTA ATTTTAGTGA CGAGAGGGAA	180
10	GAACAATTTT ACTTCTGTCC TTATTTCACT TGCTGAAAAG CTGTGGGACA AAATGTATGG	240
	AATAGACAAG GCCACTTTCT TTGTGATTTC TGCTTTTCAT GCATATTATT TTATTTACCC	300
	ATAATTTCCA AGAGGTTTGG CGTTCGCTC TCCTGCTTTT TTCTTTTCATC CACCCCTTTC	360
15	CTTTTTTTGG AAGGGGGTTA TATATGAGAG TTCATTGAAG AAGTCCAGTG AGGCTGAAGT	420
	AAAGGGGCAA GATAGGGCAG TTAACATAAG AGCACTTTAT TTCTTTGAAG CCTTTCTAAG	480
20	AAAGAAATGG GGGTGCGAGT GGCTTGAATC TCCCATGATG TTGGAGGGCA CTTAGTGGGG	540
	TTGAAGTATG ACATAATATT TCCCATGCGG GAAAGGAGAA TTTCTCTTAG AGGGTGCGAA	600
	AATGCCTTTG CCCAGTGTCC CTATTTTAGG CATCTTTTCC TTCCTTATTC CTTCAGTCA	660
25	GGGTGTGTCC TATACAAAAC TTCCCATCAG TTCTCCTCAA TATTCCCCAT TTGTAAATGA	720
	TCACTTCTCT TTTCTAAACC CTTTTCTGT TCAGATCCAT ACAGGATTTG CAAGGGTAGG	780
30	ATCATACATG CAAATGCCCC TTGTTTCATCT GTGTCTTCTG CAACTAGTC TCATGAAGAA	840
	TTCTGGCGTG CAGCAGGGTA GCTGAAGTTT GGGTCTGGGA CTGGAGATTG GCCATTAGGC	900
	NTCNCTGAGA TTCCAGCTCC CTTCCACCAA GCCCAGTCTT GCTACGTGGC ACAGGGCAAA	960
35	CCTGACTCCC TTGGGGCTC AGTTTCCCCT CCCCTTCATG AAATGAAAAG AATACTACTT	1020
	TTTCTTGTG GTCTAGCATT GCTGGACACA AAGTGTAGTC ATTATGTGTG TATTGGGTGA	1080
40	TGTGTGCAAA ACTGCAGAAG CTCACTGCCT ATAAGAGGAA ATAAGAGAGA AAGTGGAGGA	1140
	GAGGGACAAA AGGAGTAATT ATTGGTATA GATCCACCCA TCCCAACCTT TCTCTCCTCA	1200
	GTCCCTGCTC CTCATGTTTC TGGTTTGGTG AGTCCTTTGT GCCACCACCC ATAATGCTTT	1260
45	GCATGCTGTC ATCCTGGGAA GGGGTATAT GGTCTCACA GTTGTGTGCA TTGTTTTTTT	1320
	GCATGCTTTC TTAATAAAAA AAAAAAAAAA ATGTTTANAG TTTTATCTTA AAAAAAAAAA	1380
50	AAAAAAAAA ACCC	1394

55 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

5 GGMRCGAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC CGGATTATTC TATTTCCCCT 60
 CCCTCTCTCC CGCCCCGTAT CTC'TTTTCAC CCTTCTCCCA CCCTCGCTCG CGTACCATGG 120
 CGGAGCGTCG GCGGCCACTC AGTCCCATTG CATCTCCTCG TCGTCCTTCG GAGCCGAGCC 180
 10 GTCCGCGCCC GCGCGCGGCG GGAGCCCAGG AGCCTGCCCC GCCCTGGGGA CGAAGAGCTG 240
 CAGCTCCTCC TGTGCGGTGC ACGATCTGAT TTTCTGGAGA GATGTGAAGA AGACTGGGTT 300
 15 TGTCTTTGGA CACGCTGATC ATGCTGCTTT CCTTGGCAGC TTTCAGTGTC ATCARTGTGG 360
 GTTCTTTAMC TCATCCTGGC TCTTCTCTCT GTCACCATCA RCTTCAGGAT CTACAAGTCC 420
 GTCATCCAAG CTGTWCAGAA RTCAGAARAA GGCCATCCAW TCCAAAGCCT ACCTGGACGT 480
 20 AGACATTACT CTGTCTCAG AAGCTTTCCA TAATTACATG AATGCTGCCA TGGTGACAT 540
 CAACAGGGCC CTGAAACTCA TTATTCGTCT CTTTCTGGTA GAAGATCTGG TTGACTCCTT 600
 25 GAAGCTGGCT GTCTTCATGT GGCTGATGAC CTATGTTGGT GCTGTTTTTA ACGGAATCAC 660
 CCTTCTAATT CTGTCTGAAC TGCTCATTTT CAGTGTCCCG ATTGTCTATG AGAAGTACAA 720
 GACCCAGATT GATCACTATG TTGGCATCGC CCGAGATCAG ACCAAGTCAA TTGTTGAAAA 780
 30 GATCCCAAGC AAAA 794

35

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1544 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45 TTGCTTGCT AGTCTGAACC AAAGAGTTGT TTGGGCATTT GCTGTGTTGG CCATTTCTGG 60
 AGCAAGAGGG TCTTCTTCTT CCTTCCCCCA GCCAGCCAGC TGTCTGGGG CCAGGCTTTC 120
 50 CTGGGTGGAA AGAAGTATAC CTTTCCCTGG GGCCCTAGGA TAGCAAAGTG AGCCATAGTG 180
 GGCCAGGCTG CCCTCCATGC TGGGCCCCAG CCCAGGTCTG CACTCGCCTG GATCACCTTC 240
 TTTGAGCCTT AGCCATCTCC TGTCAAGTAG GAATGAACTT GCCAGCCTTC AGGYTCGTTT 300
 55 AGCTATGACC ATCTGTGCGG TCAGGGTACA CTCAGCTCTC CTCCCCAACT CCAGCAGCCT 360
 TTAAGAAGTG TCCCTTTGGC GCCCCCTGGA GGCAGAGCAC TGAGCTGGAC CCTGGGTAGA 420
 60 CTCCACAGG GAGGACGGAG CTGGCCTCAG GAGTGGGACA CCCAGACTTG GCAGGGCCTT 480

CAAGAGGCCT GTGTGGGGC CCCAGGAATC CTTAGCTGAA GCGGGGAGAC TCACTCTCCA 540
TCTCAGGAAA TTCTAGCCCT TGCCCTCAGG GAGCCACGGT TGAGGGTGAG GCCCAACACC 600
5 TGCCCTTAGGG CCCTGGGTGG GCAAGTCTGG GCCCTGGGGT AGGGAGGGAG ACTCAGGCCC 660
ACACTTGGGT ATTTTCTAAT TTCAGACAAA CACACACTCA GCGCGCACTC ACTGATTCCT 720
10 ACACATTGCC AAGATTTCAC ACATGTGACC AGGGGCCACC AAAGTCCCTG TGACCTTTGT 780
GACTAGGATC CTAATTCTC TATTTCTCC TGGGTGCCTG GGTCTGTGTC ACCTGGGGCA 840
GTGTGGATAA TGTTAGTTC TGTGACACTG TTTTGGGG GTGGCACCTG GTTCTCCGAT 900
15 GCCTGGGCTG GTGTCAGGCC CAGGACTGTA GTGCTGGGAG CAGTAAAGCT CAGCTCTGTG 960
TAATGAGTGA TGCTATGGCT TGCTCGTGTC TTATGATCCA ATCCTTTTCT ACATCAGCCC 1020
20 TTGTTTGT TTATGGCTAG TCTTATCTGG CCTGGTTATT TCCTTGCGGG GAGGAGAGGG 1080
TTTGCTAATC TGCTCCAGC CCAACCTATT ACCACCCAC CTCGCTGGGA CCTACTGCTC 1140
GGGAGGCAGC AGACAGGGAG CCACCAGCAG TGGCTTCCTG GCCCTGTGCT GGGGGTGGG 1200
25 GGAAGCTGGG GGCACATGTG GCCCTGCGCT TCTGAGCAGC TCCCAGTGCC AGGGCTTTGA 1260
GACTTTCCCA CATGATAAAA GAAAAGGGAG GTACAGAAGT TCCAATTCCC TTTTATTTT 1320
30 GCTGGTGGT ATCTGTAAAT GTTTAATAAA TATCTGAGCA TGTATCTATC AACGCCAAGA 1380
ATTTCAAAGT CTCCTTCAAC AATATGAGGC TTTTAGGATG TTTATATTCC TTCATCCCTC 1440
TTGTTTCCCA GGTTTTGCGG GGAAGGAGG TCTGGAATTA TAGATACAGC TTATTATTAA 1500
35 ATTTGTCTT GCATAAAAAA AAAAAAAAAA AACNCNNGGG GGGG 1544

40

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

50

ACCCACGCGT CCGNCTTGTC CACCCGGGGG CGTGGGAGTG AGGTACCAGA TTCAGCCCAT 60
TTGGCCCCGA CGCCTCTGTT CTCGGAATCC GGTGCTGCG GATTGAGGTC CCGGTTCTTA 120
55 AGGTGGGTCG CTGTCCACCC GGGGGCGTGG GAGTGAGGTA CCAGATTGAG CCCATTGGC 180
CCCCACGCCT CTGTTCTCGG AATCCGGGTG CTGCGGATTG AGGTCCCGGT TCCTAACGGA 240
CTGCAAGATG GAGGAAGGCG GGAACCTAGG AGGCCTGATT AAGATGGTCC ATCTACTGGT 300

60

CTTGTCAGGT GCCTGGGGCA TGCAAAATGTG GGTGACCTTC GTCTCAGGCT TTCCTGCTTT 360
TCCGAAGCCT TCCCCGACAT ACCCTCGGAC TAGTGCAGAG CAAACTCTTC CCCTTCTACT 420
5 TCCACATCTC CATGGGCTGT GCCTTCATCA ACCTCTGCAT CTTGGCTTCA CAGCATGCTT 480
GGGCTCAGCT CACATTCTGG GAGGCCAGCC AGCTTTACCT GCTGTTCCCTG AGCCTTACGC 540
10 TGGCCACTGT CAACGCCCCG TGGCTGGAAC CCCGCACCAC AGCTGCCATG TGGGCCCTGC 600
AAACCGTGGG AGAAGGAGCG AGGCCTGGGT GGGGAGGTAC CAGGCAGCCA ACAGGTTCCC 660
GATCCTTAAC GCCAGNTGCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAAATTC 720
15 TTCCGCTACC ATGGGCTGTC CTCTCTTTGC AATCTGGGCT GCGTCCTGAG CAATGGGCTC 780
TGTCTCGCTG GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 840
AATGCTTCTT CAGAAAAAAA AAAAAAAAAA A 871
20

25 (2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGCAGAGTT ATAGCATGGC ATTCATACTT TTGTTTTATT GCCTCATGAC TTTTTTGAGT 60
35 TTAGAACAAA ACAGTGCAAC CGTAGAGCCT TCTTCCCATG AAATTTTGCA TCTGCTCCAA 120
AACTGCTTTG AGTTACTCAG AACTTCAACC TCCCAATGCA CTGAAGGCAT TCCTTGTCAA 180
40 AGATACCAGA ATGGGTTACA CATTTAACCT GGCAAACATT GAAGAACTCT TAATGTTTTT 240
TTTTTAATAA GAATGACGCC CCACTTTGGG GACTAAAATT GTGCTATGC CGAGAAGCAG 300
TCTAAAATT ATTTTTTTAA AAAGAGAAAC TGCCCCATTA TTTTGGTGGG GTTGGTTTTT 360
45 AATTNTAAT NTGAAAAATT TTTTGGGGT TTTTGGGGCC ATGG 404

50

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1542 base pairs
55 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
60

	GTCAGACAGG TGGAGCCGCC GGGGCAGGAG TCTCAAAGAG CCAGGCTCCA GGAGAGGAAG	60
	GGCTCTRCGA GAGGAGAGAG GAGAGCGCTG GAGAGGAGAG GCTGGAGAGT CCTTAGCCAG	120
5	GATGGAGGCT GTTGTGAACT TGTACCAAGA GGTGATGAAG CACGCAGATC CCCGGATCCA	180
	GGGCTACCCT CTGATGGGGT CCCCTTGCT AATGACCTCC ATTCTCCTGA CCTACGTGTA	240
10	CTTCGTCTC TCACTTGGGC CTCGCATCAT GGCTAATCGG AAGCCCTTCC AGCTCCGTGG	300
	CTTCATGATT GTCTACAACT TCTCACTGGT GGCACCTCC CTCTACATTG TCTATGAGTT	360
	CCTGATGTCG GGTGGCTGA GCACCTATAC CTGGCGCTGT GACCTGTGG ACTATTCCAA	420
15	CAGCCCTGAG GCACTTAGGA TGGTTCGGGT GGCTGGCTC TTCCTCTTCT CCAAGTTCAT	480
	TGAGCTGATG GACACAGTGA TCTTTATTCT CCGAAAGAAA GACGGGCAGG TGACCTTCCT	540
	ACATGCTTTC CATCACTCTG TGCTTCCCTG GAGCTGGTGG TGGGGGTAA AGATTGCCCC	600
20	GGGAGGAATG GGCTCTTTC ATGCCATGAT AAACCTCTCC GTGCATGTCA TAATGTACCT	660
	GTACTACGGA TTATCTGCCT TTGGCCCTGT GGCACAACCC TACCTTTGGT GGAAAAAGCA	720
25	CATGACAGCC ATTCACTGA TCCAGTTTGT CCTGGTCTCA CTGCACATCT CCCAGTACTA	780
	CTTTATGTCC AGCTGTAACCT ACCAGTACCC AGTCATTATT CACCTCATCT GGATGTATGG	840
	CACCATCTTC TTCATGCTGT TCTCCAACCT CTGGTATCAC TCTTATACCA AGGGCAAGCG	900
30	GCTGCCCCGT GCACTTCAGC AAAATGGAGC TCCAGGTATT GCCAAGGTCA AGGCCAACTG	960
	AGAAGCATGG CCTAGATAGG CGCCACCTA AGTGCCTCAG GACTGCACCT TAGGGCAGTG	1020
35	TCCGTCAGTG CCTCTCCAC CTACACCTGT GACCAAGGCT TATGTGGTCA GGA CTGAGCA	1080
	GGGGACTGGC CCTCCCCTCC CCACAGCTGC TCTACAGGGA CCACGGCTTT GGTTCCTCAC	1140
	CCACTTCCCC CGGCAGCTC CAGGGATGTG GCCTCATTGC TGTCTGCCAC TCCAGAGCTG	1200
40	GGGGCTAAAA GGGCTGTACA GTTATTTCCT CCTCCCTGCC TTAAAACTTG GGAGAGGAGC	1260
	ACTCAGGGCT GGCCCCACAA AGGGTCTCGT GGCTTTTTC CTCACACAGA AGAGGTCAGC	1320
45	AATAATGTCA CTGTGGACCC AGTCTCACTC CTCCACCCCA CAACTGAAG CAGTAGCTTC	1380
	TGGGCCAAAG GTCAGGGTGG GCGGGGGCCT GGAATACAG CCTGTGAGG CTGCTTACTC	1440
	AACTGTGTC TTAATTAAAA GTGACAGAGG AAACCANAAA AAAAAAAAAA AAAA ACTCGA	1500
50	GGGGGGCCCG TACCCAAATC GCCGGTATGA TCGTAAACAA TC	1542

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(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

5	GGTAGCTCAN TGCAGTGAAA TAGTCTTACT GGAAACAAAG CCCTTTATCA AGAATAATTA	60
	ACTCTTCCCT TTTCTTTTGT GAGAGGTGCT TTGTTTCTGA TCGGACCATT TCACTGCAGC	120
10	AAGCAACACA GTATTCTRAG CAGAAGATCG GGACTTGAGG CCATGTTGCG GAGGGCCAGT	180
	RACATTATCT GGACTCTGGA GTGTGAGGAA TATGGACTCC ACTCTTCACT ATATTACAR	240
	CGATTTCAGAC TTGAGCAACA ATAGCAGTTT TAGCCCTGAT GAGGAAAGGA GAACTAAAGT	300
15	ACAAGATGTT GTACCTCAGG CGTTGTTAGA TCAGTATTTA TCTATGACTG ACCCTTCTCG	360
	TGCACAGACG GTTGACACTG AAATTGCTAA GCACTGTGCA TATAGCCTCC CTGGTGTGGC	420
20	CTTGACACTC GGAAGACAGA ATTGGCACTG CCGAGAGAG ACGTATGRGA CTYTGCCCTC	480
	AGACATGCAG TGGAAAGTTC GACCGAACTC TAGCATTCTC CATCCACGRG CTTGCAGTTA	540
	TTCTTGAGGA TCAATTGACA GCTGCAGATC TGGTTCCAAT TTTTAATGGA TTTTAAAAG	600
25	ACCTCGATGA AGTCAGGATA GGTGTTCTTA AACACTTGCA TGATTTTCTG AAGCTTCTTC	660
	ATATTGACAA AAGAAGAGAA TATCTTTATC AACTTCAGGA GTTTTGTGTG ACAGATAATA	720
30	GTAGAAATTG GCGGTTTCGA GCTGAACTGG CTGAACAGCT GATTTTACTT CTAGAGTTAT	780
	ATAGTCCAG AGATGTTTAT GACTATTTAC GTCCCATGTC TCTGAATCTG TGTGCAGACA	840
	AAGTTTCTTC TGTTCGTTGG ATTTCTTACA AGTTGGTCAG CGAGATGGTG AAGAAGCTGC	900
35	ACGCGGCAAC ACCACCAACG TTCGGAGTGG ACCTCATCAA TGAGCTTGIG GAGAACTTTG	960
	GCAGATGTCC CAAGTGGTCT GGTGCGCAAG CCTTTGTCTT TGTCTGCCAG ACTGTCATTG	1020
40	AGGATGACTG CCTTCCCATG GACCAGTTTG CTGTGCATCT CATGCCGCAT CTGCTAACCT	1080
	TAGCAAATGA CAGGGTTCCT AACGTGCGAG TGCTGCTTGC AAAGACATTA AGACAAACTC	1140
	TACTAGAAAA AGACTATTTT TTGGCCTCTG CCAGCTGCCA CCAGGAGGCT GTGGAGCAGA	1200
45	CCATCATGGC TCTTCAGATG GACCGTGACA GCGATGTCAA GTATTTTGCA AGCATCCACC	1260
	CTGCCAGTAC CAAAATCTCC GAAGATGCCA TGAGCACAGC GTCCTCAACC TACTAGAAGG	1320
50	CTTGAATCTC GGTGTCTTTC CTGCTTCCAT GAGAGCCGAG GTTCAGTGGG CATTCGCCAC	1380
	GCATGTGACC TGGGATAGCT TTCGGGGGAG GAGAGACCTT CCTCTCCTGC GGACTTCATT	1440
	GCAGGTGCAA GTTGCCTACA CCCAATACCA GGGATTTCOA GAGTCAAGAG AAAGTACAGT	1500
55	AAACACTATT ATCTTATCTT GACTTTAAKG KKWAWKMMWW KCTCAGMSRA TTATAMITSW	1560
	CWMMRARGSM WYMAAWSCTK SWGCTCYWCC KSRSTGRMKG MMRCTCTAGA AYTRGYRGAK	1620
60	CMYYYKSGCT KMWGGAARKS GGCASGAGCC AGAGACCTGC ATTGCTTTCTT CCTGGTTTPTA	1680

TTTAACAATC GACAAATGAA ATTCTTACAG CCTGAAGGCA GACGTGTGCC CAGATGTGAA 1740
AGAGACCTTC AGTATCAGCC CTAACCTCTC TCTCCCAGGA AGGACTTGCT GGGCTCTGTG 1800
5 GCCAGCTGTC CAGCCAGCC CTGTGTGTGA ATCGTTTGTG ACGTGTGCAA ATGGGAAAGG 1860
AGGGGTTTTT ACATCTCCTA AAGGACCTGA TGCCAACACA AGTAGGATTG ACTTAAACTC 1920
10 TTAAGCGCAG CATATTGCTG TACACATTTA CAGAATGGTT GCTGAGTGTC TGTGTCTGAT 1980
TTTTTCATGC TGGTCATGAC CTGAAGGAAA TTTATTAGAC GTATAATGTA TGTCTGGTGT 2040
TTTTAACTTG ATCATGATCA GCTCTGAGGT GCAACTTCTT CACATACTGT ACATACCTGT 2100
15 GACCACTCTT GGGAGTGCTG CAGTCTTTAA TCATGCTGTT TAAACTGTTG TGGCACAAGT 2160
TCTCTGTGCC AAATAAAATT TATTAATAAG ATCTATAGAG AGAGATATAT ACACTTTTGA 2220
20 TTGTTTTCTA GATGTCTACC AATAAATGCA ATTTGTGACC TGTAAAAAA AAWAAAAAA 2280
ACTCGAGGGG GGCCCGGTAC CCAAATCGCC GATATGATCT AANCATC 2327

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(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGCCGAG GCGCAACAGC CGTTCTGTCA GCTCTGGGTC CAACCGGACT AGCGAANATC 60
TTCTTCATCC TCATCATCGT CTTCCTCATC CCGATCTCGG TCCAGGTCCC TCTCCCCCCC 120
40 ACACAAGAGG TGGCGAAGGT CCAGCTGTAG TTCTCTGGA CGTTCTCGAA GATGCTCTTC 180
CTCTCTCTCG TCATCATCTT CCTCTTCGTC TTCTTCATCC TCATCATCCA GTTCTCGAAG 240
45 CCGCTCACGA ATCCCCATCC CCCC GCCGGA GRAAGTGACA GGAGGCGGCG GTACAGCTCT 300
TATCGTTCAC ATGACCATT A CCAAAGGCAA AGAGTGCTAC AAAAGGAGCG TGCAATAGAA 360
GAAAGAAGGG TGGTCTTCAT TGGAAAGATA CCTGGCCGCA TGA CTGATC AGAGCTGAAA 420
50 CAGAGGTTCT CCGTTTTTGG AGAGATTGAG GAGTGACCA TCCACTTCCG TGTCCAAGGG 480
GACAACTACG GCTTCGTAC TTATCGCTAT GCTGAGGAGG CATTTGCAGC CATTGAGAGT 540
55 GGCCACAAGC TGCGGCAGC AGATGAGCAG CCCTTGATC TCTGCTTTGG GGGCCGAAG 600
SWGTNCTGCA AGAGGAGCTA TTCTGATCTT GACTCCAACC GGGAAGACTT TGACCCAGCA 660
CCTGTAAAGA GCAAATTTGA TTCTCTTGAC TTTGACACAT TGTGAAACA GGCCCGAAG 720
60

AACCTCAGGA GGTAACCTTG GGCCCTTCCC TGCTATCCTT TTTCTCCTTT GGAGGTGCCC 780
 AACCTCCTCC ACCCCCTTCC CCTACTCTAG GGGAGAGAGC TGCTAGTGAG ATGACTGTTT 840
 5 TATAAAGAAA TGGAAAAAAG TGAAATAAAA AATATGTTGA ATCAGATTTT TTAAGGGG 900
 TATTGTGTTT TTTATAACAG GTATTGAAAC AAGTTAACTT GCATTCTCTAT GTAAGATAGG 960
 AGGGCTGAG GGGATCCCCA GTGTTTGGA CATAAGTCAC TATGCAGACT AATAACATC 1020
 10 AACTAGAGAG NAAAAAAAAA AAAAAAAAAA ATTTAAAAAA CT 1062

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 2539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

25 GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
 GCACCTACCT GTGTTGGTGA GGTITGTTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 30 AGGCTTCTCG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC AACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGIGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAAATGA AAGTTGTTGC TTCTAGACTT TYAAGMKMRA TWKCCCCMAK 300
 35 YWAWCKGAAC AMAMKCTGSW CYTCCWSYGC SKTRMKRYC GYKSTATRRC WARWKSAYKM 360
 CCYGKKMIGS RRGTAWYTSK TGCAYKAGGG AACAAATGAG GAAGTTTGTT CTTTTTTCCA 420
 40 TCGATCACCA CAACTGCTTT TAGAACTTGA CAACGTAATT TCTGTTCTTT TTCAGAACAG 480
 TAAAGAAAGG GGTAAAGAAC TGAAGGAAAT CTGCCATTCT CAGTGGACAG GCAGGCATGA 540
 TGCTTTTGAA ATTTTAGTGG AACTCCTGCA AGCACTTGTT TTATGTTTAG ATGGTATAAA 600
 45 TAGTGACACA AATATTAGAT GGAATAACTA TATAGCTGGC CGAGCATTIG TACTCTGAGT 660
 GCAGTGTCAG ATTTTGATTT CATTGTTACT ATTGTTGTC TAAAAATGT CCTATCTTTT 720
 50 ACAAGAGCCT TTGGGAAAAA CYYCMAGGGG CAAACCTCTG ATGTCTTCTT TGCKKMSRT 780
 ARMTTTTGAY ATRMARYACT RMTKSAYTY AAYGRWGTGA CWSGAWAATA TTRAASTYTA 840
 TACAATKAAT YWTRRYTSM KRMAGMYAAT CCGAAAYTGT GGMAAMYAAA CTTGATATTC 900
 55 AAATGAAACT CCTGGGAAA TTCCGCAGAG CTCACCAGGG TAACTTGGA TCTCAGCTAA 960
 CCTCTGAGAG TACTATATAA GAAACCCTAA GTGTCCAAC AGTGGAGCAC ATTATTCAGG 1020
 60 AACTTAAAGA TATATTCTCA GAACAGCACC TCAAAGCTCT TAAATGCTTA TCTCTGGTAC 1080

	CCTCAGTCAT GGGACAACTC AAATTCATA CGTCGGAGGA ACACCATGCT GACATGTATA	1140
5	GAAGTGACTT ACCCAATCCT GACACGCTGT CAGCTGAGCT TCATTGTTGG AGAATCAAAT	1200
	GGAAACACAG GGGGAAAGAT ATAGAGCTTC CGTCCACCAT CTATGAAGCC CTCCACCTGC	1260
	CTGACATCAA GTTTTTTCCT AATGTGTATG CATTGCTGAA GGTCCTGTGT ATTCTTCCTG	1320
10	TGATGAAGGT TGAGAATGAG CGGTATGAAA ATGGACGAAA GCGTCTTAAA GCATATTTGA	1380
	GGAACACTTT GACAGACCAA AGGTCAAGTA ACTTGGCTTT GCTTAACATA AATTTTGATA	1440
15	TAAACACGA CCTGGATTTA ATGGTGGACA CATATATTAA ACTCTATACR AKTAMGTCAG	1500
	MGCTYYCTAC AKAYRAYTCM SWAWMTGTGG AAARYWSSTA MGMSWGCWKK TAMMRRTMCG	1560
	GMWWTYYMK RKTYGAYMYW YGCGWMCAG AAAAAGCCGT AAGGTGTATG TAGACCACTT	1620
20	AATCACTAAA TATCTTTGCC TATAGGACTC CATTGAATAC ATTAGCCATT GATAATCTAC	1680
	CTGTTTAAAT GGGCCCTGTT TGAACCTCA AGCTTTGAAG ACCTACCTGT TCTTCCAGAA	1740
	GAGAACGTTG AAAGTGCCAT GTTTCCTTTT GCGTGATCTC TGTTGATGGC ACTCTGGAAT	1800
25	TGTTTCCAGT TTAAKTCATT TTAGACATAG CATTATTAT CACTGTGGAT CTCTACTTGT	1860
	TGGGTGTTAT GAATCTTTG AAGAATATAT TTTGAAGAGG TGTGGGAGGA AGGAATACAT	1920
30	TTTATAAAAT GTTGTAGTGA AGCCACAAAT TGACCTTKGA CTAATAGGAG TTTTAAGTAT	1980
	GTAAAAATC TATACTGGAC AGTTACAAGA AATTACCGGA GAAAAGCTTG TGAGCTCACC	2040
35	AAACAAGGAT TTCAGTGTAG ATTTGTCTT TCTTGAACCT AAAGAAACAA ATGACAAAGT	2100
	TTGAATGGAA AAGCTGCTG TTGTTCCACA TCTCGTTCCT GTTACATTC CTTTGTGGAG	2160
	CCTACATCTT CCTAAGCTTT TTAGCAGGTA TATGTTGAAC ACTTCTGTTT CATGTTGAG	2220
40	ACAGAATCAG AGGCCATGGA TACTGACAAC TGATTTGTCT GTTTTTTTTC TCTGCTTTT	2280
	TCCATGACTC TTATATACTG CCTCATCTTG ATTTATAAGC AAAACCTGGA AAACCTACAA	2340
45	AATAAGTGT CTGGTTTATC TAGAAAAATA TGGAAAATAT TGCTGTTATT TTTGGTGAAG	2400
	AAAATCAATT TTGTATAGTT TATTTCAATC TAAATAAAAT GTGAATTTTG TTWWATTAAA	2460
	AATWGSAC AAABTBHGG GGGDTCCAAA CHTWVTCGHG KAAMTCTCT WAARMATYTK	2520
50	ATAAACMSCT TCACAATTC	2539

55 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

5	AGCATGAAGC CGATGGCCGT GGTGGCCAGT ACCGTCCTGG GCCTGGTGCA AAACATGCGT	60
	GCGTTTGGCG GGATCCTGGT GGTGGTCTAC TACGTATTTG CCATCATTTG GATCAACTTG	120
10	TTTAGAGGCG TCATTGTGGC TCTTCCTGGA AACAGCAGCC TGGCCCCCTGC CAATGGCTCG	180
	GCGCCCTGTG GGAGCTTCGA GCAGCTGGAG TACTGGGCCA ACAACTTCGA TGACTTTGCG	240
	GCTGCCCTGG TCACTCTGTG GAACTTGATG GTGGTGAACA ACTGGCAGGT GTTCTCGAT	300
15	GCATATCGGC GCTACTCAGG CCCGTGGTCC AAGATCTATT TTGTATTGTG GTGGCTGGTG	360
	TCGTCTGTCA TCTGGGTCAA CCTGTTTCTG GCCCTGATTC TGGAGAACTT CCTTCACAAG	420
	TGGGACCCCC GCAGCCACCT GCAGCCCCCT GCTGGGACCC CAGAGGCCAC CTACCAGATG	480
20	ACTGTGGAGC TCCTGTTCAG GGATATTCTG GAGGAGCCCC GGGAGGATGA GCTCACAGAG	540
	AGGCTGAGCC AGCACC CGCA CCTGTGGCTG TGCAGGTGAC GTCGGGCTG CCATCCCAGC	600
25	AGGGGCGGCA GGAGAGAGAG GCTGGCCTAA CACAGGTGCC CATCATGGAA GAGGCGGCA	660
	TCCTGTGGCC AGCCAGGCAG GAAGAGACCT TTCCTCTGAC GGACCACTAA GCTGGGGACA	720
	GGAACCAAGT CCTTTGCGTG TGGCCCAACA ACCATCTACA GAACAGCTGC TGGTGCTTCA	780
30	GGGAGCGGCC GTGCCCTCCG CTTTCTTTTA TAGCTGCTTC AGTGAGAATT CCCTCGTGA	840
	CTCCACAGGG ACCTTTCAGA CAAAAATGCA AGAAGCAGCG GCCTCCCTG TCCCCTGCAG	900
35	CTTCGGTGGT GCCTTTGCTG CCGGCAGCCC TTGGGGACCA CAGGCCTGAC CAGGGCCTGC	960
	ACAGGTAAAC CGTGAGTCTG TCTCATCTAT TCACAGCTGG GAATGATACT AATACCTCCG	1020
	ATTTTAGCCC AGCACCACAG GGTACGTTCC AGTTTTCCTC TCTTTCATA GCTGTAAGGC	1080
40	CCTTCTGGG AATGGTCTC ATTCTCCTTA ATCTATTATT GGGTCAGTTT TCCTGCATGT	1140
	CCCCAGCCTC CCATCACTGC CACCCACTCC CCACAGAGAT GCCCTGCTCA TCCGACTGGG	1200
45	GCTTTGACTC CCACACTGTG TACCCCTCTT GTGTGGACGC CCTGCTGCCA AAACCTTCAG	1260
	CAAACAGCTT TCCAAATGGA AGTTGTCACT GTCAGGCCTT TACAATCAGC AACAGCAAAA	1320
	TCTACATGCT GCTGAGGGTC CTGCCTCATT AAGATGCAAT AAATATGTAA GTACATAAAA	1380
50	ACAGCAATAG AAGAAACGTA ATGCTTTATT CTCAAATATG ATGTCTACAT AGAAAAGCCA	1440
	AAATTATTAA GAATAGTAAG AATTCACCCA GCACTTTGGG AGGCCGAGGC GGGTGGATCA	1500
55	TGAGGTGAGG AGATCGAGAC CATCCTGGCT AACAGGGTGA AACCCCGTCT CTAATAAAAA	1560
	TACAAAAAAT TGGCCGGGCG CAGTGGCGGG CGCCTGTGGT CCCAGCTACT GGGGAGGCTG	1620
60	AGGCAGGAGA ATGGCGTGAA CCCGGGAAGC GGAGCTTGCA GTGAGCCGAG ATTGCCCCAC	1680

TGCAGTCCGC AGTCCAGCCT GGGCGACAGA GCGAGACTCC GTCTCAAAAA AAAAAAAAAA 1740
AAAAAAAAA A 1751

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AATGTTGTGG TGGTAGCATT TGGGTTAATT CTRATTATAG AGTCTCTTGG AGAGCAATGT 60
20 CCATAAACTA ATCCCAAACA ACATTGTCTT TTTRATGTG TAGTGAACAG CAGAGAATTT 120
CAAAGGACCT TGCTAATATC TGAAGACGG CAGCTACAGC AGGCATCATT GGCTGGGTGT 180
ATGGGGGAAT ACCAGCTTTT ATTCATGCTA AACACAATA CATTGAGCAG AGCCAGGCAG 240
25 AAATTTATCA TAACCGTTT GATGCTGTGC AATCTGCACA TCGTGCTGCC ACACGAGGCT 300
TCATTGCTTA TGGCTGGCGC TGGGTTGGA GAACTGCAGT GTTTGTGACT ATATTCAACA 360
30 CAGTGAACAC TAGTCTGAAT GTATACCGAA ATAAAGATGC CTTAAGCCAT TTTGTAATTG 420
CAGGAGCTGT CACGGGAAGT CTTTTTAGGA TAAACGTAGG CCTGCGTGGC CTGGTGGCTG 480
GTGGCATAAT TGGAGCCTTG CTGGGCACTC CTGTAGGAGG CCTGCTGATG GCATTTTCAGA 540
35 AGTACTCTGG TGAGACTGTT CAGGAAAGAA AACAGAAGGA TCGAAAGGCA CTCCATGAGC 600
TAAAACTGGA AGAGTGGAAA GGCAGACTAC AAGTTACTGA GCACCTCCCT GAGAAAATTG 660
40 AAAGTAGTTT ACAGGAAGAT GAACCTGAGA ATGATGCTAA GAAAATTGAA GCACTGCTAA 720
ACCTTCCTAG AAACCTTCA GTAATAGATA AACAAAGACA GGACTGAAAG TGCTCTGAAC 780
TTGAAACTCA CTGGAGAGCT GAAGGAGCT GCCATGTCCG ATGAATGCCA ACAGACAGGC 840
45 CACTCTTTGG TCAGCCTGCT GACAAATTTA AGTGCTGGTA CCTGTGGTGG CAGTGGCTTG 900
CTCTTGCTTT TTTCTTTTCT TTTTAACTAA GAATGGGGCT GTTGTACTCT CACTTTACTT 960
50 ATCCTTAAAT TTAAATACAT ACTTATGTTT GTATTAATCT ATCAATATAT GCATACATGA 1020
ATATATCCAC CCACCTAGAT TTAAACAGT AAATAAAACA TTTGCAAAA GATTAAAGTT 1080
GAATTTTACA GTTAAAAAAA AAAAAAAAAA AAAAAA 1117
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(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GGCAGAGGTT TTCCTATATT TTAAGTAAAT TTAAAGTGGC TATCAGAATA TTTATTCTTG 60
10 TTTGAGACTA CCAACATAAC TACGTGTTGA AGGTGCTTCA CAGAGAATAT ATTGCCPTTA 120
ATGTGAAATA ATTTTCACCA ATGTTGCTAA CTTTAATAAA GTATAAAATT TGTAGAATAT 180
15 TCAGTTAAGT AGTGGTAAC CCTTTCCTAT TTTAGTAAAA CTTAATGCAT GTTACTTTT 240
TTTTGAAAGA TGCAGACAAT CTCTTTGAAC ATGAATTGGG GGCTCTCAAT ATGGCTGCAT 300
TACTACGAAA AGAAGAAAGA GCAAGTCTTC TTAGTAATCT TGGCCCATGT TGTAAGGCGT 360
20 TGTGCTTCAG ACGGGATCTT GCAATTCGAA AGCAGCTTGT TAAAAATGAG AAGGGCACCA 420
TAAACAAGC TTACACGAGT GCTCCAATGG TAGACAATGA ATTACTTCGA TTGAGTCTTC 480
25 GGTATTTTAA GCGGAAGACT ACTTGCCATG CTCCAGGACA TGAAAGACT GAAGATAATA 540
AACTTTCACA GTCCAGTATC CAACAGGAAC TGTGTGTGTC TTAAGACCGA AGTTACAATA 600
TGGTATTTTT GGTACTGTCT TCCTTCAGCA GTGCATATTC TTMIGCAAAG TTCTTTGGTT 660
30 TGACAAGCAT TAGTGACAAA GGCAGAAAAG ATTTATCAGC CATGCTAAAA GAGTGAAGAA 720
TTTTGATCTT TAGAGACACT AGTTTGGGCC AACTTAAGAT TTTACGTTAA TTTTACATA 780
35 GTATTTGACA CTCATGCAAA ATAATGTGAA AACATCTAGA TTTAGTAGTT TATTCTGCGC 840
CTTTTGTTAA AACTGAAGAT TTTGGAAAAT GGTGTGCACT GCTCTTCCAG CCTATGAATA 900
TTTTTGTAAT ATGGAACCAT GGATTATGT CTGGATCATC CATACAGAAC CAACAATTTT 960
40 ATTCAAAAAC AATGTGTTCA TCAAAGTAAT TGCTCACATT GTGCACTACT ATGTTGTACA 1020
GACCACGTGA AAGGGAATGC TGGTCTAGCT GCGGTGGTAT GTTATAGGC GAATTTGAGC 1080
45 AGAAGGAAGC CAAAATAGTT TTTTCTTTT GAAAGTTTTT TAAAAATTAT TTCATGGGTC 1140
TTTTTTTTTAA TTAATATGTG TGCATTGTTA CAATGTATGT TGGGATGTCT TTTGACCCTA 1200
AATGCTTTTT TTGTTATCAG AGATTGTGTA CTATTTTAT TTTTAATAAA TGTATCTTCC 1260
50 CTTTTMAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 1313

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(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

5	ACAGGGACAG AATACTTTCT TTCCTTCCTT CAAGTACAAG AAGGCTTTCT CTACCATTTG	60
	CGTCTACACT TTATTTTAAA AGCTATCCTT TTCTAGTAGT ATTTTATCAT GGCAATGGCA	120
10	TGATGACAAC AACAGTCTTT CATTACAGAC TGAAGGGAAG CATGTCCTTA CTAAAATAG	180
	TTCTGCTACT TTCCCTCCTA TTATAAGGAA ATTTTACAGA TTCTAAAAAT ACCTTAATTT	240
15	TTCTTTGATT TTTATTTTAC CAAGTCACAA ATGTCTTTTT GATGTTTTGA GAATGTTCT	300
	CATAGAATCA CAAATACTGA CATTTTATTA GATGATTATT TTCCTAGAAT CCCCAAAGAG	360
	CAGTGGCAGT CCATGGCTTG GTTGAAGCTA GAAATTTTCC TGCCCTGGT GACCTGGTAA	420
20	GCCTCCTGCT CGGAACCGTG TGAGTGGGTG AGGAAGATGA GAGATGGTCA GATGGAAGAG	480
	AGRAATACAT GAACTGCTCT GGCCTCTCTG GTTCTGTTCT TGGCCAGAG TTTTGA AAA	540
	GCAGCGGANA TNGACTGACT TCACATGCTC AGCTTTCTCA GCCTTTTGT TATTTGTTG	600
25	TCCTTAGATT TCCCTGTTGT AAAAGGGGCA AGAAAAGTAA CTCATCATCT CTAACACACC	660
	ATGGCAGCTT AGCCAGGTAG TCTTAGTGGT GGTGTTTAGG CATAAGATAT GCTGATCATC	720
30	AGTCTCAGGC CACAGTTTCC TTCACTAATC GTCCAGCTTG AGTGTTCTGT TCTCTTCCTG	780
	CCCATTTCCT TGAACCTCCT GCTCTAGCCT TGGCGGAGGG AGAGTGCTAT TTGCTTTTGT	840
	TCTCCCTCTG TCTTAGGAAA AGCCATCTTT AATATAGTTC TTCACCACG TTGGGGTTGT	900
35	TTTGTGATTT TTTTTTCTT CCGAAGAACT CCTGGTTGTT ATTGGATTTT GTATTTTAAT	960
	ACAAATTATT GAATTTTATA AGCTTGTA CAATATTTAA TTAGTGTGAA AGGAAACAAA	1020
40	GAATGCAGGA AAAATAATTT AATATCAACC TCAGTTGACA AGGTGCTCAG ATTATTCAAT	1080
	TCGGGATCCT CCTTTTGTTA GGTTTTGAG ACAACCTAG ACCTAAACTG TGTCACAGAC	1140
	TTCTGAATGT TTAGGCAGTG CTAGTAATTT CCTCGTAATG ATTCTGTAT TACTTTCCTA	1200
45	TTCTTTATTC CTCTTCTTC TGAAGATTAA TGAAGTGAA AATTGAGGTG GATAAATACA	1260
	AAAAGGTAGT GTGATAGTAT AAGTATCTAA GTGCAGATGA AAGTGTGTTA TATACATCCA	1320
50	TTCAAAATTA TGCAAGTTAG TAATTACTCA GGGTTAACTA AATTACTTTA ATATGCTGTT	1380
	GAAYCTACTC TGTTCCCTTG CTAGAAAAA TTATAACAG GACTTTGTAG TTTGGGAAGC	1440
	CAAATTGATA ATATTCTATG TTCTAAAAGT TGGCTATAC ATAAATTATT AAGAAATATG	1500
55	GATTTTTATT CCCAGGATAT GGTGTTTATT TTATGATATT ACGCAGGATG ATGTATTGAG	1560
	TAAATCAGT TTTGTAAATA TGTAAATATG TCATAAATAA ACAATGCTTT GACTTATTTT	1620
60	CAAAAAAAA AAAAAATAAA NTTCGAGGGG GGGC	1654

5 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

15 GGCAAACTTT CCCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
GGGTTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATGGC GTTCCGCGAA CGTTGGCCCT 120
CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
20 CTGGMCTCA TCTTCCTGCG CCGACCTGCG CGGGTAAGG GGWAGTTTCA GACTGTGAAG 240
GACGTCGTGC TGGACTGCCT GTTGGACTTC TTACCCGAGG GGGTGAACAA AGAGAAGATC 300
25 ACACCACTCA CGCTCAAGGA AGCTTATGTG CAGAAAATGG TTAAAGTGTG CAATGACTCT 360
GACCGATGGA GTCTTATATC CCTGTCAAAC AACAGTGGCA AAAATGTGGA ACTGAAATTT 420
GTGGATTCCC TCCGGAGGCA GTTTGAATTC AGTGTAGATT CTTTCAAAT CAAATTAGAC 480
30 TCTCTTCTGC TCTTTATGA ATGTTTCTAG AATCCCAATGA CTGAGACATT TCACCCCA 540
ATAATCGGG AGAGCGTCTA TGGCGATTTC CAGGAAGCCT TTGATCACCT TTGTAACAAG 600
35 ATCATTGCCA CCAGGAACCC AGAGGAAATC CGAGGGGGAG GCCTGCTTAA GTACTGCAAC 660
CTCTTGGTGA GGGGCTTTAG GCGCCCTCT GATGAAATCA AGACCCCTCA AAGGTATATG 720
TGTTCCAGGT TTTTCATCGA CTCTCAGAC ATTGGAGAGC AGCAGAGAAA ACTGGAGTCC 780
40 TATTTGCAGA ACCACTTTGT GGGAAATGGA AGACCGCAAG TATGAGTATC TCATGACCCT 840
TCATGGAGTG GTAAATGAGA GCACAGTGTG CCTGATGGGA CATGAAAGAA GACAGACTTT 900
45 AAACCTTATC ACCATGCTGG CTATCCGGGT GTTAGCTGAC CAAAATGTCA TTCCTAATGT 960
GGCTAATGTC ACTTGCTATT ACCAGCCAGC CCCCTATGTA GCAGATGCCA ACTTTAGCAA 1020
TTACTACATT GCACAGGTTT AGCCAGTATT CACGTGCCAG CAACAGACCT ACTCCACTTG 1080
50 GCTACCTTGC AATTAGAAT CATTTAAAAA TGTCTGTGG GGAAGCCATT TCAGACAAGA 1140
CAGGAGAGAA AAAAAAAAAA AAAAAAAAAA A 1171

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(2) INFORMATION FOR SEQ ID NO: 115:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

	GGTCTGCGCC GGAAGTGCAT GAGCTGCCGA TGTGGTGCTT AGTGATGCG GTTTCGGTCC	60
10	CTCTCCCGTG TTTCCCGGGC TGGGTATTTG CCTCGCACCA TGGCGCCAA GGGCAAAGTG	120
	GGCAGGAGAG GGAAGAAGCA GATATTTGAA GAGAACAGAG AGACTCTGAA GTTCTACCTG	180
	CGGATCATAC TGGGGGCCAA TGCCATTTAC TGCCMTGTGA CGTTGGTCTT CTTTACTCA	240
15	TCTGCCTCAT TTTGGGCTG GTTGGCCCTG GGCTTTAGTC TGGCAGTGA TGGGGCCAGC	300
	TACCACTCTA TGAGCTCGAT GGCACGAGCA GCGTTCTCTG AGGATGGGCC CCTGATGGAT	360
20	GGTGGCATGG ACCTCAACAT GGAGCAGGGC ATGGCAGAGC ACCTTAAGGA TGTGATCCTA	420
	CTGACAGCCA TCGTGCAGGT GCTCAGCTGC TTCTCTCTCT ATGTCTGGTC CTTCTGGCTT	480
	CTGGCTCCAG GCCGGGCCCT TTACCTCTTG TGGGTGAATG TGCTGGGCCC CTGGTTCACT	540
25	GCAGACAGTG GCACCCGAGC ACCAGAGCAC AATGAGAAAC GGCAGCGCCG ACAGGAGCGG	600
	CGGCAGATGA AGCGTTTATA GCCATTGACA TTGTGGCCAC AGGCCACTGG CCCTGGGTGG	660
30	CTCTGTCAAG GTGCACAGCC COTCATGCCT GGAGCAATGA GGGTCTAGTC CAGGGGCCAA	720
	AAGCAGTCTG AGGTATTTGGG TATACTTATA CTCTATAGGG TCGTTGAATA AATGGCTTAG	780
	AATGTGAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCCC GGTACCCAAT TTCNCCTANA	840
35	AT	842

40

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1640 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

	GGCAGGAGGC GCGGCGCAGC GTGGCGGCGG CGCCCCCGG CGGAGCCGT TCCCTTTCCC	60
	GTGCGGAGAG GCGGGGYCGG GGCCAGGGG ACCCCGGGCC ACGGAGAGCG GGAAGAGGAT	120
55	GGATTGCCCG GCCCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAGAAGT TCAGAAGCAA	240
60	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTATCTC AGCAGTTTTC ACTTCAGAAC	300

TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT 360
 CAATCAAAAT AAGGGTAAAC CAGACTTGAA ATACAACATT GCCAATTAGA CAAACAGCAT 420
 5 CAATTTTCAA ACAACCGGTA ACCCAAAGTC ACAAATCATC CTAGTAATAA AGTGAAATCA 480
 GACCCACAAC GAATGAATGA ACAGCCACGT CAGCTTTTCT GGGAGAAGAG GCTACAAGGA 540
 CTTTAGTGCA TCAGATGTAA CAGAACAAAT TATAAAAACC ATGGAAC TAC CCAAAGGTCT 600
 10 TCAAGGAGTT GGTCCAGTAG CAATGATGAG ACCCTTTTAT CTGCTGTGTC CAGTGCTTTG 660
 CACACAAGCT CTGCGCCAAT CACAGGGCAA GTCTCCGCTG CTGTGGAAAA GAACCTGCTG 720
 15 TTTGGCTTAA CACATCTCAA CCCCTCTGCA AAGCTTTTAT TGTACAGAT GAAGACTCAG 780
 GAAACAGAAG AGCGAGTACA GCAAGTACGC AAGAAATTGG AAGAAGCACT GATGGCAGAC 840
 ATCTTGTCGC GAGCTGCTGA TACAGAAGAG ATGGATATTG AAATGGACAG TGGAGATGAA 900
 20 GCCTAAGAAT ATGATCAGGT AACTTTTCGAC CGACTTTCCC CAAGAGAAAA TTCCTAGGAA 960
 ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA 1020
 25 TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGAT TATTTTGTAT GTATATATCT 1080
 ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAATA 1140
 TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTCGAATCT ACTGGAAATG 1200
 30 TAGCACTTAC GTAAACATTT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC 1260
 TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAACA TATTTTATA 1320
 35 CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCGTCA CTGTAAAGAC AAATAAATGA 1380
 TTATATTCCA CAGAAAAAA AAAAAAAW MWSTYGARRR GSRGCMCRSW AXMMARWWCC 1440
 CCWMRIWRGS MKTCSTMTKA YTTACATTCA ACTCTGATCC CGGGCCCTTA GGTTCGACAT 1500
 40 GGGAGGTGGG AGGAAGATAG CGCATATATT TGCAGTATGA ACTATTGCCT CTGGGACGTT 1560
 GTGAGGAATT GTGCTTTCAC CAGAATTCTT AAGGATTCTT GGCTTAAATA TCACCTAGCC 1620
 45 TGTGGTAATT TTTTTCCTCT 1640

50 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

60 TGAATTTAGN AAACACTTTG GAAAACTCAT AACCTCATCA GAAACTGCCT TTAGCCACAC

60

TCCTGACCTT CTAGATGAGT AACAAAAAA TGAAATAAGT TCTTGAAAT TAAGCCATTT 120
ATTTTAATTT GCTATTTTTT TCAATGTTCT AGGTATCTTT AAATTTGTTA TTGTGGAATC 180
5 ATTTTCCTGC CAGATACCTT TATCAAAATT ATTGGCCTCA TGAGAGCTGA AGTAAGTCAG 240
CTTTTGGTG AACTTTAGTG GACTTCTGTG AGATTGTAGT TGTACTTTGT ATCTCTAAAT 300
10 CTAAAGATAG TTTTTTAAAA CTCCCAAAGA AAATCTGCTC TCCTTTCTGA TCTAAAAACT 360
CATCTTTGGG GTAAAGAGTT AAGTGTCOA AGGTGTGAC AGTTCATGAG GTCAGAGGGA 420
GCTAGCCTGG CACCTGGACT CTGCCATCC ACAGCTGACA GATTCCAACA GAAGTGATTT 480
15 TAAATTCTCC AGTAGACAAT GCTGGTAAG GGAGGGGTA GGGCTGGGT ATTAAGATAC 540
AGGCTGCTGT ATTTTACATT GGTGTGGGG GAAGGGGAGC CTGGAGAAA CAAAGTCACT 600
20 ATTCCCTTTT TTGAACAGG AAAAAAATT ATTTTGTGT CAGTAAAAAT GGTAGAGAAT 660
TCCAATGTCC CTAGCCACAA GGGACCAATT CCACTGAGAA GTGAACAGTG GGAACCAAA 720
ATTTCAGAAA CATGGGGGA AGGAAAATT GGCTTCTCT TAATTGGCAG ATGTTCCAGT 780
25 GGGGSGGGG GGCTCTGTT TTGTTGGAT GTGTTATGTT GTATGTACGC ATATATGGAC 840
CGGAGTCTGC TGACTTTATA AGGTTCCAA AATATGGTAA AATCTGGTT TTGTTAATT 900
30 TATCTCAATA AAAGCCCACT GGRACCTCAA AAAAAAAGA NN 952

35 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

45 GACGTCATAG GTAAACAGGC TCTGTATCCG TGGCAGCGGC CGTGGCAGGC TGGCTGGGTA 60
CCGGCTGTGC CTGACCCAGG AGAAGCTGCC TGTCTACATC AGCCTGGGCT GCAGCGCGCT 120
GCCGCCGCGG GGCCGGCAGC TGAAGTATGT GCTCTTCAGG GCGGGCACCG TGTGTCATTC 180
50 ATCTTTGTAC CCCCAGCATC TAGCAGTGTG GGCATGTAGT AGGCACTCAA GAAATGTGTG 240
TTGAATGAAC GATGCCTGTG ACAAGCAAGC GGACTTTATT CTTTCTGAC CCTTGCTCCT 300
55 ATGACACACC TCCTCTGAC TGCCACTGTC ACTCCTTCAG AGCAGAACTC CTCTAGGGAA 360
CCTGGATGGG AAACAGCCAT GGCCAAGGAC ATCCTGGGTG AAGCAGGGCT ACACTTTGAT 420
GAACTGAACA AGCTGAGGGT GTTGGACCA GAGGTTACCC AGCAGACCAT AGAGCTGAAG 480
60

	GAAGAGTGCA AAGACTTTGT GGACAAAATT GGCCAGTTTC AGAAAATAGT TGGTGGTTTA	540
	ATTGAGCTTG TTGATCAACT TGCAAAAGAA GCAGAAAATG AAAAGATGAA GGCCATCGGT	600
5	GCTCGGAACT TGCTCAAATC TATAGCAAAG CAGAGAGAAG CTCAACAGCA GCAACTTCAA	660
	GGCCTAATAG CAGAAAAGAA AATGCAGCTA GAAAGGTATC GGGTTGAATA TGAAGCTTTG	720
	TGTAAAGTAG AAGCAGAACA AAATGAATTT ATTGACCAAT TTATTTTCA GAAATGAACT	780
10	GAAATTTTCG CTTTATAGT AGGAAGGCAA AACAAAAAA AGCCTCTCAA AACCAAAAAA	840
	ACCTCTGTAG CATTCACCG GCTTGACCAA TGACCTATGT CACAAGAGGT GGCGTGTAAG	900
15	GAATGCAGCC CCCTGAAGAC AGCACTACAA GTCTGGGGGA GCCAGTTTTA ACATCAGTGC	960
	ACAGCTGCTG CTGGTGGCCC TGCAGTGAC GTTCTCACCT CTTATGCTTA GTTGGAACTA	1020
	AGCAGTTTGT AAACCTTCAT CCTTTTTTTT GTAAATTCAC AAAGCTTTGG AAGGAGAAGC	1080
20	AATAAATTTT TGTMTTCAA TGGCTTGATG TACCTTTTTT CCTGTTCCTC TTGAAATATG	1140
	TTTAACTCCT CATGAGAGAA CCCTGGATTC TCTATCCCCT AGTCCACAAA ACAAAACCAG	1200
25	CAGTGGTCAG CAGCTACCTT TNATTGGAT CACACACGTG AGTCAGACAG TACCAC	1256
30	(2) INFORMATION FOR SEQ ID NO: 119:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1143 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:	
40	GGCCGTAGCA GCCGGGCTGG TCCTGCTGCG AGCCGGCGGC CCGGAGTGGG GCGGCGGCAT	60
	GTACCTTCCA CATTGAGTAT TCAGAAAGAA GTGATCTGAA CTCTGACCAT TCTTTATGGA	120
	TACATTAAGT CAAATATAAG AGTCTGACTA CTTGACACAC TGGCTCGAGC AAACATGAAC	180
45	GTTGGAGTTG CCCACAGTGA AGTGAATCCA AATACCCGTG TCATGAACAG CCGGGGTATG	240
	TGGCTGACAT ATGCATGGG AGTTGGCTTG CTTCATATTG TCTTACTCAG CATTCCTTC	300
50	TTCAAGTGTTC CTGTTGCTTG GACTTTAACA AATATTATAC ATAATCTGGG GATGTACGTA	360
	TTTTTGATG CAGTGAAAG AACACCTTTC GAAACTCCTG ACCAGGGTAA AGCAAGGCTC	420
	CTAACTCATT GGAACAACCT GGACTATGGA GTACAGTTTA CATCTTCACG GAAGTTTTTC	480
55	ACAATTTCTC CAATAATTCT ATATTTCCTG GCAAGTTTCT ATACGAAGTA TGATCCAAC	540
	CACCTCATCC TAAACACAGC TTCTCTCCTG AGTGTACTAA TTCCCAAAAT GCCACAATA	600
60	CATGGTGTTC GGATCTTTGG AATTAATAAG TATTGAAATG TTTTGAACT GAAAAAAAT	660

TTTACAGCTA CTGAATTCTT TATAAGGAAG GAGTGGTTAG TAAACTGCAC TGTTCCTSTG 720
 5 ATAATGTGAA ATGAGAAGTA TTTACATTGG AGGGCCAATG GCTGGTCCTT CAAGTGCTGT 780
 TTTGAAGTGC AGATTTCCAT TAAATGATGC CTCTGTTTAA TACACCTGGT ACATTTCTGA 840
 AGAGGGGCTT TATAAGCAGG CTGGGCAGGC CCAGCTTATA AGTTAAAGGG CATCACAGTG 900
 10 AGGGTGTAGT AGATAAATTC AAGGAAATAA GAGATTGTGA AGAACTAGG ACCAGCTTAA 960
 CTTATAATGA ATGGGCATTG TGTTAAGAAA AGAACATTTC CAGTCATTCA GCTGTGGTTA 1020
 TTTAAAGCAG ACTTACATGT AAACCGGAAT CCTCTCTATA CAAGTTTATT AAAGATTATT 1080
 15 TTTATTACCG TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 GAN 1143

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(2) INFORMATION FOR SEQ ID NO: 120:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCCCG CCCCCACCC ACGTCTGCGT TGCTGCCCGG CCTGGGCCR GCCCCAAAGG 60
 35 CAAGGACAAA GCAGCTGTCA GGAACCTCC GCCGGAGTCG AATTACGTG CAGCTGCCGG 120
 CAACCACAGG TTCCAAGATG GTTGCGGGG GCTTCGCGTG TTCCAAGAAC TGCCTGTGCG 180
 CCCTCAACCT GCTTTACACC TTGGTTAGTC TGCTGCTAAT TGAATTGCT GCGTGGGGCA 240
 40 TTGGCTTCGG GCTGATTTCC AGTCTCCGAG TGTCGCGGT GGTCAATTGA GTGGGCATCT 300
 TCTGTTCCT GATTGCTTTA GTGGGTCTGA TTGGAGCTGT AAAACATCAT CAGGTGTTGC 360
 45 TATTTTITTA TATGATTATT CTGTTACTTG TATTTATTGT TCAGTTTCT GTATCTTGCG 420
 CTGTTTATAG CCTGAACCAG GAGCAACAGG GTCAGCTTCT GGAGTTGGT TGGAACAATA 480
 CGGCAAGTGC TCGAAATGAC ATCCAGAGAA ATCTAACTG CTGTGGGTC CGAAGTGTTA 540
 50 ACCCAAATGA CACCTGTCTG GCTAGCTGTG TTAAGTGA CCACTCGTGC TCGCCATGTG 600
 CTCCAATCAT AGGAGAATAT GCTGGAGAGG TTTTGAGATT TGTGGTGGC ATTGGCCTGT 660
 55 TCTTCAGTTT TACAGAGATC CTGGGTGTTT GGCTGACCTA CAGATACAGG AACCAGAAAG 720
 ACCCCCGCGC RAATCCTAGT GCATTCCTTT GATGAGAAAA CAAGGAAGAT TTCCTTTCGT 780
 60 ATTATGATCT TGTTCACCTT CTGTAATTTT CTGTTAAGCT CCAATTGCCA GTTTAAGGAA 840

	GGAAACACTA TCTGGAAAAG TACCTTATTG ATAGTGAAT TATATATTTT TACTCTATGT	900
	TTCTCTACAT GTTTTTTTCT TTCGGTGCT GAAAAATATT TGAAACTTGT GGTCTCTGAA	960
5	GCTCGGTGGC ACCTGGGAAT TTACTGTATT CATTTGCGGG CACTGTCCAC TGTGGCCTTT	1020
	CTTAGCATTT TTACCTGCAG AAAAAGTTTG TATGGTACCA CTGTGTTGGT TATATGGTGA	1080
10	ATCTGAACGT ACATCTCACT GGTATAATTA TATGTAGCAC TGTGCTGTGT AGATAGTTCC	1140
	TACTGGAAAA AGAGTGGRAA TTTATTAAAA TCAGAAAGTA TGAGATCCTG TTATGTTAAG	1200
	GGAAATCCAA ATTCCCAATT TTTTGTGGTC TTTTGTAGAA AGATGTGTTG TGGTAAAAAG	1260
15	TGTTAGTATA AAAATGATAA TTWACTKGTA GTCTTTTATG ATWACACCAA TGTATTCTAG	1320
	AAATAGTTAT GYCYTAGGAA ATTGTGGTTT AATTTTGTAC TTTTACAGGT AAGTGCAAAG	1380
	GAGAAGTGGT TTCATGAAAT GTTCTAATGT ATAATAACAT TTACCTTCAG CCTCCATCAG	1440
20	AATGGAACGA GTTTTGAGTA ATCAGGAAGT ATATCTATAT GATCTTGATA TTGTTTATA	1500
	ATAATTGAA GTCTAAAAGA CTGCATTTT AAACAAGTTA GTATTAATGC GTTGGCCCA	1560
25	GTAGCAAAAA GATATTGAT TATCTTAAAA ATGTGTTAAAT ACCGTTTCA TGAAAGTTCT	1620
	CAGTATTGTA ACAGCAACTT GTYAAACCTA AGCATATTTG AATATGATCT CCCATAATTT	1680
	GAAATTGAAA TCGTATTGTG TGGCTCTGTA TATTCTGTTA AAAAATTAAA GGACAGAAAC	1740
30	CTTCTTTTGT GTATGCATGT TTGAATTAAA AGAAAGTAAT GG	1782
35	(2) INFORMATION FOR SEQ ID NO: 121:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 610 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:	
45	GTGGCTGCA GATTGTGGT GCCTTCTGAG CCGTCTGTCC TGCGCCAAGA TGCTTCAAAG	60
	TATTATTAAA AACATATGGA TCCCATGAA GCCCTACTAC ACCAAAGTTT ACCAGGAGAT	120
50	TTGGATAGGA ATGGGGCTGA TGGGCTTCAT CGTTTATAAA ATCCGGGCTG CTGATAAAAG	180
	AAGTAAGGCT TTGAAAGCTT CAGCGCCTGC TCCTGGTCAT CACAACCAGA TTTACTTGGA	240
	GTACATGTGA AAGAAAACGT CAGTCTGCCT GTAAATTTCA GCAAGCCGTG TTAGATGGGG	300
55	AGCGTGGAAC GTCACGTAC ACTTGATATA GTACCGTTTA CTTCATGGCA TGAATAAATG	360
	GATCTGTGAG ATGCACTGCT ACCTGGTACT GCTTTTCAGT GTTTCCCCCT CAGCCCTCCG	420
60	GCGTGTCAAG CATACTCTGA GTAGATAATT TGTCATGCAG CGCATGCAAT CAGAATCTCA	480

CTGAGCCACC CATCATTTGTG AAATAATTAC CTCAGTTGTA CAGGACTTGG TGATCAGGAT 540
CCAGGCACTC ACTTGTTATTC TACTGCTCAA TAAACGTTTA TTAAACTGA AAAAAAAAAA 600
5 AAAAAAAAAA 610

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GGTACGCCCTG CAGGTACCGG TCCGGAATTC CGGGTCGCCC ACGCGTCNGG CCACGCGTCC 60
ACCCACGCGT CCGSCCAGCG GTCCGAGCCG AGCCGGA CTG CAGGATGA TCACGGACGT 120
25 GCAGTCGCC ATCTTCGCCA ACATGCTGGG CGTGTGCTC TTCTTGCTTG TCGTTCTCTA 180
TCACTACGTG GCCGTCAACA ATCCCAAGAA GCAGGAATGA AAGTGGCGCT TTCTCCGCCC 240
CAGGGTTCCA GGACATAGTC TGAGGCAAGA TGGAGGGTAT GAGGGGCCTT CACACTTCAC 300
30 TTCATCCCTT CTACCCATCA CAACATACAA AGCAACTACA CCTCGATTTT TCCAAACAAC 360
TTTTATTTC TCAGAGTCTT CCTTAATCCT ATGGAACAAG AAGCTGCCAC TGAATAGGGC 420
35 CCAGTATAGG GGCTTGCTTT TCTACTCCCT CCCCCAATA TAAAAATATA GACTTTTTAA 480
AAAAAAAAA AAAAAATTCG NGGGGGGSCC GGTACCCATC CCCCTA 526

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(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 2081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGTACCGGTC CGGAAATTC CGGGTCGACC CACGTCGTCS GGGGAACATG GCGGCTKCGG 60
AGCCGGCGGT CCTTGCCTC CCCAACAGCG GCGCCGGGGG CGCGGGGCG CCGTCGGGCA 120
55 CAGTCCCGGT GCTCTTCTGT TTCTCAGTCT TCGCGGACC CTCGTCGGTG CCACACGGGG 180
CGGGCTACGA GCTGCTCATC CAGAAGTTCC TCAGCCTGTA CGGCGACCAG ATCGACATGC 240
60 ACCGCAAATT CGTGGTGCAG CTGTTGCGCG AGGAGTGGGG CCAGTACGTG GACTTGCCCA 300

	AGGGCTTCGC GGTRAGCGAG CGCTGCAAGG TGC GCCTCGT GCCGYTG CAG ATCCAGCTCA	360
	CTACCCCTGGG AAATCTTACA CCTTCAAGCA CTGTGTTTTT CTGCTGTGAT ATGCAGGAAA	420
5	GGTTCAGACC AGCCATCAAG TATTTTGGGG ATATTATTAG CGTGGACAG AGATTGTTGC	480
	AAGGGGCCCG GATTTTAGGA ATTCTGTGA TTGTAACAGA ACAATACCCT AAAGGTCTTG	540
10	GGAGCACGGT TCAAGAAATT GATTTAACAG GTGTAAACT GGTACTTCCA AAGACCAAGT	600
	TTTCAATGGT ATTACCAGAA GTAGAAGCGG CATTAGCAGA GATTCCTCGA GTCAGGAGTG	660
	TGTATTATT TGGAGTAGAA ACTCATGTGT GCATCCAACA AACTGCCCTG GAGCTAGTTG	720
15	GCCGAGGAGT CGAGGTTTAC ATTGTTGCTG ATGCCACCTC ATCAAGAAGC ATGATGGACA	780
	GGATGTTTTGC CCTCGAGCGT CTCGCTCRAR CCGGATCAT AGTGACCAG AGTGAGGCTG	840
20	TTCTGCTTCA GCTGGTAGCT GATAAGGACC ATCCAAAATT CAAGGAAATT CAGAACTAA	900
	TTAAGGCGAG TGCTCCAGAG TCGGGTCTGC TTTCCAAAGT ATAGGACATT TGAAGAACTG	960
	GTATGCTACT CACTGGTGAA GGACAGTCAG GTGAAGGACT GTAAGCCAC ACAAGCTCTT	1020
25	CTTATCTCTA CTAGAATTAA AATGTTAAGT CAAAAACGGC TCCTTTTTTG CGCCTCCTAG	1080
	TGAAACTTAA CCAGCTAGAC CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT	1140
30	CCGGTGCTGC TTACCTTCCT TTTTGTGTA TGTGCTTTTA TTTATTAAAA AAAATTACAA	1200
	TGAAGATGCC TGTTTTGTCT CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAACT	1260
	CTGTGAAGT TTTCTTAAAT TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTGG	1320
35	CTTTTATATT ACTGTAAGAT GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG	1380
	ATTGATTGGA ATAAGATTAT TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC	1440
40	CACTCCCCTC ACAATGTTGT CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT	1500
	GTTGAATAAT TACATATCTT TCTTGACTAT ACTGATTCT TATTTTGGTC ACTATTACTA	1560
	AATCTCTGTT AATATTCTCT CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG	1620
45	CCATATTATT GGTGGAGGGC TGTTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT	1680
	ACCAACATCT TGAATATATA TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG	1740
50	GTGGAATATC ATTTTAAAAA GTTCATGTTT TGTCTATAT TTTCTTCACC TACTCTCCAA	1800
	ATATTGTAAT GCAAAAAGTC TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATTGT	1860
	TCTCTCGAT AAATTTATTT TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTTTTTCAA	1920
55	ATATGIGAAA TGTGAACTG CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG	1980
	ATTGAAATTA TTTTGNCTC CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT	2040
60	ATTTATTTAA GGINATAAAA TCTTGACATT TATAATCTTT C	2081

5 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

15 CCCC GCCGGA GCTGGACCCG CGGTGGGCTA GGGGCAGGCG CGGAGCCGCG GCGGCGGAGC 60
TGTGGATCCT TCATGATGAG AGATTGGGG ACACCTCTCT CTCCTGTGTG TAGTTGATAG 120
TTTGGTGGTG AAGAGATGCC TGACAGTGTC AAAACCTTTC TCCAGGACCT TGCCAGAGGA 180
20 ATCAAAGACT CCATCTGGGG TATTGTACC ATCTCAAAGC TAGATGCTCG AATCCAGCAA 240
AAGAGAGAGG AGCAGCGTCG AAGAAGGGCA AGTAGTGTCT TGGCACAGAG AAGAGCCCAG 300
25 AGTATAGAGC GGAAGCAAGA GAGTGAGCCA CGTATTGTTA GTAGAATTTT CCAGTGTGTG 360
GCTTGAATG GTGGAGTGT CTGGTTCAGT CTCCTCTTGT TTTATCGAGT ATTTATTCTT 420
GTGCTTCAGT CGGTAACAGC CCGAATTATC GGTGACCCAT CACTACATGG AGATGTTTGG 480
30 TCGTGGCTGG AATTCTTCCT CACGTCAATT TTCAGTGCTC TTTGGGTGCT CCCCTTGTTT 540
GTGCTTAGCA AAGTGGTGAA TGCCATTTGG TTTCAAGATA TAGCTGACCT GGCAATTGAG 600
35 GTATCAGGGA GGAAGCCTCA CCCATTCCCT AGTGTCAGCA AAATAATTGC TGACATGCTC 660
TTCAACCTTT TGCTGCAGGC TCTTTTCTC ATTCAGGGAA TGTTTGTGAG TCTCTTTCCC 720
ATCCATCTTG TCGGTCAGCT GGTAGTCTC CTGCATATGT CCCTTCTCTA CTCACTGTAC 780
40 TGCTTTGAAT ATCGTTGGTT CAATAAAGGA ATTGAAATGC ACCAGCGGTT GTCTAACATA 840
GAAAGGAATT GGCCTTACTA CTTTGGGTTT GGTGTGCCCT TGGCTTTTCT CACAGCAATG 900
45 CAGTCTCAT ATATTATCAG TGGCTGCCTT TTCTCTATCC TCTTTCCTTT ATTCATTATC 960
AGCGCCAATG AAGCAAAGAC CCCTGGCAAA GCRTATCTCT TCCAGTTGCG CCTCTTCTCC 1020
TTGGTGGTCT TCTTAAGCAA CAGACTCTTC CACAAGACAG TCTACCTGCA GTCGGCCCTG 1080
50 AGCAGCTCTA CTTCTGCAGA GAAGTTCCCT TCACCGCATC CGTCGCCTGC CAAACTGAAG 1140
GCTACTGCAG GTCACTGAGT TGCTGCCAT CCAAAGGGGA TGGGCGGGAT TGGAAGAAGC 1200
55 TGTGGCAGCT CTTTTCCTTG TTCACCTCCC GCCTGCCAGG GAAGGCAGGA CCCGCTCTGC 1260
CAAGGGCCCT CTGCGTATTC CCTTCTCTCT GAGGAATGA AATTTTGTG TCTGGTGAC 1320
60 GTAAGGCAGA ATGTTCCCTG ACACCAGTGT GTGGATTTT AACATCACC TGAGTCTGAA 1380

AGGACCACAG GTTTTTCTGC AGCTATTTTC TAGCATTTGC CAGTCCCTGT GCCTGGACTG 1440
ATTGGAACAC TTTGTTTTTC TCCCTGTGCC ATTTACCCTT CCACCTTTCC ATCCTGCCTT 1500
5 CTACCACCCT TGGATGAATG GATTTTGTA TTTCTAGCTGT TGTATTTGT GAATTTGTTA 1560
ATTTTGTGT TTTCTGTGA AACACATACA TTGGATATGG GAGGTAAAGG AGTGTCCCAG 1620
TTGCTCCTGG TCACTCCCTT TATAGCCATT ACTGTCTTGT TTCTTGTAAC TCAGGTTAGG 1680
10 TTTTGGTCTC TCTTGCTCCA CTGCAAAAAA AAAAAA 1717

15

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CCACGCGTCC GGTCACATAG TAGTGGAGGG GCAGACACCC TCCCGCAAAT TCTGGAAGGT 60
TCTTAGTCTC GACTAGGGCA GTAGCCCCAG GACTCCTAGT CGCCGGCTTC AGGTCACTGC 120
30 CGGCTGAACG GAGCTGCCGT CGCCATGTTT GGCTGCTTGG TGGCGGGGAG GCTGGTGCAA 180
ACAGCTGCAC AGCAAGTGGC AGAGGATAAA TTTGTTTTTG ACTTACCTGA TTATGAAAGT 240
ATCAACCATG TTGTGGTTTT TATGCTGGGA ACAATCCCAT TTCCTGAGGG AATGGGAGGA 300
35 TCTGTCTACT TTTCTTATCC TGATTCAAAT GGAATGCCAG TATGGCAACT CCTAGGATTT 360
GTCACGAATG GGAAGCCAAG TGCCATCTTC AAAATTTCAG GTCTTAAATC TGGAGAAGGA 420
40 AGCCAACATC CTTTGGAGC CATGAATATT GTCCGAATC CATCTGTGTC TCAGATTGGA 480
ATTTCACTGG AATTATTAGA CAGTATGGCT CAGCAGACTC CTGTAGGTAA TGCTGCTGTA 540
TCCTCAGTTG ACTCATTCAC TCAGTTCACA CAAAAGATGT TGGACAATTT CTACAATTTT 600
45 GCTTCATCAT TTGCTGTCTC TCAGGCCAG ATGACACCAA GCCCATCTGA AATGTTCAAT 660
CCGGCAAATG TGGTCTTGAA ATGGTATGAA AACTTTCAAA GACGACTAGC ACAGAACCCT 720
50 NTNTTTTGGN AACATAATT TGAATAAAT AATTTTTAAT GGATTTGNA AAAAAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAA 804

55

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
GGCACAGCCC AGGGCCTTGA AGCCAGCTGG CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG 60
GGAGGGTCTG GGATGGGGCT GCCCTGATG GCCCTGATGT GGAGTACCTT GCCAGCATCT 120
10 GCTGGGGTGA ACTTTATTTT AGCCCTTCCC TTGTTGCTCT TATGGAAGAA CAGAGGAGGG 180
GTGGGCAGGT CAGTGATGTC AGCAGTGGAG TGATTCCCAG CACAGCGGCT TCTGGGAAGA 240
15 GGGCATGGAG GCATTTCTTT CAGGGAAATG GTCCATNATT TCAGCCAGAA GGCATTGCAT 300
TAAGTTAAGT CCNGGACTTT TGTGGCCCAG CTCTGTGTTA TTAAGGGCCC TTGGCGAAGA 360
CTTCAAGGAG GGGGCAAAAN GACCTTTAAG TTTTtaggtt TAACACAGGG AACCNCAAA 420
20 GGGTTATTTT G 431

25 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 3752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:
35 NGGCACGAGG AGAGTCACCT GGACTCAGAA CTAGAGATAT CCAATGACCC AGACAAAATT 60
AAACTTCAGC TTTCTAAGCA TAAGGAGTIT CAGAAGACTC TTGGTGGCAA GCAGCCTGTG 120
40 TATGATACCA CAATTAGAAC TGGCAGAGCA CTGAAAGAAA AGACTTTGCT TCCCAGAGAT 180
ASTCAGAAAC TTGACAATTT CCTAGGAGAA GTCAGAGACA AATGGGATAC TGTTTGTGGC 240
AAGTCGTGG AGCGGCAGCA CAAGTTGGAG GAAGCCCTGC TCTTTTCGGG TCAGTTCATG 300
45 GATGCTTTGC AGGCAITGGT TGA CTGGTTA TACAAGGTGG AGCCACAGCT GGCTGAGGAC 360
CAGCCCGTGC ACGGGGGACC TTGACCTCGT CATGAACCTC ATGGATGCAC ACAAGGTTTT 420
50 CCAGAAGGAA CTGGNGAAG CGAACAGGAA CCGTTCAGGT CCTGAAGCGG TCAGGCCGAG 480
AGCTGATTGA GAATAGTCGA GATGACACCA CTGGGTAAA AGGACAGCTC CAGGAAGTGA 540
GCACTCGCTG GGACACTGTC TGTAAGTCT CTGTTTCCAA ACAAGCCGG CTTGAGCAGG 600
55 CCTTAAACA AGCGGAAGTG TTTGAGACA CAGTCCACAT GCTGTTGGAG TGGCTTTCTG 660
AAGCAGAGCA AACGCTTCGC TTTGGGGAG CACTTCCTGG ATGACACAGA GGCCCTGCAG 720
60 TCTCTCATTG ACACCCATAA GGAATTCATG AAGAAAGTAG AAGAAAACG AGTGGACGTT 780

	AACTCAGCAG TAGCCATGGG AGAAGTCATC CTGGCTGTCT GCCACCCCGA TTGCATCACA	840
	ACCATCAAAC ACTGGATCAC CATCATCCGA GCTCGCTTCG AGGAGGTCCT GACATGGGCT	900
5	AAGCAGCACC AGCAGCGTCT TGAAACGGCC TTGTCAGAAC TGGTGGCTAA TGCTGAGCTC	960
	CTGGAAGAAC TTCTGGCATG GATCCAGTGG GCTGAGACCA CCTCATTTCA GCGGGATCAG	1020
10	GAGCCAATCC CGCAGAACAT TGACCGAGTT AAAGCCCTTA TCGCTGAGCA TCAGACATTT	1080
	ATGGAGGAGA TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1140
	AAAAACATAG AGCCTACTCA CGCGCCTTTC ATAGAGAAAT CCCGCAGCGG AGGCAGGAAA	1200
15	TCCCTAAGTC AGCCAACCCC TCCTCCCATG CCAATCCTTT CACAGTCTGA AGCAAAAAAC	1260
	CCACGGATCA ACCAGCTTTC TGCCCGCTGG CAGCAGGTGT GGCTGTTAGC ACTGGAGCGG	1320
20	CAAAGGAAAC TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1380
	GACTTTGATG TCTGGAGGAA AAAGTATATG CGTTGGATGA ATCACAACAAA GTCTCGAGTG	1440
	ATGGATTTCT TCCGGCGCAT TGATAAGGAC CAGGATGGGA AGATAACACG TCAGGAGTTT	1500
25	ATCGATGGCA TTTTAGCATC CAAGTTCCCC ACCACCAAGT TAGAGATGAC TGCTGTGGCT	1560
	GACATTTTCG ACCGAGATGG GGATGGTTAC ATTGATTATT ATGAATTTGT GGCTGCTCTT	1620
30	CATCCCAACA AGGATGCGTA TCGACCAACA ACCGATGCAG ATAAAATCGA AGATGAGGTT	1680
	ACAAGACAAG TGGCTCAGTG CAAATGTGCA AAAAGGTTTC AGGTGGAGCA GATCGGAGAG	1740
	AATAAATACC GGTTCCTCCT CGGCAATCAG TTTGGGGATT CTCAGCAGTT GCGGCTGGTC	1800
35	CGTATTCGTC GCAACCGTGA TGGTTCGGCT TGGTGGAGGA TGGATGGCCT TGATGAATT	1860
	TTTAGTGAAA AATGATCCCT GCCGAGCAG AGGTAGAAGT AACATTGAAC TTAGAGAGAA	1920
40	ATTCATCCTA CCAGAGGGAG CATCCCAGGG AATGACCCCC TTCCGCTCAC GGGGTCTGAAG	1980
	GTCCAAACCA TCTTCCCGGG CAGCTTCCCC TACTCGTTCC AGCTCCAGTG CTAGTCAGAG	2040
	TAACCACAGC TGTACATCCA TGCCATCTTC TCCAGCCACC CCAGCCAGTG GAACCAAGGT	2100
45	TATCCCATCA TCAGGTAGCA AGTTGAAACG ACCAACACCA ACTTTTCATT CTAGTCGGAC	2160
	ATCCCTTGCT GGTGATACCA GCAATNAGTT CTCCCCGGC CTCCACAGGT GCCAAAACAA	2220
50	ATCGGGCAGA CCTAAAAAG TCTGCCAGTC GCCCTGGAG TCGGGCTGGG AGTCGAGCCG	2280
	GGAGTCGAGC CAGCAGCCGG CGAGGAAGTG ACGCTTCTGA CTTTGACCTC TTAGAGACGC	2340
	ATTGCTTGTT CCGACACTTC AGAAAGCAGC GCTGCAGGGG GCCAAGGCAA CTCCAGGAGA	2400
55	GGGCTAAACA AACCTTCCAA AATCCCAACC ATGTCTAAGA AGACCACCAC TGCTCCCCC	2460
	AGGACTCCAG GTCCCAAGCG ATAACACTGT CTAAGCACCC CCAAGCCACT ATCCACTTTG	2520
60	AATCCTGCTC CATACTTGG GTGTATATTT ATTCTGAACG GGAGAAGTTA TATTGTAA	2580

AGTGTAAAAG AATAATGTG TTATGAAGCT GCCTTATTTT TTTCTTTTTT GTAAGTTACT 2640
 ATTTTCATGT GAATATTTAT GTAGATAAAA TTTGCCTCCT GGTAACCCCTG TAATGGATGG 2700
 5 GGCCCAAGAA TGAAATATTT GAGAAAAACA AGTGAAAAGG TCAAGATACA AATGTGTATT 2760
 AAAAAAAAAA AAGCCTATTA ATAGGGTTTC TCGCGGTGC AGGGTTGTAA ACCTGCTTTA 2820
 10 TCTTTTAGGA TTATTCCTAA ATGCATCTTC TTTATAAACT TGACTTGCTA TCTCAGCAAG 2880
 ATAAATTATA TTAATAAAT AAGAATCCTG CAGTGTAA GGAACCTTT TTTGTAAAT 2940
 CACGGACACC TCAATTAGCA AGAACTGAGG GGAGGGCTTT TTCCATGTT TAATGTTTTG 3000
 15 TGATTTTTAG CTAAAGAGAG GGAACCTCAT CTAAGTAACA TTTGCACATG ATACAGCAAA 3060
 AGGAGTTCAT TGCAACTCTG TCTTTGGATA TTGTTTCAGT ACTGGGTGTT TAAAGGACAA 3120
 20 ATAGCTGCTA GAATTCAGGG GTAAATGTAA GTGTTGACAA AACGTCAGAA CATTTGGGGT 3180
 TTTAACTGA TTTGTGCTC CCTATCCAGC CTAGACACCA GTAACCTTG TGTCACCAG 3240
 GACCCAGACC CTTGGCAAGG GATAGGCTCG TTGGTGACAT TGTGAATTC AGATTTGTTT 3300
 25 TATCCACTTT TTTTGCTATT TATTAAATG GTCGATCAAC TTCCCACAA CTGAGGAATG 3360
 AATCCACGA GCCTGTCTG AAAATGTGGA CGTAAGACAA ACACGTGCTC GTCCTTTAAT 3420
 30 GGAGTTCACC AGCACACTTG TTAACCAGTC CTGTTTGCIT TCGTCTTTTT TTGTGCGTAA 3480
 TAAAGTCAAC TGACCAAGTG ACCATGAAAA GGGGCTGTCT GGGGCTCCTG TTTTTAGCT 3540
 GCTGTCTTC AGCTCCGACC ATGTTGCTGT GTGATTATCT CAATTGGTTT TAATTGAGGC 3600
 35 AGAACTGAA GCTCTACCA TGAAGTGTG AGAAACAAGA CACACTTTTG TATTAAAT 3660
 GCTTGCACTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACCTGAGG GGGGCCCCGT 3720
 40 ACCCAATTCG CCGTATATGA TCGTAAACAA TC 3752

45 (2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1144 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55 TGACCCTCTG CCTGCCGGGC TCAGTGCTGG ACGCTTCTG TTTGTGCGA GTCGGTCTC 60
 GGTAACACCA GCGGCCTGTG GTCCACCACT CCATTCAGCA GCTCCATTG GTCCAGCAAC 120
 CTTAGCAGCG CCTTCCCTTC ACCACTCCAG CAAACACGCT GGCAAGCATC GGCCTCATGG 180
 60

	GCACAGAAAA CTCCCCTGCT CCTCACGCTC CCTCCACCTC CAGTCCAGCT GACGACTTGG	240
	GACAGACCTA CAACCCGTGG CGGATATGGA GCCCCACGAT TGAAGAAGA AGCTCGGACC	300
5	CTTGGTCTAA TTCGCACTTT CCTCACGAGA ATTAAATTAA GCAAAAAACA AACAAACATA	360
	GTGGGCCCTC GTCTAGATCA TGATGTGCCA GTTCTGAGA CATCTTTTA AGGCTCTTAC	420
	TGCAGCTCCC CTCCCACCC TCCTCTTCTT TGCAAAACAG ACCCAAGCAG GGCAGGCTCA	480
10	GACCACTCGC TTCTTTCAGA TCTTCTTGC AATTATGATA ACATGAGATT TGCTGTTGTG	540
	CTTTTAGAGA AAAGTCTGGA CTCAGCCACA AACTCTAATA AGACCTGTAC ATCTGAGAAC	600
15	CTTTCCCGTT ACTGCGTTTT CACCACCTGT CTTCCCATG CTTTATTTAT CTGTATGAAC	660
	ACAGATTTGA CATTACAGCT AAGGAAATAA TTTGAGTTGA TTCAGAAATC CTGGCATGTG	720
	ACAATTTTGT TAAATTACCA AGTTTGGTTT TTAATAATTT CTCATATTA TGCGCCAAGA	780
20	TCTAATTTTA AAAGTGTATG AGGACTTTGT GCTGAAAATA GAGTATTTT TTAAAGTAAG	840
	GCTGTCTTGG TTTAAAGCA GATTACAGAA ATGTAAGTCA ACTTAAGAAC RGTGAATGAA	900
25	TGTAAAAACA TTCAGTYGAG ACCATATGCA TTTTCTGTGC TGTTTGTACT TGAGGTATGT	960
	AACATTTGTA TACCTGAAC TATTTTAAAG ATGAAC TGAA ATGCACATAG CCAAGTCTTG	1020
	AGATACAAGA TTGAATGTGT ATTTCTTAAA AATACAAC TTGTGTGTAC TTGAAATAA	1080
30	ATGATGCTTT TTTCAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCCCGGTACC	1140
	CAAT	1144

35

(2) INFORMATION FOR SEQ ID NO: 129:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	GCATGCAGAG GAGCACCTG AGCGTGYCC TGGAGCAGGC GGCCATSTTG GCACGGAGCC	60
50	ACGGGTGCT GCCCAAGTGC ATCATGCAGG CCACGGACAT CATGCGGAAC AGGGCCCAAG	120
	GGTGGAGATT CTGGCCAAA ACCTGCGAGT CAAGGACCAG ATGCCCCAGG GTGCTCCGG	180
	CCTCTACCGC CTCGTCCAGC CGCCGTGGA TGGGACCTC TGAACACCCA AATGCCCCAC	240
55	GCTGGGCCG GGCCTCTGGA GCTGGGATTT GGGAGGACAC AGCAGGCAGC GCTGGCCTTC	300
	TCCAGGGATG GCCCAANGCT TCCGCARCCG CCCGTTCCGG GACCTGCCCA GCGTCTCCC	360
60	TGCCTCCTC CGGACAAGC CTGGCCACCC TCGCTGTGAT GACGAGCTGG CTGATTGGCC	420

	CTGGGCCGGC CCATTCTTCA CACGCCCTGCC AGAAGCTGGA GGGGTGCTGG AGACCCATAG	480
	AGCTGATGGG AGCAGCTGGT GCCTGGCCTT CCGCTCCTGC GTCCCCAGAA CCCAAGGGAA	540
5	CGTCATGGAG GCCACATGGG GCCACCCGGC TCCTCGGGA TGGCTCCGCT GCACTTTTGA	600
	AACCCCGGTT TCCTTCAACG TCCACATTCC AGGTGACCAC ACGTGTCTCC TCCTCCTCAT	660
10	CTTAGCTTCC AGGTTACACC TAACCTGTGA CTAACCTGCT TGGTGGACTT GGAAAAGACT	720
	TGGCTCTGTC GGGAAAGGAG AGACGGGGCC TCCATCACGC CTGTTACCAG AGGATCCCCG	780
	AGAGCCACAC CAGCTCTGGA CATCACCACC CCTGGAAC TG GGGCCACCAG CCTGGGCAC	840
15	GAGATTTGCT CTGACTTTAT TTATATGGCA TGAATCTCT GGTTTATTTT GGGATTTTTT	900
	GTTGTGGTG TTGTCAAAGT TTGTTTTTTC TAAAGTTGTG TGATTATATA TTTGACATTT	960
20	TACATTTCAA AGAAAGGTAT GTTGTCTAAC AGGGGACCAA CAGAAGGTAG TATTGACAAC	1020
	TGTTCTGCT TCTACTAAAA AAAAAAGAGC ACAAAGAAA AACTAAATTA TTGAAAAATT	1080
	AAAAAATGTC ATTGTTTCCT GTTGTGTAAT ATTAGGGTGG TAAGGTGTCG TTTTGAGGTA	1140
25	TCGACTGTGA TTCCTTCCCC CACCCTCCAT TCTCCAGCGG TTGGCCGGTG TTAGAACTCG	1200
	CTCTCTTTGA GTGACTGGCT ACAAGGGCCT GAGAGGTGGC CAGCCAGGGT TGGAGCTGGA	1260
30	GGGGATGGAG CCCACCTGA GGTGCCGTGT CACACGGGTT AGAGGGTCAC TGGGAAACAC	1320
	CGGGCGGTGG CTCTGTGAT TTATTTTCTT GATGGTAACT TCTCAGAGCA GGGCRATTGG	1380
	GACATCACCA GCCAGAGCAC AGGAAGCCAC CCTGCCTGCT GGGGAGGAGG GACCCACACA	1440
35	AGCCCCCTCG GCAGTTGTG CCCCCAGCTT CGGTATGCCT TCAGGGAAAG GTCACAGCTG	1500
	GGGAGGAAGC GGGGGGACGC CTGTCACCCC TGGCAGGTGG TGAGTTCAGG TGGGGGCTCC	1560
40	CTGCTKCCCC CAGGCCTGGG AGCTTGAAGC CCTCCCGGCA TCTGGCATCC GAGCCTCCCG	1620
	CCCTCCAGGG TGGCCTTCCC TCTCTTGCCG CAGCATACAC GAGGGCAGGC AGTGGCCTTG	1680
	TCACTGTATC TTGCATCAGA GACAAAGGAG GACCCGCTTT AGCCCTGCTG CGGGAAATGG	1740
45	GGGATGGCCC AGGGCCAGCG CATGTGCAC TGGTTTACTT TAAATGTAC AGATTCTTCT	1800
	CGTTAAATTC TTGATAGATT TTTTATTATT	1830
50		

(2) INFORMATION FOR SEQ ID NO: 130:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	GGCCGCCCGG ATGGCGACCC CAGCCTCGGC CCCAGACACA CGGGCTCTGG TGGCAGACTT	60
5	TGTAGGTTAT AAGCTGAGGC AGAAGGGTTA TGTCTGTGGA GCTGGCCCCG GGGAGGGCCC	120
	AGCAGCTGAC CCGCTGCACC AAGCCATGCG GGCAGCKGGA GATGAGTTCC AGACCCGCTT	180
10	CCGGCGCACC TTCTCTGATC TGGCGGCTCA GCTGCATGTG ACCCCAGGCT CAGCCCCAACA	240
	ACGCTTCACC CAGGTCTCCG ATGAACTTT TCAAGGGGGC CCCAACTGGG GCCGCCTTGT	300
	AGCCTTCITTT GTCTTTGGGG CTGCACTGTG TGCTGAGAGT GTCAACAAGG AGATGGAACC	360
15	ACTGGTGGGA CAAGTGCAAGG AGTGGATGGT GGCCTACCTG GAGACGCGGC TGGCTGACTG	420
	GATCCACAGC AGTGGGGGCT GGTATATCCA GATCACTGAA GCTGAGATGG CTGATGAAGT	480
20	AATTTCAGT GAAATTTTAA GCGACTGTGA CTCTGCTGCA AGTTCCCAG ATCTTGAGGA	540
	GCTGGAAGCT ATCAAAGCTC GAGTCAGGGA GATGGAGGAA GAAGCTGAGA AGCTAAAGGA	600
	GCTACAGAAC GAGGTAGAGA AGCAGATGAA TATGACTCCA CCTCCAGGCA ATGCTGGCCC	660
25	GGTGATCATG TCCATTGAGG AGAAGATGGA GGCTGATGCC CGTTCCATCT ATGTTGGCAA	720
	TGTGGACTAT GGTGCAACAG CAGAAGAGCT GGAAGCTCAC TTTCATGGCT GTGGTTCACT	780
30	CAACCGTGTT ACCATACTGT GTGACAAATT TAGTGGCCAT CCCAAAGGGT TTGCGTATAT	840
	AGAGTTCTCA GACAAAGAGT CAGTGAGGAC TTCCCTGGCC TTAGATGAGT CCCTATTTAG	900
	AGGAAGGCAA ATCAAGGTGA TCCCAAAACG AACCAACAGA CCAGGCATCA GCACAACAGA	960
35	CCGGGGTTTT CCACGAGCCC GCTACGCGC CCGGACCACC AACTACAACA GCTCCCCTC	1020
	TCGATTCTAC AGTGGTTTTA ACAGCAGGCC CCGGGGTCGC GTCTACAGGG GCCGGGCTAG	1080
40	AGCGACATCA TGGTATTCCC CTACTAAAA AAAGTGTGTA TTAGGAGGAG AGAGAGGAAA	1140
	AAAAGAGGAA AGAAGGAAAA AAAAAAGAAT TAAAAA AAAA AAAAAA ACAGAAGWTG	1200
	MCCTTGATGG AAAAAAATA TTTTTAAAA AAAAGATATA CTGTGGAAGG GGGGAGAATC	1260
45	CCATAACTAA CTGCTGAGGA GGGACCTGCT TTGGGGAGTA GGGGAAGGCC CAGGGARTGG	1320
	GGCAGGGGGC TGCTTATTCA CTCTGGGGAT TCGCCATGGA CACGTCTCAA CTGCGCAACT	1380
50	GCTTGCCCAT GTTCCCTGC CCCACCCAC CCTCTTCTC CGGCTCCCTG CCCCTCCAGA	1440
	TTGCCTGGTG ATCTATTTTG TTTCCTTTG TGTTCITTT TCTGTTTGA GTGTCTTTCT	1500
	TTGCAGGTTT CTGTAGCCGG AAGATCTCCG TTCCGCTCCC AGCGGCTCCA GTGTAAATTC	1560
55	CCCTTCCCC TGGGGAATG CACTACCTTG TTTTGGGGG TTAGGGGTG TTTTGTTTT	1620
	TCAGTTGTTT TGTTTTTTG TTTTTTMIT TTCTCTTGC CTTTTTCCC TTTTATTTG	1680
60	AGGGAATGGG AGGAAGTGG AACAGGGAGG TGGGAGGTG ATTTTGTTTA TTTTTTTAGC	1740

	TCATTTCCAG GGGTGGGAAT TTTTPTTTTAA TATGTGTCAT GAATAAGTT GTTTTGA	1800
	AKAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1860
5	AAAA	1864
10	(2) INFORMATION FOR SEQ ID NO: 131:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2041 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:	
20	GGCAGGAGCG GCGGCAGGG CCTTGGACCC GCGCGGCTCC CGGGGATGGT GAGCAAGGCG	60
	CTGCTGCGCC TCGTGTCTGC CGTCAACCGC AGGAGGATGA AGCTGCTGCT GGGCATCGCC	120
	TTGCTGGCCT ACGTCGCCCTC TGTTTGGGGC AACTTCGTTA ATATGAGGTC TATCCAGGAA	180
25	AATGGTGAAC TAAAAATTGA AAGCAAGATT GAAGAGATGG TTGAACCACT AAGAGAGAAA	240
	ATCAGAGATT TAGAAAAAAG CTTTACCCAG AAATACCCAC CAGTAAAGTT TTTATCAGAA	300
30	AAGGATCGGA AAAGAATTTT GATAACAGGA GCGCAGGGT TCGTGGGCTC CCATCTAACT	360
	GACAAACTCA TGATGGACGG CCACGAGGTG ACCGTGGTGG ACAATTTCTT CACGGGCAGG	420
	AAGAGAAACG TGGAGCACTG GATCGGACAT GAGAACTTCG AGTTGATTAA CCACGACGTG	480
35	TGGAGCCCCT CTACATCGAG GTTGACCAGA TATACCATCT GGCATCTCCA GCCTCCCCTC	540
	CAAACATCAT GTATAATCCT ATCAAGACAT TAAAGACCAA TACGATTGGG ACATTAAACA	600
40	TGTTGGGGCT GGCAAAACGA GTCGGTGCCC GTCTGCTCCT GGCCTCCACA TCGGAGGTGT	660
	ATGGAGATCC TGAAGTCCAC CCTCAAAGTG AGGATTACTG GGGCCACGTG AATCCAATAG	720
	GACCTCGGGC CTGCTACGAT GAAGGCAAAC GTGTTGCAGA GACCATGTGC TATGCCTACA	780
45	TGAAGCAGGA AGGCGTGGA GTGCGAGTGG CCAGAATCTT CAACACCTTT GGGCCACGCA	840
	TGCACATGAA CGATGGCGCA GTAGTCAGCA ACTTCATCCT GCAGGCGCTC CAGGGGGAGC	900
50	CACTCACGGT ATACGGATCC GGGTCTCAGA CAAGGCGGTT CCAGTACGTC AGCGATCTAG	960
	TGAATGGCCT CGTGGCTCTC ATGAACAGCA ACGTCAGCAG CCGGTCAAC CTGGGGAACC	1020
	CAGAAGAACA CACAATCCTA GAATTTGCTC AGTTAATTAA AAACCTTGTT GGTAGCGGAA	1080
55	GTGAAATTCA GTTCTCTCC GAAGCCCAGG ATGACCCACA GAAAAGAAAA CCAGACATCA	1140
	AAAAGCAAA GCTGATGCTG GGGTGGGAGC CCGTGGTCCC GCTGGAGGAA GGTTTAAACA	1200
60	AAGCAATTCA CTACTTCCGT AAAGAACTCG AGTACCAGGC AAATAATCAG TACATCCCCA	1260

5 AACC AAAAGCC TGCCAGAATA AAGAAAGGAC GGACTCGCCA CAGCTGAACT CCTCACTTTT 1320
 AGGACACAAG ACTACCATG TACACTTGAT GGGATGTATT TTGGCTTTT TTTGTGTGTC 1380
 GTTTAAAGAA AGACTTTAAC AGGTGTCATG AAGAACAAAC TGGAAATTCA TTCTGAAGCT 1440
 TGCTTTAATG AAATGGATGT GCCTAAAAGC TCCCCTCAAA AAAGTGCAGA TTTTGCCTTG 1500
 10 CACTTTTGA ATCTCTCTT TTATGTAAAA TAGCGTAGAT GCATCTCTGC GTATTTTCAA 1560
 GTTTTMTTAT CTGCTGTGA GAGCATATGT TGTGACTGTC GTTGACAGTT TTATTTACTG 1620
 GTTCTTTTGT GAAGCTGAAA AGGAACATTA AGCGGGACAA AAAATGCCGA TTTTATTTAT 1680
 15 AAAAGTGGGT ACTTAATAAA TGAGTCGTTA TACTATGCAT AAAGAAAAAT CCTAGCAGTA 1740
 TTGTCAGGTG GTGGTGC GCCATTGATT TTAGGGCAGA TAAAGAATT CTGTGTGAGA 1800
 20 GCTTTATGTT TCTCTTTTAA TTCAGAGTTT TTCCAAGGTC TACTTTTGAG TTGCAAACCT 1860
 GACTTTGAAA TATTCCTGTT GGTGATGATC AAGGATATTT GAAATCACTA CTGTGTTTGT 1920
 CTGCGTATCT GGGGCGGGG CAGGTTGGG GGCACAAAGT TAACATATTC TTGGTTAACC 1980
 25 ATGGTTAAAT ATGCTATTTT AATAAAATAT TGAAACTCAC CAAAAAAAAA AAAAAAAAAA 2040
 A 2041

30

(2) INFORMATION FOR SEQ ID NO: 132:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2012 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TACCAAGCTG CAAGAATCTA CTATATCATG GCAGAAGAAG TAGAGTGGGA CTATTGCCCT 60
 45 GACCGGAGCT GGGAACGGGA ATGGCACAAC CAGTCTGAGA AGGACAGTTA TGGTTACATT 120
 TTCTTGAGCA ACAAGGATGG GCTCCTGGGT TCCAGATACA AGAAAGCTGT ATTCAGGGAA 180
 TACACTGATG GTACATTGAG GNTCCCTCGG CCAAGGACTG GACCAGAAGA AACTTTGGGA 240
 50 ATCTTGGGTC CACTTATCAA AGGTGAAGTT GGTGATATCC TGACTGTGGT ATTCAAGAAT 300
 AATGCCAGCC GCCCCTACTC TGTGATGCT CATGGAGTGC TAGAATCTAC TACTGTCTGG 360
 55 CCACTGGCTG CTGAGCCTGG TGAGGTGGTC ACTTATCAGT GGAACATCCC AGAGAGGTCT 420
 GGGCCTGGGC CAATGACTCT GCTTGTGTTT CCTGGATCTA TTATCTGCA GTGGATCCCA 480
 TCAAGGACAT GTATAGTGGC CTGGTGGGTC CCTTGGCTAT CTGCCAAAAG GGCATCCTGG 540
 60

	NAGCCCCATG GAGGACGGAN TGACATGGAT CGGGAATTG CATTGTTGTT CTGATTTTT	600
	GATGAAAATA AGTCTTGGTA TTTGGAGGAA AATGTGGCAA CCCATGGGTC CCAGGATCCA	660
5	GGCAGTATTA ACCTACAGGA TGAACTTTC TTGGAGAGCA ATAAAATGCA TGCAATCAAT	720
	GGGAAACTCT ATGCCAACCT TAGGGGTCTT ACCATGTACC AAGGAGAACG AGTGGCCTGG	780
10	TACATGCTGG CCATGGGCCA AGATGTGGAT CTACACACCA TCCACTTTCA TGCAGAGAGC	840
	TTCTCTATC GGAATGGCGA GAACTACCGG GCAGATGTGG TGGATCTGTT CCCAGGGACT	900
	TTTGAGGTTG TGGAGATGGT GGCCAGCAAC CCTGGGACAT GGCTGATGCA CTGCCATGTG	960
15	ACTGACCATG TCCATGCTGG CATGGAGACC CTCTTCACTG TTTTCTCTCG AACAGAACAC	1020
	TTAAGCCCTC TCACCGTCAT CACCAAAGAG ACTGAAAAAG CAGTGCCCCC CAGAGACATT	1080
20	GAAGAAGGCA ATGTGAAGAT GCTGGGCATG CAGATCCCCA TAAAGAATGT TCAGATGCTG	1140
	GCCTCTGTTT TGGTTGCCAT TAGTGTCAAC CTCTGCTCG TTGTTCTGGC TCTTGGTGGA	1200
	GTGTTTGGT ACCAACATCG ACAGAGAAAG CTACGACGCA ATAGGAGGTC CATCCTGGAT	1260
25	GACAGCTTCA AGCTTCTGTC TTTCAAACAG TAACATCTGG AGCCTGGAGA TATCCTCAGG	1320
	AAGCACATCT GTAGTGCACT CCCAGCAGGC CATGGACTAG TCACTAACCC CAACTCAAA	1380
30	GGGGCATGGG TGGTGGAGAA GCAGAAGGAG CAATCAAGCT TATCTGGATA TTTCTTTCTT	1440
	TATTTATTTT ACATGGAAAT AATATGATTT CACTTTTCTT TTAGTTTCTT TGCTCTACGT	1500
	GGGCACCTGG CACTAAGGGA GTACCTTATT ATCCTACATC GCAAATTTCA ACAGCTACAT	1560
35	TATATTTCTT TCTGACACTT GGAAGGTATT GAAATTTCTA GAAATGTATC CTTCTCACAA	1620
	AGTAGAGACC AAGAGAAAAA CTCATTGATT GGGTTTCTAC TTCTTTCAAG GACTCAGGAA	1680
40	ATTTCACTTT GAACTGAGGC CAAGTGAGCT GTTAAGATAA CCCACACTTA AACTAAAGGC	1740
	TAAGAATATA GGCTTGATGG GAAATGAAG GTAGGCTGAG TATTGGGAAT CCAAATTGAA	1800
	TTTTGATTCT CCTTGGCAGT GAACTACTTT GAAGAAGTGG TCAATGGGTT GTTGCTGCCA	1860
45	TGAGCATGTA CAACCTCTGG AGCTAGAAGC TCCTCAGGAA AGCCAGTTCT CCAAGTTCTT	1920
	AACCTGTGGC ACTGAAAGGA ATGTTGAGTT ACCTCTTCAT GTTTTAGACA GCAAACCCTA	1980
50	TCCATTAAAG TACTTGTTAG AACACTGAAA AA	2012

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

5	GAGCAGTATT TTAACCAACT TGTATTACAG ATGTTACAGT TCATGTTAGG AAGTCAGAAA	60
	AGACTTTGTT TGTCTTTGTT CTGCTGATGT GAGTCATGTT TTGTGGGGTC TTCCATGGCA	120
	CATTTACCTG TTGCTCCGTC CAGATGTTGA GGGCCAGTCT AGGCTGACAC ATCCTACCCG	180
10	AGGACAAGCC TGTCTCCAT TTCTTCACTC TCCCCTCCCC ATATAGCAAC TCTCCCAGGT	240
	TTAGATTACC GTTTTCGACG ACAGATTAAC CAAAAATGCC CCACACAGGT TTTATTACTG	300
15	TTATATACTA TACTTTTAAC AGTACAGACC CTAAATTTTA TTATTTGTTG CTCCCCCAAT	360
	CTGATACCAA ATGTTTAAAG TTGTTTGAAA TCCAAACATG GTAGTGTTCA TGGGTAAATA	420
	TTTTCTAGGC TATGTAAGAG TTAGCAGCCC ATAGCATAGA AGTAATCAAG TAGCATCTGA	480
20	GA CTGTTGGA GGCAC TAGGG CCTCTCTGGG CCTAACAGCC TCACCTCCCC AGCCTCACCT	540
	TGCTGTCTC TGACACTGCC ATCAGGGCTG TTAGTGGCAC CTGTATGAGG CCAAGTGTC	600
25	GTCCAGGGGA ACAGCACAGG TTAATGCGTC TCCCTAGAAC TCATGAAGTC AGTTTAATTC	660
	ATGCATGAAC ATGAGTTCAT TTTATGTTTT ATATAGCTTT CTAGACATA CCAAACCATC	720
	ATTCATAAAT CAGATAAATT ATTCAATTTT TGTGTTTGA AAGCTAAGTA TGTGTAGCTG	780
30	GAAACAAAAA TGAGCGTGT TTCTCTCTG TTAATCTAGA GTGTGCAGTT ACACATGTGT	840
	GGATAATTTC ATGTTCCAGG GGCCTTGGC ATCTCCCATG GACTGATTCC CAGGAAGAAA	900
35	AGCCCAAAGG GAAACCCACG ATTCTTTTCG AGTAGATGTG GGAAAGAGCC CATTTGGAGGA	960
	TATGAGGTCC TGTGAAATTC AGTTGTGTGT GTGGCTCCTT GTTAGCAGTC ATGTTGACAT	1020
	GGTGTAGGA GGCTCCCCAT CCACCTTTA CATGATGTAG GGACCACTGT CTTGTGAGAT	1080
40	TAACCTTGGG ACACAGTGGG TTAGCCTGGA GAAAATGAGA GGCCCTGCCT GGACCCAGGG	1140
	AGAGGAGCCA GTGACACAGG CAGAGCGGTG CAGCCCTCCT TCCCTTCCAT TTGGAGGAGG	1200
45	TGGTGCCAGG AGCCTGCCCG CTTACCTCTG CTGAAGCATA AGTGGACTTT GCTTTTGGGG	1260
	CTTATCTCTG ATACATGCTG GAGCCCTGCC TCTCCACTGC TAGATGGAAC CTGGAATCTC	1320
	TCATCTACCT CTTAGTCTGT CAGTTTCTAC GTGTGAGAAG CAAGCTTGTG GGCCAGTGTG	1380
50	CTTGACATG CTGTAGCACT TAAAAAATAA TTCCAGGGTT CCCTGGAAAA CCACTCCCAG	1440
	GGTTCCTATG ATCTGTAGTT TCTACCTGGA TTATAACTGG TTTTGGGTAC CTGAATTTTG	1500
55	ATTGGTTAGC CTTAATTATA GTCTGGCGTG ATCATGTAGA ATCTTTTCTG GTGAACAGAT	1560
	CATAAAGTTC TATCAAGGAG TTCTATCAAG GCATCCATGT CAGTGGTGCT ATGCTGGTTA	1620
	CAACTTGAGA TTTTGAAT AAAAAATTG TCATAAAAAA AAAAAAAA	1669
60		

(2) INFORMATION FOR SEQ ID NO: 134:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CACTTTTGCT ATATAACCTA AGTGATAACC CTCMTTAGT TACCTGCCAA ACTCTGGNCT 60
15 TGGTMTATAT TGCAGTTAAC ACAGTTACAA AGCTGTAATG GTGTCMTTTT TTCCTTTGTA 120
ACCGAATGTG TAAATCAAAG TATATACATT GTGTGGTGTT CCTGTTCTG GAGTTTCATG 180
AGGATTTACA CATGGCATTG AGTGTCTGT ATAGATCTGC CTACCTTTGT GAATTCATCT 240
20 GTTAACCCCT CTCCTTTGA GAGAGCACCG GCGATGGTGG TTAACCTCT GTGTTTCTC 300
TCTCTCCTAC TGGTTATTCT TGAATTAAGC ACAGACTCGT CAGCTCGGTT GCTTTATCAT 360
25 GAATAATGTG TGTGACCTTG CAGTTCCTCC ACAGTTCAGC AAACAAGTGC TAGCTTCACT 420
GACCAAAAAT TAAGGAAGGA AAACACAGTT TTAAAACGA TCCATCTTTT AACAGCCGAA 480
ACCGATGTGT CTATGGTGCT GCACCTTGCT GTTGTACTTC TGAAATCAGA CGTGTGTGAA 540
30 CGATCATTTT TGACTTAACC GTGAGATGCT CACGAGTACC CTCCTGTTG TTTTGTTAGC 600
ATTGAAATCG AGACTATTTA TTTGGAATAT ATACAACAGT GTTTTCCAC TGTATTTTAT 660
35 TTGCAAAAGT TGAGAACTGC TTTCTCTACC TTTTGCAAAA TAATTGATAT TCCATATGG 720
ATTCTCAAAG ACTTCGATAT GGTGAACCTA TTAAACCTAG AAATTGTATT CATCCTTTCA 780
TGACTGTGGC CTGAGTCCC CAGCCCCTCT CCTCCTTTTT TTTAGATGAG ATTTAGCACA 840
40 CTCTCAGTTA TTTAAACATG CAACATTTCT TGAGTATGTA TGTGAGGCC ATCTGAGCTC 900
ATAGCTGATT CAGTAACCAG TTTTCATGCTG TGTCAITCAC ACTCACTACT TAATACTGCC 960
45 ATGGTGAAAA TGTGGAGGAA AAATGTATCC ATGTGTGTCT GGGAAGCATA TACACTTGTA 1020
CATTTTTTAA TACTCTGATT CTGTAACATT TCTGAGTTT GTTTTGTITT ACAGNAAAAA 1080
AAAAAAAGT GATAAAGCAA TCAGAAGACC AAGAGGTTA CTATTGATGC TTAGGGTCGT 1140
50 CTGACCTTGG CTGGCCAATA GACCTACAG GCCAAATTAA TTTACGAGAG TAATAATTTT 1200
TCAAAAGCCA ATTTTTTTTC TGTATTTTCT GTATGAACT GCCAATATCA TGAATAGAAA 1260
55 GGGAGAACCA TAAAGGAGAA AGAACGTGAT GTTCTGTTAT GTTCATGTAA ACCTAAAGAA 1320
ACAGTGTGGA GGCAGGCGG ATCAGCCGAA CTCTAGGGAC TTGGTGTGTC TTGGAAGGCA 1380
TCCATACCTG CATTTTGCAT TCTTCGTATG TAATCATATT GCCAAAGACA AACTATTTCA 1440
60

TCATTTATG TAAATAACAC TTTTCCCCAG ACCTACCATA AAGTTTCTGT GATGTATTGT 1500
CTTCCAGTTG CAATAAAAT TACTGAGTTG CATCAATTGA AGAAAAAAAA AAAAAAAAAA 1560
5 CTCGA 1565

10 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2007 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

20 TCTAAAGCC CCCTTATACC CCACTTTGTG CAGCAAAGAT CCCCCTGCAG GTCACAGCCT 60
GATTTGTGGC CAGGCTGGAC AAATTCCTGA GGCACAACCT GGCTTCAGTT CAGATTTCAA 120
GCTGTGTTGG TGTGGGACC AGCAGAAGGC AAACGTCCAG CCAACACACA GGA CTGTAAG 180
25 AGGACTCTGA GCTACGTGCC CTGTGAAGAC CCCCAGGCTT TGTCATAGGA GGTGTTTCAG 240
CTTCCCCAAA GTCAGAGGTG ATTTGATTG GGAAGACTG AATATTCACA CCTAAGTCGT 300
GAGCATATCC TGAGTTTAC TTCCTTATGG CTGCCCCTCC AAGTTCTCTC TCTCATACAC 360
ACACACACCC TTGCTCCAGA ATCACCAGAC ACCTCCATGG CTCCAGCTAT GGAACAGCT 420
GCATGGGGC TGCCTTTCTG TTTGGCTTAG GAACTTCTGT GCTTCTTGTG GCTCCACTCG 480
35 CGAGGCAGCT CGGAGGTGTG GACTCCGATT GGGCTGCAGG CAGCTCTGGG ACGGCACAGG 540
GCGGGCGCTC TGATCAGCTC GTGTAAACA CACCGTCTTC TTGGCCTCCT GGCAGTTCTT 600
40 TCTGCGAATA GTCCTCTCCC TGGCCAGTTG AATGGGGGAA GCTGCTGGCA CAGGAAGGAG 660
AGGCGATCCC GGCTGAGGCT TAGGAAATTG CTGGAGCCGG CTCCAAGCAG ATAATTCAT 720
GGGAGGTTT TCAGAGTCAA ACATCATTTT GCCTGTTTGT GGGGCCAGGT GTGTACACA 780
45 AGCATCTCAA AGTCAAAAGC CATCTGGGGC TGCTGCTTCT CTTTCTCAGG CTC TGGGGAA 840
AGGAATCTCC CTCTCCTCTC ACTTGATTCC AAGTGTGGTT GAATTGTCTG GAGCACTGGG 900
50 ACTTTTTC TCTTTTCCTT GATGGACCAA CAGTGCAAAT GCAATCTCGC CATTTAACCT 960
TCAGGTCGAT TTCCTTTCCT GATCAGACAT CTTTGTGCCC CCTTTAGGAA GGAAAAGAAT 1020
ACACCTACGA TGTGCCAGGC ACTGTGTTAG GCGCTTTTAT ATAGATCCTC GTTAGGATGA 1080
55 GACTAAGGGA TGAGGACATC TCTTTATAAA AGGCCCTAA GTAATGGATA AACAGAAACA 1140
CTTAGAGGTG AGAAGGTCTG TCTTCAAGAT CCAAGGTAAG ATTGCCTTCA GTCTGATGTT 1200
60 TGTCTCAAG GACTTATCCC CTACAATATT CTCCACTCC ATACTTCTCC TTCTACCCCA 1260

5 CCATGTGCTC CCGTGCACTC CTCAGATGGT CAGAGGGGTA ACCCAAGTCC TTAGAGAATT 1320
 TGGGGACCAA TAGAATATGT GATGTGTGAA TTTTCTTTAA AAACTTAAG GAGTCTTTGC 1380
 TACCTTCTGC TTGTTGAGTT GTTTTGGCAT TCATATTAAA AGCCAGCATC TCACTATTTA 1440
 TTGACAGGTT GGGCTGTGTG TGTGCGCATG TGTGTATACA TTTCCAGGCG TGCCTGTGTC 1500
 10 CTGTAGCTTT TTAAGGAA ACCCAGTCAT CCCACTATGA ATCTGGCATC TTCTTATGCT 1560
 TCTAGTGTTC TGGCCATACA TCAACCAAGG GGTTTAATTT ATCCAATGCT TGACGACATG 1620
 TTCAGGAGGG GCTGGATCAA ATTTTGAGAG GGTTATGGGA AAGGGAGGGG GAGAAGAAAT 1680
 15 TGACATTTAT TTTATTATTT ATTTTAAATG TTTACATCTT CTMTATGTTG TATCAAGCCT 1740
 GAATAGAAAC TGATAGCATT AAAATACTCC GTTCCTCTCT CTCTTCTCGC TTCCTTTTTT 1800
 20 TTTTTTTTTA AATTTAGGAT AACACATTTT TGTTCCTAAA GTGATTTGTG ATTTGTGCTG 1860
 TATAAACTGT ATAAAAGGTT CTGTTTTTAA AGGTGGATTT TCATTCCTCT GGGGACAGTG 1920
 25 GTCGCCAAGA CATCTACATT GTAAGAGAAC ACAGTGAAG ATCCTGTCCT GATTCTCAAA 1980
 AATTATTTTC TCTGTATGAT TAAAAGT 2007

30

(2) INFORMATION FOR SEQ ID NO: 136:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CTTTAAACCC TCCCCCTTCA CACACATACA TATCAGGTTG TTTCTAGTT AAAAACCCTAA 60
 GTAGCTCAGA TTCTACTTTA ATGTCAGTGC AGATTTGCAT TGAATCATGC CATTATGTTT 120
 45 TTTCTCATTT TTATGCTGTT GGGTCTTAGT TTTTAAATG ATATAAAGAA CTCAGCAATG 180
 GTTTATTTT CTACTCATAC TTAGGGTTTA GGAACACTA CCACTAGTTA TCATTTAATC 240
 AACTTCAATG GTCTACTGAA ACAAAAATGG TAACTTTTC TTAGTGGATT ATTTAGAGTT 300
 50 ATAGTAGTTG TTTCCAGAAA ACACCTCCTC ACAATGTGAC TTCCCAATCA AATCATGTGA 360
 TCATACAGTT ATTCCCATGA AAGGCAGAAT GTTTGTTTCA AAATTAATCT AGTTTCTGT 420
 55 ACATTTAAAT TTGAGAAGGT GACAACTGGC TCTTTTCCAG TCTTCCTTCA TGTCAGTTT 480
 CTGATAGACC ACTATTGGCA AACAGTATCT GTCAACTACC AAATGTGTAA AATTTCTGT 540
 60 ATTTCACTTT GTCTTATTTG TAAATAGTGA ACTAAAATT TTGGCAGATC AGCAACATTT 600

	GCTGAGCCTG TTTTAAAGC TAATGTGTAT TCTTACTAAT GTTCCTATCA AGAATGGATT	660
	TGTAATATAT GCTGTCTATT TCTAATGTC ACATTCATAT TTTGAGGTC TATCTTATT	720
5	TAATAGAGAA CAGACTTCTC AAAAAATCTT CAGAAGCAGC TTATTATTGA AATATCGAAA	780
	TATTGAAATA AACCCGGTGG GTTAGATTAC TCATCTGTCC ACCAAGTGGG ACATTTCAT	840
10	GGACTGGGGG CTAAAGGAC TTAGAAGAGA CCTGTAAGTA AATCCTGAAA ATGAGCCAAT	900
	CCCCACTTGA ATGGTTACTG GAGTAAACCC ACCTTTACCA CCCCAATTAC AGCACCCGAG	960
	GCCGATAAAC CAACTTGGCT CTGGTTCATT TTTCTTTTCT TCATTTGTGA TGCTCAGATT	1020
15	CAAAATGTGT GTTCTACACT GTTACAGGCT TCTCTTTTGT TTGATTAAAG ATTTTAGTCC	1080
	TACTTTTGTA TGGACACATT AGAATATTCA GAGACCAAAA TAGAAGAATT TGCTGTTAGA	1140
20	TATTTTTCAG AAGTCAGCAG ATTTGTGGCA AATCATTTAT TTGCCTTTTT AAAAATTCAT	1200
	TTAAGCAGTT CAGAGAGTAG ACTACTCAGA AAATTATTTC ACGTAATTGT CTAAGAGGTC	1260
	AATATTTTTT AATGCATATT GAATCAAATA A	1291

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(2) INFORMATION FOR SEQ ID NO: 137:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

	GGCAGGAGGA CCTACTTTTG TAACAGACCA TGGTGTGTGC CAAGGTAAAA CCACAGTGAT	60
40	ATTTTGGGAT GCTTTGTCTG CAATCTTGAC TTGTTTTTGC AGTATCATTA TTCAGACTTC	120
	AAATGTGAA TCTTTTAAAC ATCTTGATAA TTTGTTGTG AGAGCTGTTC ATTCTAAAAT	180
45	GTAATGAAAT TCAGTCTAGT TCTGCTGATA AAGATCATCA GTTTTGAAAG GTTACTGATT	240
	TTCTCTTCC CTCTTAGTTT TTTACCCAAT ATATGGAGAA GAGTAATGGT CAATCTTAAC	300
	ATTTGTTTT AATTGTTTAA TAAAGCTGCT GGGCAGTGGT GCAGATTCC TACCTAGTGT	360
50	CATAAAGCA AAATACTTAC ATAGCTTTCT TAAATATAG GAATGACATT ACATTTTATG	420
	GAGAAAGTAA GTTGCTTTGC ACCGCCTACT TAAITCCTTT CCATATATTG TGATACAAAC	480
55	TTTTGAATAT GGAATCTTAC TATTTGAATA GAAATGTGTA TGTATAATAT ACATACATAC	540
	ATAAGCATAT ATGTGTGTGT GTGTGTGTAT ATATATATAT ATGCATGCTG TGAAACTTGA	600
	CTACACAACA TAAATCACTT TTTAAATTCC AGGAACGGGT AGTCTGACAC GGTGATTATC	660
60	CTTTTGAGGC TGAATCCGTT ATTAACCTGT TATTTAGGTT TTAATCCAG TAGCAAGGGA	720

	TTCTAAGTTA GTTGCACTTA CATGATTATT GTGATTTAAA ACTAAGAATA AAGGCTGCAT	780
	TTTCAAAGAT AAATTGGAAT TGCTGTTGGT GAAATAACAA CCAAATACT GAATCTGATG	840
5	TACATACAGG TTTCTACAGG AAGAGATGGT ATAATTTACA ATTTGGAGAT TTAATAACCA	900
	GGGCTACCCA GAAAAAGTGA CTTGATAACA TGGTACCAAT AAGTAAGGGA TGCTCTCTCG	960
10	GTTTGCTTTT GCCACTTTCA AGATTTTAAAC TTCTCAGGTT ATTAATCAAA ATTATTGTAT	1020
	AAGTTAGCCA ATAGAATTTT TAGGTTAAAA CAACAGATGG GGGGTTTGTG GAGTGTTTAA	1080
	TGTCATGGGC ATTTTTAGTA GCATAGACCC TTTGTTCTGC ATTTGAATGT TTCGTATATT	1140
15	TTTGTTTCAC AGTTAATCTT CCCTCCCCAA GTTTGCTATT CAAATCAACT GCCTGAATGA	1200
	CATTTCTAGT AGTCTGATGT ATTTTCTGA GGAATAGTTT GTGATTCCAA TGCAGGTGTC	1260
20	TTCAATTACCA TTACCTCTAC ACTGCAGAAG AAGCAAAACT CCTTTATTAG AATTACTGCA	1320
	CATGTGTATG GGGAAAATAG TTCTGAAAGG CTAGAATGAT ACAAGTGAGC AAAAGTTGGT	1380
	CAGCTTGGCT ATGGAGTGGT GGCAATAATC TCTAAACATT CCAAAGACC ATGAGCTGAA	1440
25	CCTAAACTCC CTTGGGAATC TGAACAAAG GAATATGAAA ATTGCCATTT GAAAACTGAC	1500
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	1560
30	AATTATAGAG ACTACAGCTA AATAAATTG AACATTAAAT ATAATTTTAC CACTTTTGT	1620
	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	1680
	GATACTGAGT TGACTGTTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	1740
35	GTGCACAACT TAGGTTATTT TTGCTCCGA ATTTGAATGA AAAACTTAAT GCCATGGATT	1800
	TTTTTCTTTT GCAAGACACC TGTATTATCAT CTGTTTAAA TGTAATATGC CCCTTATGCT	1860
40	TTTGAAATAA ATTTCTTTT GTAAAAAAA AAAAAAAA AAAAAA	1906

45 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1935 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

55	TCTGAACATA TGCTAACAGA TCCCCCTGAG GGATTTCTGA TGGGCTGAGC AGCTGGCTGG	60
	AGCTAGTACT GACTGACATT CATTTGTATG AGGGCAGCTT TCTGGTACAG GATTCTAAGC	120
60	TCTATGTTTT ATATACATTT TCATCTGTAC TTGCACCTCA CTTTACACAA GAGGAACTA	180

	TGCAAAGTTA GCTGGATCGC TCAAGGTCAC TTAGGTAAGT TGGCAAGTCC ATGCTTCCCA	240
	CTCAGCTCCT CAGGTCAGCA AGTCTACTTC TCTGCCTATT TTGTATACTC TCTTTAATAT	300
5	GTGCCTAGCT TTGGAAAGTC TAGAATGGGT CCCTGGTGCY TTTTFACTTT GAAGAAATCA	360
	GTTTCTGCCT CTMTTGGAA AAGAAAACAA AGTGCAATTG TTTTFACTG GAAAGTTACC	420
10	CAATAGCATG AGGTGAACAG GACGTAGTTN AGGCCTTCCT GTAAACAGAA AATCATATCA	480
	AAACACTATC TTCCCATCTG TTTCTCAATG CCTGCTACTT CTGTAGATA TTTCATTCA	540
	GGAGAGCAGC AGTTAAACCC GTGGATTMTG TAGTTAGGAA CCTGGGKTCA AACCCCTCTC	600
15	CACTAATTGG CTATGTCTCT GGACAAGTTT TTTTMTTMTT TTTTMTTAA ACCCTTCTG	660
	AACTTTCATC TTCTATGTCT ACCTCAAAGA ATTGTTGTGA GGCTTGAGAT AATGCATTTG	720
20	TAAAGGGTCT GCCAGATAGG AAGATGCTAG TTATGGATTT ACAAGGTTGT TAAGGCTGTA	780
	AGAGTCTAAA ACCTACAGTG AATCACAATG CATTTACCCC CACTGACTTG GACATAAGTG	840
	AAAAGTAGCC AGAAGTCTCT TTTTCAAATT ACTTACAGGT TATTCAATAT AAAATTTTGT	900
25	TAATGGATAA TCTATTTAT CTAAACTAAA GCTTCCTGTT TATACACACT CCTGTTATTC	960
	TGGGATAAGA TAAATGACCA CAGTACCITA ATTTCTAGGT GGGTGCCTGT GATGGTTCAT	1020
30	TGTAGGTAAG GACATTTTCT YTTTTTCAGC AGCTGTGTAG GTCCAGAGCC TCTGGGAGAG	1080
	GAGGGGGGTA GCATGCACCC AGCAGGGGAC TGAAGTGGGA AACTCAAGGT TCTTTTFACT	1140
	GTGGGGTAGT GAGCTGCCTT TCTGTGATCG GTTTCCTTAG GGATGTTGCT GTTCCCCTCC	1200
35	TTGCTATTTC CAGCTACATA CAACGTGGCC AACCCAGTA GGCTGATCCT ATATATGATC	1260
	AGTGCTGGTG CTGACTCTCA ATAGCCCCAC CCAAGCTGGC TATAGGTTTA CAGATACATT	1320
40	AATTAGGCAA CCTAAATAT TGATGCTGGT GTTGGTGTGA CATAATGCTA TGGCCAGAAC	1380
	TGAAACTTAG AGTTATAATT CATGTATTAG GGTCTCCAG AGGGACAGAA TTAGTAGGAT	1440
	ATATGTATAT ATGAAAGGGA GGTATTAGG GAGAACTGGC TCCCACAGTT AGAAGGCGAA	1500
45	GTGCGACAAT AGGCCGTCTG CAAGCTGGGT TAGAGAGAAG CCAGTAGTGG CTCAGCCTGA	1560
	GITCAAAAAC CTCAAACTG GGAAGCTGA CAGTGCAGCC AGCCTTCAGT CTGTGGCCAA	1620
50	AGGCCAAGAG CCCCTGGCAA CCAACCCACT GGTGCAAGTC CTAGATTCCA AAGGCTGAAG	1680
	AACCTGGAGT CTGATGTCCA AGAGCAGGAA GAGTGAAGA AAGCCAGAAG ACTCAGCAAA	1740
	CAAGGTAGAC AGTGTCTACC ACCAYAGTGG CCATACCAA GAGGCTACCG ATTCCTTCCT	1800
55	GCTACCTGGA TCCCTGAAGT TGGCCTGGTC TCTGCACCTT CTAAACCTAG TTCTTAAGAG	1860
	CTTTCATTA CATGAGCTGT CTCAAAGCCC TCCAATWAAT TCTCAGTGA AGYTTCAAAA	1920
60	AAAAAAAAAA AAAAA	1935

(2) INFORMATION FOR SEQ ID NO: 139:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

NGCCCCCTTG GCACAAGTCA GATGAAGCAC GTTCTGCCGG GGAGGCCCTC AMCTTCCAGA 60
15 GAGGACAGAC ACAGATTTC TCTGGGGGA GGGAGGAGTC CACGCATCCT GATGCTGCCT 120
GGAAGCTTAT TTTCCCGTGG CCAGGATGCA TTTCTCTGAG TGGAAACAGG TTCTTGCA TG
20 TGGATGTGTG TTTCCCCAGG CAGACGGCCC CTCTTTTCCC AGCACTTCCC TGCCTCCCCC 240
AGGCCTCAGG CCAGCACCCA GTTCTCCTC ACATGGCAGG TGAGCACAGA CTTCTAGTTG 300
GCAGGAGCTG AGGAGGGTGA ACAAAACCCG AGGGAGGCCG GGCCTTGCT CCCGAGTTGG 360
25 GGGGAGGGGG TGTGGCAACG TGCCCCCGC AGAGGCCACG CATGTTTGAC CAAAGCCCTC 420
ATTGTGGTCC GAGGACAGCC TTTCCCCAG GCCTCARAGC ATTGCTCATC CGTGCCAAAC 480
30 TGGGTAGGTG GATTGTAGCG GAAAGACTCC CAAAATGTGC CAAGAATTC CCRGTCCCAG 540
GCAGGGCAGG GGAAACTAAG GGCAAGCAGG ATACAGGGCG AGGGATGTGG CAGGTGAGGG 600
GGCTCCCGCC TGTGCCCTT CTCCTCACCA TGTCTCCCC ACCCTGCCTC AGTTCTCGT 660
35 TCCCCTCAT CTCCTCCCC CTCTTTGAAG CTGTCCCCAT CTCAGTGCA GACCAGCCTT 720
CTCCTCAKCT GACCACCTC CTCTGACCSA CGCCCCCTCC TTGTCTGAAA AAAGGAGCCT 780
40 TGAATGGTGG AGGGAGGCAG TGGGAGAGAA GGTCTCACC GACAGGTGG GAGAATGAGG 840
TCAGCGGTGC TGGGGAACAG ATGGAGGGGG CAGTGGGGAC AGGGCTTGGG CAGACACCAG 900
CAGGAATAAT TTGAATGTG TGAGGTGACT CCCCAGAGG CTTGGGCTTG GGCATTTGGG 960
45 AAAAGAATGA TGTCTGGAAG GGCTTAAGG ACACAGTGA CGAGGGGAGA GTCCTCATCT 1020
GCTGGCATTT TGTGGGGTGT TAGTGCCAAA CTTGAATAGG GGCTGGGGTG CTGTCTTCCA 1080
50 CTGACACCCA AATCCAGAAT CCCTGGTCTT GAGTCCCAG AACTTTGCCT CTTGACTGTC 1140
CCTTCTCTTC CTACCTCCAT CCATGGAAAA TTAGTTATTT TCTGATCCTT TCCCCTGCCT 1200
GGTCTAGCTC CTCTCCAAAC AGCCATGCCC TCCAAATGCT AGAGACCTGG GCCCTGAACC 1260
55 CTGTAGACAG ATGCCCTCAG AATTGGGGCA TGGGAGGGGG GSTGGGGGAC CCCATGATTC 1320
AGCCACGGAC TCCAATGCCC AGCTCCTCTC CCAAAACAA TCCCACAAT CCCTTATCCC 1380
60 TACCCCAACC CTTTGCGGCT CTGTACACAT TTTTAAACCT GGCAAAAGAT GAAGAGAATA 1440

TTGTAA

1446

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(2) INFORMATION FOR SEQ ID NO: 140:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTTTTTTTTT TTTGATATGA AATTGTCTTT CTCCATTGCA GAAATAAGCT AGGGAAACAC 60
TAACCCAAAA ACTTCTGTGA GAGCTGTTCC TTTGGAGGCA GCATCACTTA TTGGCAGTAA 120
20 AGACTCAGTA TAAAAGCACC AGCATCCCTA CTTGGGTGAT GGGGATTAAT TTTATAGCAT 180
TCCATTTTCC TAGTGCCACA TGTGAAATTG GATTTTGATG ATCTTAATCT ATATTCTACC 240
25 CTTATAATAA AAGATCAAAA GATATATCTC CTATGAACAG AITGGAGATA GGAGATGAAA 300
AGTTGGGAGG ATGTCTTTAT TCTAATGTGA GGGTAGGGAA AATGTGGATA ACATTACTGG 360
GGTGARGGAG GCATGTCTCT TTAGTTGGAG TTCTCATTTT TATTCTCCAG TACTGACTTG 420
30 TGGGGAAGC ATACTTTTTC ACTGCCAGGT ACTGAATGCA GAGGCTCAGT GAAGTATATA 480
TGTGGGAAGT GCATGCATTT CGTTTATTAG CAAACATAGC TGGATTAAGA CAAAGTTGTT 540
35 GGTTTGGAAA GGGTTAAAG CCTTAAGTGA ACAAATCTAG CTAACAGTGA ATGAACTAGG 600
TAATATAACT TGCATATTTT TAATTTCCIT TGGTTAAAGG TCCCCCATAC TTCTCTGTTT 660
GGAGACATGA GAAGTATGAT TACTTCAGTG TTAGTTTCTT TAATTTTTTT TTTCCTCTAT 720
40 TTGTCCTTGT TCACTTTGTT GCAAGCTAGA AATCTGTGGG TTATACATAG GGCAGCTCTT 780
TGTGAAAGTG GTTTATTCCA CTGGAGAAAG GGGATTGAAA ATCAGTTAGA ACCAATGTAT 840
45 TTCTTGCCCC ACGGAACACT ATTCTATAA GATAGCTGAA AGAAGCTGCT GTGAGGAGCT 900
CAGCTCCAAA CACAGGATCA GCACCTTGTA TAGGAATCC CATGAATTAT GACTTCTCAT 960
TCTGTTTTAT CAGAGTGCAT ATATGTCCTA CTTGAGGAAA AGTAAAACAG TCATTTACGA 1020
50 AAGAAAGTCA ATCTGTATCC TAAGCATTTT AATAAAAAGT TAAAACAAAA AATTAAAAGG 1080
GACACTCGAG GGGGGGCCCC AAACCCAAT 1109

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(2) INFORMATION FOR SEQ ID NO: 141:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TAGGACTAAC TTAAATCTCT TTATTCATCT TTTATTTATT AAAAAATTTT ATTTCTTTGA 60
10 ATTTTCCTGT AATTTCCTTA RGCTCTTCTA TAAAAATGTA TATTCATGTG AACCATACCT 120
CATTATCCTT AACATTTACT CTCAAAAAGC TTTTATTTT TATTTTTTTG AAGGTAGTTT 180
15 TTCTGTGTGT ACTCTGTAAC ATGATTTTGC TTTCAAATCA TTGTGTGCC CCCATACAAA 240
ATGCCTTTTA TTTTGGAGGA TCGTGGACTT TTTAGTATGG CATGAGTGTG CTAAGGCCA 300
GATATCTTTC CACATTCACT GGTGGCTTTG ACACCTAGTT TTTAATCTCC CATCCTTACT 360
20 TTAAACCTG ACAGTGCAGT CCTCAGTCAG GGCCAGGACC GGGCTGAGGC CCTTTGTGGA 420
GATGCTGCAC CACCAGCAGA AGGCTGAGAC CTGTTTACCT GTACCTGTTT ACTTGTAAATA 480
AAAAGAATTA TCTAAAA 497

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(2) INFORMATION FOR SEQ ID NO: 142:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAGGCAGA GGCAAGCTGC CTGCCAAGCC CCTCCCTCAA GGAATGGCCT TGCCAGGAA 60
40 TGCCACCAC ACATACCCTC TTCTTTTCTT CTAGTCAAAC TCTTGTTTAT TCCTTGCTT 120
GCCTCCCTCC TTCTCTCCC TCTCAACCTT TACTTCTGG TTTCTATTTC ATGGGATTG 180
45 GGGTGAAGT TAAACTTACA ACAGTGCCGC CAACACCAAG TCTTGAGGA AAAAAATACA 240
AAGAAATTTA ACAAAAAAAA AAAAAAAA 269

50

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

	TTGATTGACT ATGGTCTCTC CGGCTACCAG GAAGAGTCTG CCGAAGTGAA GGCCATGGAC	60
	TTTCATCACCT CCACAGCCAT CCTGCCCTTG CTGTTCGGCT GCCTGGGCGT CTTGGGCTC	120
5	TTCCGGCTGC TGCAGTGGGT GCGCGGAAG GCCTACCTGC GGAATGCTGT GGTGGTGATC	180
	ACAGGCGCCA CCTCAGGGCT GGGCAAAGAA TGTGCAAAAG TCTTCTATGC TCGGGTGCT	240
10	AAACTGGTGC TCTGTGGCG GAATGGTGG GCCCTAGAAG AGCTCATCAG AGAACTCACC	300
	GCTTCTCATG CCACCAAGGT GCAGACACAC AAGCCTTACT TGGTGACCTT CGACCTCACA	360
	GACTCTGGGG CCATAGTTGC AGCAGCAGCT GAGATCCTGC AGTGCTTTGG CTATGTGAC	420
15	ATACTTGTC ACAAATGCTGG GATCAGCTAC CGTGGTACCA TCATGGACAC CACAGTGGAT	480
	GTGACAAGA GGGTCATGGA GACAACTAC TTTGGCCAG TTGCTCTAAC GAAAGCACTC	540
20	CTGCCCTCCA TGATCAAGAG GAGGCAAGGC CACATTGTCG CCATCAGCAG CATCCAGGGC	600
	AAGATGAGCA TTCTTTTCG ATCAGCATAT GCAGCCTCCA AGCAGCAGC CCAGGCCTTC	660
	TTTGACTGTC TCGTGCCGA GATGGAACAG TATGAAATTG AGGTGACCGT CATCAGCCCC	720
25	GGCTACATCC ACACCAACCT CTCTGTAAAT GCCATCACCG CGGATGGATC TAGGTATGGA	780
	GTTATGGACA CCACCACAGC CCAGGGCCGA AGCCCTGTGG AGGTGGCCCA GGATGTTCTT	840
30	GCTGCTGTGG GGAAGAAGAA GAAAGATGTG ATCCTGGCTG ACTTACTGCC TTCCTTGGCT	900
	GTTTATCTTC GAACCTGGC TCCTGGGCTC TTCTTCAGCC TCATGCCTCC AGGGCCAGAA	960
	AAGAGCGGAA ATCCAAGAAC TCCTAGTACT CTGACCAGCC AGGGCCAGGG CAGAGAAGCA	1020
35	GCATCTTAG GCTTGCTTAC TCTACAAGG ACAGTTGCAT TTGTTGAGAC TTTAATGGAG	1080
	ATTTGTCTCA CAAGTGGGAA AGACTGAAGA AACACATCTC GTGCAGATCT GCTGGCAGAG	1140
40	GACAATCAAA AACGACAACA AGCTTCTTCC CAGCGTGAGG GGAAACACTT AAGGAATAAA	1200
	TATGGAGCTG GGTTTTAACA CTAAAACTA GAAATAAACA TCTCAAACAG TAAAAAATAA	1260
45	AAAAAAAC	1269

(2) INFORMATION FOR SEQ ID NO: 144:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

60

AAAAGGCAAA CTATAGGATA ACACAGAGCC CTTTGTGAAA ATAAATTGGC ATTGGAGTGT 60

	TTTACCCTCT AGCTGTTTTA CTTAGAATGT AACATATGCT GCCTACCCAC CTCAAAATGT	120
	CTGTACTGCA AGAGGGCCCT GGGCCTCTGC TTTCCATATT CACGTTTGGC CAGAGTTGTA	180
5	GTCCCAAAGA AGAGCATGGG TGGCAGATGG TAGGGAATTG AACTGGCCTG TGCAATGGGC	240
	ATGGAGCACA AGGGGTGACA GCATGCCCTCC TGCCCTACCG TGGCAGTACG GAGACAGTCC	300
	AGAACATGGT CTTCTTGCCA CGGGGTGTTG TTGTCTCTGG TGGTGCTGCA TGTCTGTGGC	360
10	TCACCTTTAT TCTTGAAACT GAGGTTTACC TGGATCTGGC TACTGAGGCT AGAGCCCACA	420
	GCAGAAATGGG GTTGGGCCTG TGGCCCCCAA ACTAGGGGGT GTGGGTTCAT CACAGTGTG	480
15	CCTTTTGTCT CCTAAAGATA GGGATCTACT TTTGAAGGGA ATGTTCCTC CCAAATAAAT	540
	TTGCTTTACC TTGGTCTTTT CTTTGTGCC AGTATTCAAG TGGTATAGCT CTGAGCAGGG	600
	TCACATTTGG CCAAACCTGA CACTGTCTTG CTGCATTCTC CTTTGGCAAA CATCAGGGTC	660
20	AGAATTCAGG ATAGCCCTTC CTAGGGCACT GGACTTTCTG GCATGGGGC TGTGTTTGCA	720
	CAAGTTATTT TCATGTTACC TGGAGAGTGT CCAGAGGCTG CTCTGAGGCT GAGGTGTGTT	780
25	CCCCCTTGCC TGGTTCAGC TGTGAGAGG ATACCATCCT AGGGTCTGGG AATCCAAGGC	840
	CACGAGACTC CTTGGTTTGT GGTCCGAGAT CCTGTACTAA GGAGGGTCTG GCCAGAGGAA	900
	CAGACCAGCT TTTGCACAAT GAAGCGCAAG CGAACAAGTG GTTTCCTGG TGTCTACCT	960
30	GTCCTGAACC TGGTCTGTG GGCCATTGAA AAGTTAGATC TGTGATCTCT GGGGTTTTTG	1020
	TGGCTTTGTT CAATGCTTCC ACTCTAGGGC AGGCAGAGCA GTCTATACTC TCCCAGCCT	1080
35	GCTTGACCTC CAAGTAGAGC TGATACAGAG ATCTGTGAAT ATTGTGATAG AAATTCTTTG	1140
	GTATTCATAC ATTTTCAGCTG CAAGTCAGCA ATTTCCAGG TACCATGTAA GCTATAAAAC	1200
	AGTCATTCCT AAAGACAGAG GATAGCTGTG ACTCATGGGA TCATGAGGTC CATGGCTGGT	1260
40	TGCAGGTTC CTTTTCCTT CCTCAGGTTT TGTCTCTTCC TGTGTTGTCC CCAGCAAGGG	1320
	AGAGACTGTG GGGTGGATTG GGAGAACAGA TTAGGAGTAT AGCAAATGAA CCCAGAATGG	1380
45	AACAGTGGG AGCTAACTGT GAATGAGGAG AGTACCTGCT GCAGGACCTG GAGGTCAGGT	1440
	GTGAATGCTG TATTGCCACA GGAATAAAT ATCTGGCGT CTGGAGCCTT CACCTCTCCG	1500
	TCAAGTCCTT CCTGTGATAC TGCCATGGCA CAGGATCTGA GTTGCAGCTC TGCACCCTAA	1560
50	ATCACACCTT GGCATGTGC TGGGCTGCAG GGCTGCCAGG TTCTGTACTT GTGTCCAGCT	1620
	GTGGCCCTGG ATGCTGGAGC TGGAGGGTTT TCTGTGCTCA GACTGTAGCC TGTAGCTCTT	1680
55	GGCCTGTGTA GAGCCCCCTC CTGTGCCCTC AGTGGCTGTC GTTTGTTAAC ATCATCAGGA	1740
	AGATGGGAAA GGTGAGGAG AATTTTCTG CCCTACAAAG GGTGGAAGAG AAAGGACACA	1800
60	GTATTTTCAT GAATTTACCA TATATCTTTG TTTTCTTCA ACGAAAAAGT TAATTGAGGC	1860

AATGTCATCT GCTCAAAGTT GAGTGGTTTA TTCACAATAA ACTGTAAGTT TCTGATTATA 1920
AAAAAAAAAA AAAAAAAAAA AAAG 1944

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(2) INFORMATION FOR SEQ ID NO: 145:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

TCGACCCACG CGTCCGGGGT GCGCAACGGG GAGTTCGGC TGGAGACCCG TGCTCTGGGC 60
CGGCGCCTTC ACCATGGCCT CGGCAGAGCT GGAATACACC ATCGAGATCC CGGATCAGCC 120
CTGCTGGAGC CAGAAGAACA GCGCCAGCCC AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC 180
TGTTGGTGATT CTYTTGGGCT GGGGTGGCTG CAAGGACAAG AACCTTGCCA AGTACAGTGC 240
CATCTACCAC AAAAGGGGCT GCATCGTAAT CCGATACACA GCGCCGTGGC ACATGGTCTT 300
CTTCTCCGAG TCACTGGGTA TCCCTTCACT TCGTGTMTTG GCGCAGAAGC TGCTCGAGCT 360
GCTCTTTGAT TATGAGATTG AGAAGGAGCC CCTGCTCTTC CATGCTCTCA GCAACGGTGG 420
CGTCATGCTG TACCGCTACG TGCTGGAGCT CCGCAGACC CGTCGCTTCT GCGCCTGCG 480
TGTTGGTGGC ACCATCTTTG ACAGCGCTCC TGGTGACAGC AACCTGGTAG GGGCTCTGCG 540
GGCCCTGGCA GCCATCCTGG AGCGCCGGGC CGCCATGCTG CGCCTGTGTC TGCTGGTGGC 600
CTTTGCCCTG GTGGTCGTCC TGTTCCACGT CCTGCTTGCT CCCATCACAG CCNTCTTCCA 660
CACCACCTTC TATGACAGGC TACAGGAGCG GGGCTCTCGC TGGCCCGAGC TCTACCTCTA 720
CTCGAGGGCT GACGAAGTAG TCCTGGCCAG AGACATAGAA CGCATGGTGG AGGCACGCCT 780
GGCAGCCCGG GTCCTGGCGC GTTCTGTGGA TTTCGTGTCA TCTGCACAGC TCAGCCACCT 840
CCGTGACTAC CCTACTTACT ACACAAGCCT CTGTGTCGAC TTCATGCGCA ACTGCGTCCG 900
CTGCTGAGGC CATTGCTCCA TCTCACCTCT GCTCCAGAAA TAAATGCCTG ACACCTCCCC 960
50 ACAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGGCCCGGTA CCCAATTGCG CCTATAAAGG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO: 146:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

GGCACGAGGA GGGCCACGGC AGCCATCGCG CTTTGCAGTT CGGTCTCCTG GTGTACGGCC 60
AACGCCAAGT AGGGGATTGC GTTCCCTCCA GTCGCAGACC CTATCAGATT TGGATATGTC 120
10 CTTCATATTT GATTGGATTT ACAGTGGTTT CAGCAGTGTG CTACAGTTTT TAGGATTATA 180
TAAGAAAAC TGTAACTGG TATTTCTTGG ATTGGATAAT GCAGGAAAA CAACATTGCT 240
15 ACACATGCTA AAAGATGACA GACTTGGACA ACATGTCCCA ACATTACATC CCACTTCCGA 300
AGAAGTACC ATTGCTGGCA TGACGTTTAC AACTTTTGAT CTGGGTGGAC ATGTTCAAGC 360
TCGAAGAGTG TGGAAAAACT ACCTTCCTGC TATCAATGCC ATTGTATTC TGGTGGATTG 420
20 TGCAGACCAC GAAAGGCTGT TAGAGTCAAA AGAAGAACTT GATTCACTAA TGACAGATGA 480
AACCATTGCT AATGTGCTTA TACTGATTCT TGGGAATAAG ATCGACAGAC CTGAAGCCAT 540
25 CAGTGAAGAG AGGTTGCGAG AGATGTTTGG TTTATATGGT CAGACAACAG GAAAGGGGAG 600
TATATCTCTG AAAGAACTGA ATGCCCAGCC CTTAGAAGTT TTCATGTGTA GTGTGCTCAA 660
AAGACAAGGT TACGGAGAAG GCTTCCGCTG GATGGCACAG TACATTGATT AACACAACT 720
30 CACATTGGTT CCAGGTCTCA ACGTTCAGGC TTAATCAGAG ATTTGATTGC TCAACATGCA 780
TAACITGAAT TCAATAGACT TTTGCTGGTT ATAAACAGA TGTTTTITAG ATTATTAATA 840
35 TTAAATCAAC TTAATTGAA TGAGAATTGA AACTGATTC AAGTAAGTTT GAGTATCACA 900
ATGTTAGCTT TCTAATTCCA TAAAAGTACT TGGTTTTTAC AGTTTATAAT CTGACATCAC 960
CCCAGCGCCA TTGTAAAGA GCAACTTCC AGCAGTACAT TTGAAGCACT TTTTAACAAC 1020
40 ATGAACTAT AAACCATATT TAAAAGCTCA TCATGTTAAA TTTTTATGT ACTTTTCTGG 1080
AACTAGTTTT TAAATTTTAG ATTATATGTC CACCTATCKT AAGGTACAG TTAATAATTA 1140
45 GCTTATCAA TGATTGCATG ATGCTTACA GTTTCAATA ACTTTTTTTC TTATGCAAAC 1200
GTCATGCAAT AAAACAACT CTAATGTTTG GCAAAAAAAA AAAAAAAAAA NTCGAGGGGG 1260
GGCCCGTACC CAATTCGCCC TAAAG 1285
50

55 (2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5	GGCACGAGGT GCGCAGGGG TCAGTGGTTC TCTCGGGTCT CGGGACAGGT GAGCACCTG	60
	ATGAAGGCCA CGGTCTGAT GCGGCACCTG GCGGGTGCA GGAGATCGTG GCGCCCTCC	120
	GCAAGGGCGS CGGAGACCGG TTACAGGTGA TTTCTGATTT TRACATGACC TTGAGCAGGT	180
10	TTGCATATAA TGGAAAGCGA TGCCCTTCTT CTTACAATAT TCTGGATAAT AGCAAGATCA	240
	TCAGTGAGGA GTGTCGAAA GAGCTCACAG CGCTCCTTCA CCACTATTAC CCAATTGAGA	300
	TCGACCCACA CCGGACCGTC AAGGAGAAGC TACCTCATAT GGTGGAATGG TGGACCAAAG	360
15	CGCACAATCT CCTATGTCAG CAGAAGATTC AGAAGTTTCA GATAGCCAG GTGGTTAGAG	420
	AGTCCAATGC AATGCTCAGG GAGGGATATA AGACCTTCTT CAACACACTC TACCATAACA	480
20	ACATTCCCCT TTTTCTTTT TCTGCGGGCA TTGGTGATAT CCTGGAAGAA ATTATCCGAC	540
	AGATGAAAGT GTTCCACCCC AACATCCACA TCGTGTCTAA CTACATGGAT TTTAATGAAG	600
	ATGGTTTCTT CCAGGGATTT AAGGGCCAGC TGATACACAC ATACAACAAG AACAGCTCTG	660
25	TGTGTGAGAA CTSTGGTTAC TTCCAGCAAC TTGAGGGCAA AACCAATGTC ATCCTGCTGG	720
	GAGACTCTAT CGGGGACCTC ACCATGGCCG ATGGGGTTCC TGGTGTGCAG AACATTCTCA	780
30	AAATGGCTT CCTGAATGAC AAGGTGGAGG AGCGCGGGA NCGCTACATG GACTCCTATG	840
	ACATCGTGCT GGAGAAGGAC GAGACTCTGG ATGTGGTCAA CGGGCTACTG CAGCACATCC	900
	TGTGCCAGGG GGTCCAGCTG GAGATGCAAG GCCCTGAAG GCGCAGGCTN CCAGNCCGCC	960
35	TGCAGGCCGT GGTGAGGAGG GGCGCCTCCC CAGAGTCTGC TCCCCGTGA ACACAGAGCA	1020
	GANGCCAGGG TGGCCAGCAG TGGCTGGGTC CTTCCGCGCC CCTCCGTCCT CTTTCCCTG	1080
40	AGCACCTTCA TCACCAGAGG CTTGAAGGAA CCCCGCCATG TGGCAGGGCA CAGGCACTGT	1140
	TCCTGGTGAA CCTTGGACCA CAGCATGTCA GTGCTCTAGG GATTGTCTAC TCCAGGGATT	1200
	TTCTTCAAAA TTTTAAACA TGGGAAGTTC AAACAAATAT AATGTGTGAA ACAGATCAAA	1260
45	ATTTTAAAAA TGAAAAAAA GCTGCTCTGA TTCAGGGGAT GTGGGTCGGG GTAGAACCTG	1320
	GACCTCTTGG CCTGGGGGCA CATGGGATGC TTCTAGGAAC ACAGTTTGAG AACCACCAAA	1380
50	AAAAAA	1386

55 (2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2098 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

5	AGCCCTTCTC CCCGCGCTTG GGA CTCTGAC ATCTTAAGGC TGCACGGTCG TGTCCCTGTG	60
	TGGGTGAGGC CATGTCTGTG ATCCAAGGTT CCTGGAAGTG ACACAGGAAG GGGCTGTGAA	120
	CCCTAAGTGG GTGTATCTC CTCRACCGA GGCTTCTMAC CCTGGAGATG GCAGTTACTC	180
10	CTGGCCATGG TTGCTGAGCA TGGGCAGACC AGTGGAGGCC ACCCTACTGT GTTATCTGCG	240
	CCTTCRATGA AGTGAGACCC TTGGGGAGAA CGGGCTGTGG ATGAAGGAGT GGA CTGCAGC	300
15	CTTGGCCTAG CCACTGGGCT GGGATCTTCT GGGTCATGTG ACTGTGTATC CAGGAGCAGA	360
	AACTGTGATT CTCAGGATTC AGGATCTACC CAGCACCAA GATGTATTTT CAGGAGAACA	420
	GACCTAGAAA TGGGCCTGTC TGGCATTTCA GAGTCAGGCA AAGCAGGCAG GGCCAGGGAG	480
20	CTTCTGTGGG TCTACACAAG AAGGTTCTTG TGAGGGCTAT CAGTTGTGTC CTTCTAGCTT	540
	GCTGGTAACT TTGGCGCCTC CGCCAAGCCC TGCCAGACTC CCCTGGCTGT GATGGCATTC	600
25	TGTGCCATCC TGCCTTGTC CCAGCCTCTG CAGGATGCCC TCCCTACCCA MCTYTYCCTG	660
	GGCCTTCCCT GTCCACTGGG CTGGATTCAT GTTCAAACCA CTGGACTGGC AGGGCAACGA	720
	CTTCTTCCCA CCTCAAGATG AGGTCTCTGC CCCCTTGTCT TGGCATAAAA ACACCTTTAA	780
30	AGCATGAGCC ATGTGCTTCT TTGCCCTTCT CTGTCCGTGT CCAATCTTCT GCCTCCAGT	840
	CACTCCCTGG GGA CTATGGG ATCACTGTCC CCCCACCTGT GTGGCCACAC CATGTGTCTT	900
35	GTCAATCCAG AACTGCCTCT GAGCTCCAGG CTGACCACAG ATCAGCCACA GCCTGATGCC	960
	TGCAGCCCCA CTTTGCTCAC CCTTCCCTC CCCTCCTCCT TCCTTCCACA CAGCAAGCCT	1020
	ACCTTTYTCC ATCCATGCTC ACCATAGCCC CCTTCCCTGT GACCTGGACC CTCCATGTGA	1080
40	CCTGGCTGAG ACTGTCAGCC TCCTGGAGGA GTGGGGTCCA CCTTCTTCTT GCCCTATGCA	1140
	GTGCAAGCTT CACTTCTCAC CCAGCAAGGT TGACTCATCT GCCTCCATGT CTCTGGGGCT	1200
45	TTGCTGTGTC CCTGAAACCT AGCTGGGCTG GTCTTGCTCC CAGCTTGCTT CCCCCTCCTC	1260
	GGATGTCCCT TTGCAGGCCC CTGTCTGTCC TCCGGCACCA GTGTCTTGG CTGCCATGGC	1320
	AAGCTCATCA GGGGCTTGTA CCCTGGTCAC CAAGCATGGT AGCAGCTGCC TGCATTGTAT	1380
50	CTCCATCTGG TCACTGCAGG TGCCAACCTT TCATCCCCCA TGTTTCTCTG GGCCATGGAG	1440
	GGCTGACCTC CGTTTCTGGG GAATGTGGCT GAGCTGTGGT AACCAGCTAC ACCCCAGGTG	1500
55	CTCTTTCCAT GGTGGTGCTT GCTCATCTTG CTGATGCAAA CTAGGAAGTT AGGCTGCATC	1560
	TCGGAGTGGC TTTGCTGGA GAGGTGCTTT GCTGTCTCTC AGACTCAGTC ACTGTGTTCC	1620
60	CTCCCCGCCT CTCTTATCTC CATGGCTGTT TGCAGCTCTC CCAGGACTT TGGGGTCTGA	1680

GCTGGAATTC CTTTGTGGTT TGCTCTTCTG CTTCTCACTC TTGTATTAAG AAGGATTCCA 1740
 CAAAGGGAGA GTGGCATCCC TGCTGCTGCT GTGCCAGACC AGAGTTTCCT GAGGGGCCCT 1800
 5 GACCCTAACC CTCCAGCTCA GCCCTGTACA CCTGACCCCTG TAAATGAGTG GGGTTTGCTG 1860
 ACTGTAATCC CTGACACCAG TAAAACCAAA AGGACTCTTG GGGGCTCAGT GTGAGAGCCA 1920
 GGGTTACCTA CTCTGCCAAG TGAGGACAAA CTGCTAGGCT GTATCCATA ATTTCAGGAT 1980
 10 GAGAAACATT AACAATAAAA ATTTGTAGTA AACATAACCT CATGANGACT AAAAAAAAAA 2040
 AAAAACYGG GGGGGGGCCC GTAACCCATT GGGCCCTTNG GGGGGNGTT TAAAAAT 2098

15

(2) INFORMATION FOR SEQ ID NO: 149:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGACCCACG CGTCCGAAC T GAGGCGGCGG CGGGAGCCGG TTGGKGTCTG GTCTTCGCGT 60
 30 CGGCCCCGCG GACCAGACGC TGCCCCCGGC GCGGGGAGAA GATGGTGCK AGCGGCCTCG 120
 GGCCCGCCAC GCGCCGCCAC GAGTGAGCCC AGCGCGACCG CGGGCGTCCG CCGAGCAGCT 180
 GGCCCGGCTG GGCCCGGGGC GCGCANTGCC CGCCGGGGCG GGGTGAGCT GATCAGAATA 240
 35 ATGTTTCAGCA TCAACCCCTT GGAGAACCTG AAGGTGTACA TCAGCAGTCG GCCTCCCTCG 300
 GTGTCTTCA TGATCAGCGT AANGCCCATG GCCATAGCTT TCCTGACCCT GGGCTACTTC 360
 40 TTCAAAATCA AGGAGATTAA ATCCCCAGAA ATGGCAGAGG ATTGGAATAC TTTTCTGCTA 420
 CGGTTCATG ATTTGGACTT GTGTGTATCA GAGAAATGAA CCCTCAAGCA TCTCACAAAC 480
 GACACCACAA CTCCGGAAAG TACAATGACC AGCGGGCAGG CCCGAGCTTC CACCCAGTCC 540
 45 CCCCAGGCC TGGAGGACTC GGGCCCGGTG AATATCTCAG TCTCAATCAC CCTAACCTG 600
 GACCCACTGA AACCTTTCGG AGGGTATTCC CGCAACGTCA CCCATCTGTA CTCAACCATC 660
 50 TTAGGGCATC AGATTGGACT TTCAGGCAGG GAAGCCACG AGGAGATAAA CATCACCTTC 720
 ACCCTGCCTA CAGCGTGGAG CTCAGATGAC TGCGCCCTCC ACGGTCACTG TGAGCAGGTG 780
 GTATTACAG CCTGCATGAC CCTCACGGCC AGCCCTGGGG TGTTCCTCGT CACTGTACAG 840
 55 CCACCCACT GTGTTCTGA CACGTACAGC AACGCCACG TCTGGTACAA GATCTTCACA 900
 ACTGCCAGAG ATGCCAACAC AAAATACGCC CAAGATTACA ATCCTTCTG GTGTTATAAG 960
 60 GGGGCCATG GAAAAGTCTA TCATGCTTTA AATCCCAAGC TTACAGTGAT TGTTCAGAT 1020

	GATGACCGTT CATTAATAAA TTTGCATCTC ATGCACACCA GTTACTTCCT CTTTGTGATG	1080
	GTGATAACAA TGTTTGTGCTA TGCTGTTATC AAGGGCAGAC CTAGCAAATT GCGTCAGAGC	1140
5	AATCCTGAAT TTTGTCCCGA GAAGGTGGCT TTGGCTGAAG CCTAATTCCT CAGCTCCTTG	1200
	TTTTTTGAGA GAGACTGAGA GAACCATAAT CCTTGCCTGC TGAACCCAGC CTGGGCCTGG	1260
10	ATGCTCTGTG AATACATTAT CTTGCGATGT TGGGTTATTG CAGCCAAAGA CATTTCAAGT	1320
	GCCTGTAAC TATTTGTACA TATTTATAAA AATCTATTCA GAAATTGGTC CAATAATGCA	1380
	CGTGCTTTGC CCTGGGTACA GCCAGAGCCC TTCAACCCCA CCTTGGACTT GAGGACCTAC	1440
15	CTGATGGGAC GTTTCACGT GTCTCTAGAG AAGGATTCCT GGATCTAGCT GGTACGACG	1500
	ATGTTTTCAC CAAGGTCACA GGAGCATTCG GTGCGTGATG GGGTTGAAGT TTGGTTTGGT	1560
20	TCTTGTTC AATCAATATG TAGAGAACAT TTGAAACAGT CTGCACCTTT GATACGGTAT	1620
	TGCATTTC AAGCCACCA TCCATTTTGT GGATTTTATG TGCTGTGGC TTAATAATCA	1680
	TAGTAACAAC AATAATACCT TTTCTCCAT TTGCTTGCA GGAAACATAC CTTAAGTTTT	1740
25	TTTTGTTTG TTTTGTGTTT TTTGTTTTTT GTTTTCCTTT ATGAAGAAAA AATAAAATAG	1800
	TCACATTTA ATACTACCAA AAAATGGACA AAAAAAGTCG AGGGGGG	1847
30		

(2) INFORMATION FOR SEQ ID NO: 150:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1569 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	GACGCTGACG AGAGAAGGCC TCTTCCTTGA GGGTTGGTGC TGTGTTGCAG TGACCGTGGC	60
45	GGATTACGCC AACTCGGATC CGGCGGTCGT GAGGTCTGGA CGAGTCAAGA AAGCCGTAGC	120
	CAACGCTGTT CAGCAGGAAG TAAAATCTCT TTGTGGCTTG GAAGCCTCTC AGGTTCTGCTG	180
	AGAGGAAGCT CTTTCTGGGG CTGGTGAGCC CTGTGACATC ATCGACAGCA GTGATGAGAT	240
50	GGATGCCCAG GAGGAAAGCA TCCATGAGAG AACTGTCTCC AGAAAAAGA AAAGCAAGAG	300
	ACACAAAGAA GAACTGGACG GGGCTGGAGG AGAAGAGTAT CCCATGGATA TTTGGCTATT	360
55	GCTGGCCTCC TATATCCGTC CTGAGGACAT TGTGAATTTT TCCCTGATTT GTAAGAATGC	420
	CTGGAAGTTC ACTTGCACTG CTGCTTTTGG GACCAGGTTG TACCGAAGCA CTACACGCTG	480
60	GATGCTTCCC TGCCTTTGCG TCTGCGACCA GAGTCAATGG AGAAGCTGCG CTGTCTCCGG	540

	GCTTGTGTGA TCCGATCTCT GTACCATATG TATGAGCCAT TTGCTGCTCG AATCTCCAAG	600
	AATCCAGCCA TTCCAGAAAG CACCCCCAGC ACATTAAAGA ATTCCAAATG CTTACTTTTC	660
5	TGGTCAGAA AGATTGTTGG GAACAGACAG GAACCAATGT GGAATTCAA CTTCAAGTTC	720
	AAAAACAGT CCCCTAGGTT AAAGAGCAAG TGTACAGGAG GATTGCAGCC TCCCGTTCAG	780
10	TACGAAGATG TTCATACCAA TCCAGACCAG GACTGCTGCC TACTGCAGGT CACCACCCTC	840
	AATTTCATCT TTATTCCGAT TGTATGGGA ATGATATTTA CTCTGTTTAC TATCAATGTG	900
	AGCAGCGACA TCGGCATCA TCGAGTGAGA CTGGTGTTC AAGATTCCCC TGTCCATGGT	960
15	GGTCGGAAC TCGCAGTGA ACAGGGTGTG CAAGTCATCC TGGACCCAGT GCACAGCGTT	1020
	CGGCTCTTTG ACTGGTGGCA TCCTCAGTAC CCATTCTCCC TGAGAGCGTA GTTACTGCTT	1080
20	CCCATCCCTT GGGGGCAGCC TCGAGTGTAG TCCATTAGTA ATCAGATTCC AGTTTGACA	1140
	GGTGGCTGG ATTGTATATC TCGTTAGTAA TGTACATGCT CTTCAGGTTT TAGGGCTCCT	1200
	GTTAGGGGAG GGAGAAATGT TGAATCAAGA GGGAAAACAA CTACTATGAT TTATAACAT	1260
25	ATTTTAATGT AAAAATTGTC ATTTAAAAGG AGTGGCCCTG TTTTCTGTGT TAAAACCCCA	1320
	TTTGGTGCTA TTGAGTTTGT TCTTTATTCT TTTATCCCAG TGAAAATTGT TGATCTTGCT	1380
30	GTAGGAAAA ATTAACCTCT TTGAATCTCC AAACAAGGAA GTTTCAGCAT TCCCTTATGG	1440
	ATCAGAGGAA CCTTAGAGGC CTGAAATTGT TGCTTCCAGT TTAGCTGCCC CTCAAATTCA	1500
	AGTGAATATT TTCCCTTCTC CCTTACCCT TCTCCAGAAA TAAAGCAGGT GACAGGGTTT	1560
35	CAGAATCTT	1569

40 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

50	CCCACGCGTC CGGAAGGATT GACCAGTTAA CCAACATCTT AGCCCCCATG GCTGTGGGCC	60
	AGATTATGAC ATTTGGCTCC CCAGTCATCG GCTGTGGCTT TATTTGCGGA TGGAACCTGG	120
	TATCCATGTG CGTGGAGTAC GTCCTGCTCT GGAAGGTTTA CCAGAAAACC CCAGCTCTAG	180
55	CTGTGAAAGC TGGTCTTAAA GAAGAGGAAA CTGAATGAA ACACCTGAAT TTACACAAAG	240
	ATACTGAGCC AAAACCCCTG GAGGGAATC ATCTAATGGG TGTGAAAGAC TCTAACATCC	300
60	ATGAGCTTGA ACATGAGCAA GAGCCTACTT GTGCCTCCCA GATGGCTGAG CCGTTCCGTA	360

CCTTCCGAGA TGGATGGGTC TCCTACTACA ACCAGCCTGT GPTTCTGGCT GGCATGGGTC 420
 TTGCTTTTCT TTATATGACT GTCCTGGGCT TTGACTGCAT CACCACAGGG TACGCCTACA 480
 5 CTGAGGGACT GAGTGGGTTC CATCCTCAGT ATTTTGATGG GAGCATCAGC TATAACTGGA 540
 ATAATGGGAA CTGTAGCTTT TACTTGGCTA CGTCGAAAAT GTGGTTTGGT TCGGCAGGTC 600
 10 TGATCTCAGG ATTGGCACAG CTTTCTGTG TGATCTTGTG TGTGATCTCT GTATTCATGC 660
 CTGGAAGCCC CCTGGACTTG TCCGTTTCTC CTTTGAAGA TATCCGATCA AGGTTCATTC 720
 AAGGAGAGTC AATTACACCT ACCAAGATAC CTGAAATTAC AACTGAAATA TACATGTCTA 780
 15 ATGGGTCTAA TTCTGCTAAT ATTGTCCCGG AGACAAGTCC TGAATCTGTG CCCATAATCT 840
 CTGTCACTCT GCTGTTTGCA GGCCTCATTC CTGCTAGAAT CGGTCTTTGG TCCTTTGATT 900
 20 TAACTGTGAC ACAGTTGCTG CAAGAAAATG TAATTGAATC TGAAAGAGGC ATTATAAATG 960
 GTGTACAGAA CTCCATGAAC TATCTTCTTG ATCTTCTGCA TTTCATCATG GTCATCCTGG 1020
 CTCCAAATCC TGAAGCTTTT GGCTTGCTCG TATTGATTTC AGTCTCCTTT GTGGCAATGG 1080
 25 GCCACATTAT GTATTTCCGA TTGCCCCAAA ATACTCTGGG AAACAAGCTC TTTGCTTGCG 1140
 GTCTGTATGC AAAAGAAGTT AGGAAGGAAA ATCAAGCAAA TACATCTGTT GTTTGAGACA 1200
 30 GTTTAACTGT TGCTATCTG TTAGTAGATT ATATAGAGCA CATGTGCITA TTTTGTACTG 1260
 CAGAATTCCA ATAAATGGCT GGGTGTTTTG CTCTGTTTTT ACCACAGCTG TGCCTTGAGA 1320
 ACTAAAAGCT GTTTAGGAAA CCTAAGTCAG CAGAAATTAA CTGGATTAAT TTCCCTTATG 1380
 35 TTGAGGGCCA TGGRAAAAAA ATTGGGAAAA GGAAAACTC AGTTTAAAT ACGGGAGACT 1440
 ATAATGGATA AACTGTRATT CCCCTATTTC TCATGAGTAG ATACAATCTT ACGTAAAAGA 1500
 40 GTGGTTAGTC ACGTGAATTC AGTTATCATT TGACAGATTG 1540

45 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1719 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

55 TACTTATGAG GTCAATTGGA AATAAGAACA CCATTTTACT GGGTCTAGGA TTTCAAATAT 60
 TACAGTTGGC ATGGTATGGC TTTGGTTCAG AACCTTGGAT GATGTGGGCT GCTGGGGCAG 120
 TAGCAGCCAT GTCTAGCATC ACCTTTCTCTG CTGTCAGTGC ACTTGTTCCTA CGAACTGCTG 180
 60

	ATGCTGATCA ACAGGGTGTC GTTCAAGGAA TGATAACAGG AATTCGAGGA TTATGCAATG	240
	GTCTGGGACC GGCCCTCTAT GGATTCATTT TCTACATATT CCATGTGGAA CTTAAAGAAC	300
5	TGCCAATAAC AGGAACAGAC TTGGGAACAA ACACAAGCCC TCAGCACCAC TTTGAACAGA	360
	ATTCCATCAT CCTTGGCCCT CCCTTCCTAT TTGGAGCCTG TTCAGTACTG CTGGCTCTGC	420
10	TTGTTGCCTT GTTTATTCGG GAACATACCA ATTTAAGCTT AAGGTCCAGC AGTTGGAGAA	480
	AGCACTGTGG CAGTCACAGC CATCCTCATA ATACACAAGC GCCAGGAGAG GCCAAAGAAC	540
	CTTTACTCCA GGACACAAAT GTGTGACGAC TGAAATCAGG AAGATTTTTT TATCAGCACC	600
15	CAGGCTTAG TTTTCACCTC TAGTCTGGA TGTACATTCC ATTTCCATCC ACAGTGTACT	660
	TTAAGATTGT CTTAAGAAAT GTATCTGCAT GAACTCCGTG GGAACATAAG GAAGTGGGAA	720
	CTTAGAACCA GACAGTTTTT CAAAGATGTT ACAATTTCTT TTGAAAAACC TTTTGTATTAT	780
20	TAGCACCAAT TTCTYGCCAC TAAGCTATTT GTTTTATTAT ACATCCTTTA ATTAAAAACT	840
	ATATATGTAA CTTCCTAGAT ATTAGCAAAT GTCTCTGCTA CCATTTCCCTT AAGGTGTGA	900
25	GCTTTAACTC TATGCTGACT CAGTGAGACA CAGTAGGTAG TATGGTTGTG GACCTATTTG	960
	TTTTAACATT GTAAATTTT GAGTCAGATT TTAATATTGT AAAATCTTGG GTCAAATAAT	1020
30	TCAAAGCCTT AATGCAGATG CACTAAAACA AAGAAATGGT AAATGAATTG TTTGCATTTA	1080
	AAAAAAAAA CTCTTAAGAA AACTGTACTA AATCTGAATC ATGTTTGTGAG CTGTGTTGCA	1140
	GTACTTTTAA ACATTATTCA CTACTGTTTT TGAAGTGAGA AAGTATCAGC CATTTAGCAT	1200
35	TTAAGTTGGG GTATTTAGAG CCTGTAATCT AAATGCTGGC TCAAATTTAT TCCCCAGCTA	1260
	CTTCTTATAC CACTATTCTT TTAATGTTTG CATAATCATA AGCACCTCAA CACTGAATA	1320
40	CATAATCTAA AAATTATATA GTAAAGCTGG TAGCCTTGAA AATGTCAGTG TGATATCTAT	1380
	TATGTAGATA AATATATATA GTGGCCTTTC AGGACTGTCA CAGTAACACT TTATTTACAG	1440
	AGCTAATGTT TGTCTTAAAT TTTCAGGACC CTAGAGGAGA GCTTTATACA ATTACCGATG	1500
45	TGAATTTCTC TAAAGTGAT ATTTTGTGT CCAGTTATAT TATTTAAAA AGTGTTACTT	1560
	TGTAAAAATT GTATATAAAG AACTGTATAG TTTACTCTGT TTTTATCTTG TGTGTGGTTA	1620
50	TTGCTTAATG CTTTITAAC TTGGAACACT CACTATGTTT AAATAAGGTC TTTAAAGAAA	1680
	TGTAAATATT YGTTAATAA AGTTAAATAT TTTAATGAT	1719

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(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 863 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

5	GGCACGAGGG AAGCCGGGAC GATGTCCGCA TGACAACCGA CGTTGGAGTT TGGAGGTGCT	60
	TGCCTTAGAG CAAGGGAAC AGCTCTCATT CAAAGGAAC AGAAGCCTCT CCCTCAGTGG	120
10	TAGGGAGACA GCCAGGAGCG GTTTCTGGG AACTGTGGGA TGTGCCCTTG GGGGCCGAG	180
	AAAACAGAAG GAAGATGCTC CAGACCAGTA ACTACAGCCT GGTGCTCTCT CTGCAGTTCC	240
	TGCTGCTGTC CTATGACCTC TTTGTCAATT CCTTCTCAGA ACTGCTCCAA AAGACTCCTG	300
15	TCATCCAGCT TGTGCTCTTC ATCATCCAGG ATATTGCAGT CCTCTTCAAC ATCATCATCA	360
	TTTCCCTCAT GTTCTTCAAC ACCTTCGTCT TCCAGGCTGG CCTGGTCAAC CTCCTATTCC	420
20	ATAAGTTCAA AGGGACCATC ATCCTGACAG CTGTGTACTT TGCCCTCAGC ATCTCCCTTC	480
	ATGTCTGGGT CATGAACTTA CGCTGGAAAA ACTCCAACAG CTTTATATGG ACAGATGGAC	540
	TTCAAATGCT GTTTGTATT CAGAGACTAG CAGCAGTGT GTACTGCTAC TTCTATAAAC	600
25	GGACAGCCGT AAGACTAGGC GATCCTCACT TCTACCAGGA CTCTTTGTGG CTGCGCAAGG	660
	AGTTCATGCA AGTTCGAAGG TGACCTCTTG TCACACTGAT GGATACTTTT CCTTCCTGGA	720
30	TAGRAGGCCA CATTTGCTGC TTTGCAGGGG AGAGTTGGGC CCTATGCATG GGGCAAAACA	780
	GGTGGGATTT TCCAAGGGAA GGGTTCAGAA TTAGGCNTGT TGTTTCAGCC ATTTCCAAGG	840
35	AAGGGGAAGG GTTCCCTNC CCT	863

(2) INFORMATION FOR SEQ ID NO: 154:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

50	AACAGCAAAA AAGAATGATT TCTTCTGAAA TTGTGGAACA TGAGGATTCA AGTTTTTATT	60
	TTGTACTAG GTGCTGGAGG AACATCCAG TTCACAAAGC CCCCATCTCT TCCTCTGGAG	120
	CCAGAGCCTG CGGTGGAATC AAGTCCAAC GAAACATCAG AACAAATAAG AGAGAAATAA	180
55	GAATAGAATG AATGACCCCA AAATARGGTT TTCTTGGGCG AGGATGTGCT GGATTAGGAA	240
	AGGTGACATG ACACAGGCAG AGCAGAGTGG CACCCACCAC AGAATACAGT GTGTGTTATT	300
60	ACGAGGAGCC AGCAGTTGAG CCTAAGGTCC TTCTACCTAC CTGGTATTGG CATTTGAGGT	360

	CGGAAACCCT CTAAGCCCC ATAAGCCAGG AAAAGTGAAA AGAGAACACA GTTCCTTTAA	420
	GAAGTGGCAG CAAGGCTTGA GGCCTTATGT ATGTAGCTGA GTCAGCAAGG TACATGATGC	480
5	TGTCGCTTT CAAAAGGACT TTTCTCTCCT AGCTGACTGA CTCCTTCCTT AGTTCAAGGA	540
	ACAGCTGAGA CAGACCTCTG CTGAGTAGCT CTGTGATGAC AAAGCCTTGG TTAACTGAG	600
	GTGATCCTCA GGTGTGAGG TTTATTAGTC CCCAAGGCAA ACACAAATAT TAGATTAAATA	660
10	ATCCAACCTT AATAGTATAC ATTTAAAAGA AAAAAACAA AAGCCCTGGA AGNTTGAGGC	720
	CAAGCCTGCT GAGTATTGCA GCTGCATTTG CCCAAAGGGA ATCCAGAACA AGTCCCTCCC	780
15	TGTATTTTGT TCTTGAGAGG GGTGAGTCTA GAAGCTAGAT CCTATCAGGA TGAGGAGCAG	840
	CAGCCAGGG CTGTCTGGA TCAGACCAA CGATTTTAAA GAAAAAGGA AGAGTTTCTT	900
	AGATGAGTAA TTGTTATTGA AGATAGTCAG TGATAACCAC TGACCAGATG CTATCAATAC	960
20	ACTATGTGTC CTTTTAGAA TAAAGATTAC ATATCATCAT TCCTTTGGG AAAATTGTTA	1020
	TTCAGGTATA AAAACAAGAG ATTATAATAA AAAANTAAAA GAACCCTAAA AAAAAAAAC	1080
25	CTCGTGCCGA ATCCCTGCA G	1101

30 (2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2031 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40	CAATTAACCC GTTTGAGGCC TAGGTTGTTT GGCAAGCCCC NGGCCTAAAG TTTTAATTCG	60
	GCAGAGCCAA GGCCTGAAA GGAAGGGAAA GGGGAGGGTA GCGGGAGGGT AGCAGGTGAG	120
	TTCTAGGGC TGAAGGTTT AGCAGCAGCC TGGTGAGTG CCCTGTCATC AAGACAAACC	180
45	CACGGTCTC CTGGGTGCCT ACCAAGCTTG GTTTGTACAA AAGCAAGGTG GGAGTCTATT	240
	TTGTACATG AGATACATCA CACTTACCTG TGGGCCAGTA TTGTGAAGTG AGTCTGAGTT	300
50	GTTTACACTG ATGCCTTCCC TGCCACCCAC AAATTGTGTA CATAGTCTTC AGAATGATAC	360
	CACCCCTTTC CCCAGCTCCC AACCAAGAGC TGGTCTAGG CCTGTGTTAT ATGTCATATT	420
	TAGCGTTTT ATATATGACC TTTGATTCT GTTGTGTGTA TTTAGCACA GTGTATGCAC	480
55	CTTCATTTAA ATACATCTGT GTGCATACAG ATACGCATAT ATGTGTGTGC GTATGCATAT	540
	ATCTCTCATC TGTAGTTTCC AAGAGTTCAG CTGAAGCAGA TGGAGTCCTG CAGCCCAGGA	600
60	GACACCCTGC ATCCCTGCTA ATAGTGTTCG CCACAAGTAT TAGTGAGTCT TCCTTATTAA	660

TATTTTCATT TCAGAAGACT GAAGCAAAGC TGATAGTGTT TGCTGTTTCT TTGGCAGCTA 720
 AGTGAGGGTC TTGGGATGAC TTGCTGTGTT CCTCAAGCTG CACTTTGGGG CCATCTCTGC 780
 5 AGTATTAAGC CCCCTTTTTC CTGGGTGGTA CTCTGTCTGT GCCTGTGTGT GTGTGTGATA 840
 GTCACTCTTG CATGGCTTCC ATGTCTGGTT TGTGGCATTG GGGGATAAGT GCTGAACCAG 900
 10 AGCATTTGCA GTTTGTTTGA GGCTCGTTG CCAATGATAG ATCACTCCTG TTGACCTGGT 960
 ATGTCTGCTT GCTTGCTGCT TTTCTTGCT TTCTCTTGGA AGAGGAAAGG ACTCTGGTCA 1020
 GGCCCAAGGCT GAGTGAGATG AGCTGCAGCT GGCTCATGGC CTCTTAGAG CAGAGAGAGG 1080
 15 AGTATGTCAT TTTACTAAGT TCCTAAACAA ACATTTATGC AGGCAACACT CCTTGCAGAT 1140
 CCAGAAACTG AGGCACAATA GGGTTATGAC TTGCTCAAGA ATATGTAGCT GCTAGGGGGT 1200
 20 AAATCAAGGC ATCACAATTT CTGTTACGCG GGCAGGAATA GGCTGTGAAT TGCTAGCACT 1260
 TTTTTTTAA GCAATTACTT TTTGACTTGT TCCTCTGAAA GTGCAAGAGG CGTACACCTT 1320
 TCCCAAATGT AGACTAGAAT CTGCAGGATG CCACCCACTG TATAGTTCTG CTTTCCCAGA 1380
 25 GAGGAAGAAC TTTTAGAAAC CAAATGATCT TAATTGTTAT TGCCACCCC TGGCTTTTCC 1440
 GGGTAGAAAA TTCACAGTAG GAATGATTGT TAAGAGAGAG TGCTTGAAC CATGGGTAA 1500
 30 CAGGAAAGGC TACCTAACTT CACATATCTG CAACCAGAGC AGCCACCAAG CATTACTTAG 1560
 CAGCAGGAAA ATGATTGTAT TTGAGTTCCT GTGTGTCCAA AACTGAGGCA CCATGTTCTT 1620
 TGAAAACATG CCACCTCAAG GCTGGGCGCG GTGGCTCACA CCTGTTAATC CCAGCACTTT 1680
 35 GGGAGGCCGA GCGGGCGGA TCACCGGAGT CGGGGAGTTT GAGACCAGCC TGGACCAACA 1740
 TGGGAGAAAC CCCATCTCTA CCTAAAAATA CAAAATTAGC CGGGCGTGGT GGCATGCGCC 1800
 40 TATAATCTCA GCTACTTGGG AGGGYTGAGG CAGGRGAATT GCTTGAACCC RGGANGGCGG 1860
 AGGTTTGCGG TTGAGTTGAG GATCGTGCCA TTGCACTTCC GGGCCTTGGG GCAACAACAG 1920
 CAAAAAYTCC GTCTTCAAMW MRTGCCGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC 1980
 45 TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGNGATC GTATTACAAT C 2031

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	CCTGCACCCT GAGCCCTTCA CCCCTCCGAG TTCCCCCAG GTTGGCTTCC TTCGATTCTT	60
	TTTCTTGGTA TCAACGTTTG ATTGGAAGAA CAACCCCTC TTTGTCAACC TCAATAATGA	120
5	GCTCACTGTG GAGGAGCAGC TCGGGCAGAG CTCMCCGTYA TGGTCATTGT TACCCCCCAA	180
	GACCGCAAAA ACTCTGTGTG GACACAGGAT GGACCCTCAG CCCAGATCCT GCAGCAGCTT	240
	GTGGTCTTGG CAGCTGAAGC CCTGCCCATG TTAGAGAAGC AGCTCATGGA TCCCCGGGGA	300
10	CCTGGGGACA TCAGGACAGT GTTCCGGCCG CCCTTGGACA TTTACGACGT GCTGATTTCG	360
	CTGTYTCTTC GCCATATCCC GCGGCACCGC AGGCTTGTGG ACTCGCCAGY TGCCTCTCTC	420
15	TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC TCATCCCTGA TGCCCGTGCT GGGTATGAT	480
	CCTNCTCAGC TCTATCTGAC GCAGCTCAGG GAGGCCTTTG GGGATCTGGC CCTTTCTCTC	540
	TATGACCAGC ATGGTGGAGA GGTGATTGGT GTCCTCTGGA AGCCACCAG CTTCAGCCG	600
20	CAGCCCTTCA AGGCCTCCAG CACAAAGGGG CGCATGGTGA TGTCTCGAGG TGGGGAGCTA	660
	GTAATGGTGC CCAATGTTGA AGCAATCCTG GAGGACTTTG CTGTGCTGGG TGAAGGCCTG	720
25	GTGCAGACTG TGGAGGCCCC AAGTGAGAGG TGGACTGTGT GATCCCAGCT CTGGAGCAAG	780
	CTGTAGACGG ACAGCAGGAC ATTGGACCTC TAGAGCAAGA TGTAGTAGG ATGACCTCCA	840
	CCCTCCTTGG ACATGAATCC TCCATGGAGG GCCTGCTGGC TGAACATGCT GAATCATCTC	900
30	CAACAAAACC CAGCCCCAAC TTTCTCTCTG ATGCTCCAGC ATTGGGGCAG GGGCATGGTG	960
	GCCCATGTAG TCTCCTGGGC CTCACCATCC CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA	1020
35	GGAAGTGAAC CCAGGAGATC CATCCACCTA TTAGCCCTGG GCCTGGACCT CCCTGCGATT	1080
	TCCCACTCCT TTCTTAGTCT TCTTCCAGAA ACAGAGAAGG GGATGTGTGC CTGGGAGAGG	1140
	CTCTGTCTCC TTCTGTCTGC CAGGACCTGT GCCTAGACTT AGCATGCCCT TCACTGCAGT	1200
40	GTCAGGCCTT TAGATGGGAC CCAGCGAAAA TGTGGCCCTT CTGAGTCACA TCACCGACAC	1260
	TGAGCAGTGG AAAGGGGCTA TATGTGTATG AATAGACCAC ATTGAAGGAG CACAATGCCC	1320
45	TCCTGTGTTG ATGCCACTTC CCAGGGTGGG GACAGTGGAA AAGAACCGAG GACAGGAAAG	1380
	GATTGGGTAG GTGAAGGGGT CAGGGGACTG GTAGTCACCC AATCTTGGAG AGGTGCAAAA	1440
	AGCACTGGGG GCTACCCGTT AGCTGCATCT GCCTGGCTG TTTGCCCGTT CATGTCACAA	1500
50	ACTGCCACTA CTATGTACCT GCAGTGGGGT TGCAGAGATG GGGGAGACTC AAGTCTTACT	1560
	CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG AATGCTGCCT CCTTTCAGTC TGGTCTACAC	1620
55	CCACTTTCTG GTAGCCTCTC TGCTTCTGT ATTCTGGCT GTTTTTCAG ACTCAGCTCA	1680
	AATAGTGCCC CTCCTTAAGC CCATCCCTCG CCCCAGCCT GAGGTGATCT TTCCCTCCTC	1740
60	TGAAGTATTA GAGCAGTTAC TGTCTGTCA GTTCGTTTGG CAGGCACACA CAGTGGCATA	1800

AATTCTATTG TTTTGAAGTC TGATTTAAAA TTAAATTGCA GCTGGGCGTG GTGGCTCATG 1860
CTTGTAATCC CAACACTTAG GGAGTMAGGR GAATCACTTG ASCYCAGGAG TYCTAGACCA 1920
5 ATCTGGGCAA MAGAGAGACC CCATCTCTTT TAAATAAAAA GTTAAATTGC TTAAAAAATA 1980
A 1981

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(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GAATTCGGCA CGAGCGCGGC CATGCGGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60
GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120
25 GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
TACCAGCCAG ATCCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAACT GCTGGCTGGG 240
30 TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAACPTGTT CTTGATTCTG 300
CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
CCAGCCATTG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420
35 ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
40 ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600
ATTTTGCTTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660
ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
45 TTAAATCAA CAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780
TACCTCTGAA CTTTTTCTG TGCCTTAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
50 AACCATATAT CCTATTTTAT TTCCTCCTTT TAAACCTTA TAACTATAA MAAAAAATAA 900
AAAAAATAA CTCGA 915

55

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 2117 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

	AGAGCGAAGC GAGGGTGGCG CGGGTCCGGG CATGAAGCTG GGCCGGGCGG TGCTGGGCCT	60
	GCTGCTGCTG GCGCCGTCCG TGGTGCAGGC GGTGGAGCCC ATCAGCCTGG GACTGGCCCT	120
10	GGCCGGCGTC CTCACCGGCT ACATCTACCC GCGTCTCTAC TGCCTCTTCG CCGAGTGTG	180
	CGGGCAGAAG CGGAGCCTTA GCCGGGAGGC ACTGCAGAAG GATCTGGACG ACAACCTCTT	240
15	TGGACAGCAT CTTGCAAAGA AAATCATCTT AAATGCCGTG TTTGGTTTCA TAAACAACCC	300
	AAAGCCCAAG AAACCTCTCA CGCTCTCCCT GCACGGGTGG ACAGGCACCG GCAAAAATT	360
	CGTCAGCAAG ATCATCGCAG AGAATATTTA CGAGGGTGGT CTGAACAGTG ACTATGTCCA	420
20	CCTGTTGTG GCCACATGC ACTTTCCACA TGCTTCAAAC ATCACCTTGT ACAAGGATCA	480
	GTTACAGTTG TGGATTCGAG GCAACGTGAG TGCCTGTGCG AGGTCCATCT TCATATTTGA	540
25	TGAAATGGAT AAGATGCATG CAGGCCTCAT AGATGCCATC AAGCCTTTCC TCGACTATTA	600
	TGACCTGGTG GATGGGTCT CCTACCAGAA AGCCATGTTT ATATTTCTCA GCAATGCTGG	660
	AGCAGAAAGG ATCAGAGATG TGGCTTTGGA TTTCTGGAGG AGTGGAAGC AGAGGAAGA	720
30	CATCAAGCTC AAAGACATTG AACACGCGTT GTCTGTGTG GTTTTCAATA ACAAGAACAG	780
	TGGCTTCTGG CACAGCAGCT TAATTGACCG GAACCTCATT GATTATTTTG TTCCCTTCCT	840
35	CCCCCTGGAA TACAAACACC TAAAAATGTG TATCCGAGTG GAAATGCAGT CCCGAGGCTA	900
	TGAAATTGAT GAAGACATTG TAAGCAGAGT GGCTGAGGAG ATGACATTTT TCCCCAAGA	960
	GGAGAGAGTT TTCTCAGATA AAGGCTGCAA AACGGTGTTC ACCAAGTTAG ATTATTACTA	1020
40	CGATGATTGA CAGTCATGAT TGGCAGCCGG AGTCACTGCC TGGAGTTGGA AAAGAAACAA	1080
	CACTCAGTCC TTCCACACTT CCACCCCCAG CTCCTTTCCC TGGAAGAGGA ATCCAGTGAA	1140
45	TGTTCTGTGT TGATGTGACA GGAATTCTCC CTGGCATTGT TTCCACCCCC TGGTGCCTGC	1200
	AGGCCACCCA GGGACCACGG GCGAGGACGT GAAGCCTCCC GAACACGCAC AGAAGGAAGG	1260
	AGCCAGCTCC CAGCCCCTC ATCGCAGGGC TCATGATTTT TTACAAATTA TGTTTTAATT	1320
50	CCAAGTGTGT CTGTTTCAAG GAAGGATGAA TAAGTTTAT TGAAAATGTG GTAACTTTAT	1380
	TTAAAATGAT TTTTAACATT ATGAGAGACT GCTCAGATTC TAAGTTGTG GCCTTGTGTG	1440
55	TGTGTTTTTT TTTAAGTTCT CATCATTATT ACATAGACTG TGATGTATCT TTACTGGAAA	1500
	TGAGCCCAAG CACACATGCA TGGCATTGT TCCACAGGAG GGCATCCCTG GGGATGTGGC	1560
60	TGGAGCATGA GCCAGCTCTG TCCCAGGATG GTCCCAGCGG ATGCTGCCAG GGGCAKTGAA	1620

GTGTTTAGGT GAAGGACAAG TAGGTAAGAG GACGCCTTCA GGCACCACAG ATAAGCCTGA 1680
AACAGCCTCT CCAAGGGTTT TCACCTTAGC AACAAAGGGA GCTGTGGGAG TGATTTTGGC 1740
5 CACACTGTCA ACATTTGTTA GAACCACTCT TTTGAAAGAA AAGTATTTCC AACTTGTAC 1800
TTGCCAGTCA CTCCTTTTGG CAAAAGGTGG CCCTTCACTG TCCATTCCAA ATAGCCCACA 1860
CGTGCTCTCT GCTGGATTCT AAATTATGTG AATTTTGCCA TATTAAATCT TCCTCATTTA 1920
10 TACTATTATT TGTACGTTT AATCAGAATC CCCGAAACCT CCTATAAAGC TTAGCTGCCC 1980
CTTCTGAGGA TGCTGAGAAC GGTGTCCTTC TTTATAAATG CAAATGGCTA CCGTTTAC 2040
15 ATAAATTTT GCATGTGCAA AAAAAAAAAA ANAAAAAAAA AAAATCCCGG GGGGGGGCCG 2100
GTAACCAATT TGNCCCC 2117

20

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 2395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:
30

TGTTCTTAA TCCCTTTTCT AAAAAGGGGG GAAATCCCG ATGGATTTTA GGGATTGGTC 60
TGGTGTGAGC TGTGTTTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG 120
35 CAAAGCCTTT ATTTTGGCAG TTAAGSCAAA TGTGTTTCC AGAAAGTTAG TTATTTTCTC 180
CTCTTTCTTT CCTTCTTTC CTCCCTTTT CCCGTCTGAC CCCAAACGTT ATGTGCCAAA 240
40 CATGACTGGA CAGCAGCTTT TGTTCCTTGA CCCTGTAATA TGACAGTCTG CTAATATTGA 300
CAGAAGGTGC AGTTTTTGGG TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA 360
AAAAAAKGA CTGTTTCTG TTGTACTTGA GTCTTAAGAA AAAGTGCCC ATAGTTTAGT 420
45 GGACAATTT CAAAGGCTTT AGTACCACCT GTATTTCAAA ATGGGGGACC CAAACTCCCG 480
GAAGAAACAA GCTCTGAACA GACTACGTGC TCAGCTTAGA AAGAAAAAG AATCTCTAGC 540
50 TGACCAGTTT GACTTCAAGA TGTATATTGC CTTGTATTG AAGGAGAAGA AGAAAAAGTC 600
AGCACTTTTT GAAGTGTCTG AGGTATATAC AGTCATGACA AATAATTATG AAGAAAATAT 660
CCTGAAAGGT GTGCGAGATT CCAGCTATTC CTGGAAGT TCCCTAGAGC TTTTACAGAA 720
55 GGATGTGTA CAGCTCCATG CTCCTCGATA TCAGTCTATG AGAAGGGATG TAATTGGCTG 780
TACTCAGGAG ATGGATTICA TTCTTTGGCC TCGGAATGAT ATTGAAAAA TCGTCTGTCT 840
60 CCTGTTTCT AGGTGGAAG AATCTGATGA GCCTTTTAGG CCTGTTGAG CAAATTTGAG 900

	TTTCATCATG GTGACTATGA AAAACAGTTT CTGCATGTAC TGAGCCGCAA GGACAAGACT	960
5	GGAATCGTTG TCAACAATCC TAACCACTCA GTGTTTCTCT TCATTGACAG ACAGCACTTG	1020
	CAGACTCCAA AAAACAAAGC TACAATCTTC AAGTTATGCA GCATCTGCCT CTACCTGCCA	1080
	CAGGAACAGC TCACCCACTG GGGCAGTTGG CACCATAGAG GRTCACCTCC GTCCTTATAT	1140
10	GCCAGAGTAG AGTACTGACC AGCAAAATGG AGAAGATCAG AGAATGCAGC AGCAGTTTTT	1200
	TTTCTTGTTT TCTTACCACT TTATTCTTTC AGAGTTTAAA GAAAATGGAC TCATGCACAG	1260
15	AACACTATGC ATTTTGAAAC TTGTTTCATCC TGGATTTTTT TAAATCATT TTATCTCAGA	1320
	ACTTAAACAA AAATTAGATG TCGTGCACGG ACTGTGTGAA AGAAGATGCT TTGCATATTT	1380
	GCTGCAGTGC ATCAGTATCT TACTAAAAAT GTGAAATGAA AGGACTATTG TACACTGAAA	1440
20	TGCTTAAATG TATCTGAAAG CACAAGGTGA TACTCATTTT TATGGTCTTC CCATTTGTGC	1500
	TGGTTTTTGC CTCTTTGACA TCTGTATCA GTATTTAGAG GGTGAGAAGT GAATGTAACA	1560
25	GGTATAATA ACATTTTTAA AAACAATAAC TTTGCTATA TCACAGTTGT TCCAGAGCAC	1620
	TGTCAGATAC ATTCTAATGA CCAGAACTGG TTTAAAAAAA GAAAATACAA CCATGGGAAA	1680
	GAAATCTTAA ATGAAAAACG CATCTCATTG TAGGCATTTT TGCCTCATAT TTTACTGGGC	1740
30	CATGTTTGTT TCCTGGTACT CATGTATTTT TTTTTCAG ATCTCTTTCC CCAAGTTGCT	1800
	ATTGTAAGAG TATTCTGCTG CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT	1860
35	CTGAAGTAGC TATAAAGCAG CTATAAACA GAAATACATG CATAGCTGCA GAAACCATGA	1920
	TAGGTAGAGG ACTTTTCTTT TGGTTTGT TTGTTTGT TTGTTTGT TTTGGTTTTA	1980
	CAGAGAAGAG ATTTTTATTA CAAAGAAAAA AATCCAGTG AATTGTGCAG AAATGCTGGT	2040
40	TTTTACACCA TCCTAAAGAA AAACTTTACA AGGGTGTTTT GGAGTAGAAA AAAGGTTATA	2100
	AAGTTGGAAT CTTAAATTGT AAAATTAACC ATTGAGTGTC AAAGTTCTAA AAGCAGAACT	2160
45	CATTTTGTGC AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TTCTCCTTTT	2220
	AAATGAAGAA AAGCTTTGCT TAAGGGTTGC ATACTTTTAT TGGAGTAAAT CTGAATGATC	2280
	CTACTCCTTT GGAGTAAAC TAGTGCTTAC CAGTTTCCAA TTGTATTTAG CTCTGGTTG	2340
50	GAATTTGAAA AAAAAAGAAA AAAAGAAAAA GAAACCTAA ATAAAATAGG TGAAA	2395

55 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

5	CCCCGGATAC CGCCTGACGT AGTGCCAATC ACACCTCTCG CGTCTCGGCG CCTCGGAGGC	60
	TAATGAGGAC GCCTGGCGAA ACGCAGTAAC GGATTTCGGG GTGGACCTTC GCTTTACGGC	120
	TCGTGAGTTC TTCCGCCCAA CCCAGAGGAA GCGGGAGAGC AGTTTACGAC AGCGCCGGTC	180
10	GTGTTTACGG CGGCGCCCCG TCGCGCGCA TGTTCCTCT TTTCTGGTT TCTCAAGAGT	240
	GCTGCTGCTA ACGCGGTCCC CGGCACGCAC CATCTGTTGC CATCCGGCC GGCCGAGGCA	300
15	TTGCAGATTT TGGAAGATGG CAAAGTTCAT GACACCCGTG ATCCAGGACA ACCCCTCAGG	360
	CTGGGGTCCC TGTGCGGTT CCGAGCAGTT TCGGGATATG CCCTACCAGC CGTTCAGCAA	420
	AGGAGATCGG CTAGGAAAGG TTGCAGACTG GACAGGAGCC ACATACCAAG ATAAGAGGTA	480
20	CACAAATAAG TACTCCTCTC AGTTTGGTGG TGGAAGTCAA TATGCTTATT TCCATGAGGA	540
	GGATGAAAGT AGCTTCCAGC TGGTGGATAC AGCGCGCACA CAGAAGACGG CCTACCAGCG	600
25	GAATCGAATG AGATTGCCCC AGAGGAACCT CCGCAGAGAC AAAGATCGTC GGAACATGTT	660
	GCAGTTCAAC CTGCAGATCC TGCCTAAGAG TGCCAAACAG AAAGAGAGAG AACGCATTGG	720
	ACTGCAGAAA AAGTTCCAGA AACAAATTGG GGTTAGGCAG AAATGGGATC AGAAATCACA	780
30	GAAACCCCGA GACTCTTCAG TTGAAGTTCG TAGTGATTGG GAAGTGAAAG AGGAAATGGA	840
	TTTCTCTCAG TTGATGAAGA TCGCTACTT GGAAGTATCA GAGCCACAGG ACATTGAGTG	900
35	TTGTGGGGCC CTAGAATACT ACGACAAAGC CTTTGACCGC ATCACCACGA GGAGTGAGAA	960
	GCCACTGCGG ASATNCAAGC GCATCTTCCA CACTGTCACC ACCACAGACG ACCCTGTCAT	1020
	CCGCAAGCTG GCAAAACTC AGGGGAATGT GTTTGCCACT GATGCCATCC TGGCCACGCT	1080
40	GATGAGCTGT ACCCGCTCAG TGTATTCTTG GGATATTGTC GTCCAGAGAG TTGGGTCCAA	1140
	ACTCTTCTTT GACAAGAGAG ACAACTCTGA CTTTGACCTC CTGACAGTGA GTGAGACTGC	1200
45	CAATGAGCCC CCTCAAGATG AAGGTAATTC CTTCAATTCA CCCCACAACC TGGCCATGGA	1260
	GGCAACCTAC ATCAACCACA ATTTCTCCCA GCAGTGCTTG AGAATGGGA AGGAAAGATA	1320
	CAACTTCCCC AACCCAAACC CGTTTGTGGA GGACGACATG GATAAGAATG AAATCGCCTC	1380
50	TGTGCGTAC CGTTACCGCA GTGNAAGCT TGGAGATGAT ATTGACCTTA TTGTCCGTTG	1440
	TGAGCAGGAT GGCCTCATGA CTGGAGCCAA CGGGGAAGTG TCCTTCATCA ACATCAAGAC	1500
55	ACTCAATGAG TGGGATTCCA GGCAGTGTAA TGGCGTTGAC TGGCGTCAGA AGCTGGACTC	1560
	TCACGAGGG GCTGTCATTG CCACGAGCT GAAGAACAAC AGCTACAAGT TGGCCCGGTG	1620
60	GACCTGCTGT GCTTGTCTGG CTGGATCTGA GTACCTCAAG CTTGGTTATG TGTCTCGGTA	1680

CCACGTGAAA GACTCCTCAC GCCACGTCAT CCTAGGCACC CAGCAGTTCA AGCCTAATGA 1740
GTTTGCCAGC CAGATCAACC TGAGCGTGA GAATGCCTGG GGCATTTTAC GCTGCGTCAT 1800
5 TGACATCTGC ATGAAGCTGG AGGAGGGCAA ATACCTCATC CTCAAGGACC CCAACAAGCA 1860
GGTCATCCGT GTCTACAGCC TCCCTGATGG CACCTTCAGC TCTGATGAAG ATGAGGAGGA 1920
AGAGGAGGAG GAAGAAGAGG AAGAAGAAGA GGAAGAAACT TAAACCAGTG ATGTGGAGCT 1980
10 GGAGTTTGTC CTTCCACCGA GACTACGAGG GCCTTTGATG CTTAGTGGAA TGTGTGTCTA 2040
ACTTGCTCTC TGACATTTAG CAGATGAAAT AAAATATATA TCTGTTTAGT CTTAAAAAAA 2100
15 AAAAAAAAAA AAAAAAAAAAN 2120

20 (2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

30 GGAAGCTGAA GTCCTTCCAG ACCAGGGACA ACCAGGGCAT TCTCTATGAA GCTGCACCCA 60
CCTCCACCCT CACCTGTRAC TCAGGACCAC AGAAGCAAAA GTTCTCACTC AAAGTGGATG 120
CCAAGGATGG GCGCTGTTC AATGAGCAGA ACTTCTTCCA GCGGGCCGCC AAGCCTCTGC 180
35 AAGTCAACAA GTGGAAGAAG CTGTACTCGA CCCCCTGCT GGCATCCCT ACCTGCATGG 240
GTTTCGGTGT TCACCAGGAC AAATACAGGT TCTTGGTGT ACCCAGCCTG GGGAGGAGCC 300
40 TTCAGTCGGC CTGGATGTC AGCCCAAAGC ATGTGCTGTG CAGAGAGGTC TGTGCTGCAG 360
GTGGCCTGCC GGCTGCTGA TCCCTGGAG TTCCTCCATG AGAATGAGTA TGTTCATGGA 420
AATGTGACAG CTGAAATAT CTTGTGGAT CCAGAGGACC AGAGTCAGGT GACTTTGGCA 480
45 GGCTATGGCT TCGCTTCCG CTATTGCCA AGTGGCAAAC ACGTGGCCTA CGTGAAGGC 540
AGCAGGAGCC CTCACGAGG GACCTTGAG TTCATTAGCA TGGACCTGCA CAAGGGATGC 600
50 GGGCCCTCCC GCCGRCGA CCTCCAGAGC CTGGGCTACT GCATGCTGAA GTGGCTCTAC 660
GGGTTTCTGC CATGGACAAA TTGCCTTCCC AAMAMTGGG ACATCATGAA GCAAAAACAG 720
AAGTTTGTG ATAAGCCGG GCCCTTCGTG GGACCTGCG GTCAGTGGAT CAGGCCCTCA 780
55 GAGACCTGC AGAAGTACCT GAAGGTGGTG ATGGCCCTCA CGTATGAGGA GAAGCCGCC 840
TACGCCATGC TGAGGAACAA CCTAGAAGCT TTGCTGCAGG ATCTGCGTGT GTCTCCATAT 900

60

(2) INFORMATION FOR SEQ ID NO: 162:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GGCACGAGAT GAGGGGCACC CAGTGCCTCT AGGCGAGGCT GGGTGGTGGT CCCCTAGGTA 60
15 TCAGCCTCTC TTACTGTACT CTCGGGAAT GTTAACCTTT CTATTTTCAG CCTGTGCCAC 120
CTGTCTAGGC AAGCTGGCTT CCCCATGGC CCCTGTGGGT CCACAGCAGC GTGGCTGCCC 180
CCCAGGGCCA CCGCTTCTTT CTTGATCCTC TTTCCTTAAC AGTGACTTGG GCTTGAGTCT 240
20 GGCAAGGAAC CTGCTTTTA GCTTCACCAC CAAGGAGAGA GGTGACATG ACCTCCCCGC 300
CCCCTACCA AGGCTGGGAA CAGAGGGGAT GTGGTGAGAG CCAGGTTCTT CTGGCCCTCT 360
25 CCAGGTGTT TTCCACTAGT CACTACTGTC TTCTCCTTGT AGCTAATCAA TCAATATTCT 420
TCCCTTGCCT GTGGGCAGTG GAGAGGCTGC TGGGTGTACG CTGCACCTGC CCACTGAGTT 480
GGGAAAGAG GATAATCAGT GAGCACTGTT CTGCTCAGAG CTCCTGATCT ACCCCACCCC 540
30 CTAGGATCCA GGA CTGGGTC AAAGCTGCAT GAAACCAGGC CCTGGCAGCA AACCTGGGAA 600
TGGCTGGAGG TGGGAGAGAA CCTGAATTC TCTTTCCCTC TCCTCCTCC AACATTACTG 660
35 GAACTCTATC CTGTTAGGAT CTTCTGAGCT TGTTCCTG CTGGGTGGGA CAGAGGACAA 720
AGGAGAAGGG AGGCTCTAGA AGAGGCAGCC CTCTTTGTC CTCTGGGGTA AATGAGCTTG 780
ACCTAGAGTA AATGGAGAGA CCAAAGCCT CTGATTTTAA ATTTCCATAA AATGTTAGAA 840
40 GTATATATAT ACATATATAT ATTTCTTTAA ATTTTGAGT CTTTGATATG TCTAAAAATC 900
CATTCCTCT GCCCTGAAGC CTGAGTGAGA CACATGAAGA AAAGTGTGTT TCATTTAAAG 960
45 ATGTTAATTA AATGATTGAA ACTTGAAAAA AAAAAAAAAA AAA 1003

50 (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2196 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

60 AAGAAGCGGC ACACGGATGT GCAGTTCTAC ACAGAAGTGG GAGAGATAAC CACGGACTTG 60

	GGGAAACATC AGCATATGCA TGACCGAGAT GACCTCTATG CTGAGCAGAT GGAACGAGAA	120
5	ATGAGGCACA AACTGAAAAC AGCCTTTAAA AATTTCATTG AGAAAGTAGA GGCTCTAACT	180
	AAGGAGGAAC TGGAATTTGA AGTGCCTTTT AGGGACTTGG GATTTAACGG AGCTCCCTAT	240
	AGGAGTACCT GCCTCCTTCA GCCCACTAGT AGTGCCTGG TAAATGCTAC GGAATGGCCA	300
10	CCTTTTGTGG TGACATTGGA TGAGGTAGAG CTGATCCACT TTRAGCGGGT CCAGTTTCAC	360
	CTGAAGAACT TTGATATGGT AATCGTCTAC AAGGACTACA GCAAGAAAGT GACCATGATC	420
15	AACGCCATTG CTGTAGCCTC TCTTGACCCC ATCAAGGAAT GGTGGAATTC CTGCGACCTG	480
	AAATACACAG AAGGAGTACA GTCCCTCAAC TGGACTAAAA TCATGAAGAC CATGTGTTGAT	540
	GACCCCTGAGG GCTTCTTCGA ACAAGGTGGC TGGTCTTTCC TGGAGCCTGA GGGTGAGGGG	600
20	AGTGATGCTG AAGAAGGGGA TTCAGAGTCT GAAATTGAAG ATGAGACTTT TAATCCTTCA	660
	GAAGATGACT ATGAAGAGGA AGAGGAGGAC AGTGATGAAG ATTATTCATC AGAAGCAGAA	720
25	GAGTCAGACT ATTCTAAGGA GTCATTGGGT AGTGAAGAAG AGAGTGAAA GGATTGGGAT	780
	GAAGTGAGG AAGAAGCCCG AAAAGCGGAC CGAGAAAGTC GTTACGAGGA AGAAGAAGAA	840
	CAAAGTCGAA GTATGAGCCG GAAGAGGAAG GCATCTGTGC ACAGTTCGGG CCGTGGCTCT	900
30	AACCGTGGTT CCAGACACAG CTCTGCACCC CCCAAGAAAA AGAGGAAGTA ACTTCTGAAC	960
	TTTGGCCCTG AGCTCCATTG TTCTCCAGC CAACCCCTGA AAATTTTACA TGACATAGAA	1020
35	ACTGTATTTT TCCTTTCGTT TTCAATTGAA GTTTTGCCAT TTGTGTTTAT GGGTTTAGGG	1080
	GGCCATTGT GTGGACCAAT CTAATCGGGG AATTCCAGGC CCACCAGGAC ACGTGCCAAT	1140
	GGCCCCATTG AGATGGCAAG GGAGGAGGTG TTCTTGAAGA CAGGAGGAGG CTCCCGCTGT	1200
40	TAATAAATAT TGTTCATTG TTCTCTCTC CTGTACCTT CTGCCAAGAC ATTGATGGCT	1260
	TCTGACATCT TATTTGGTGT CTCAAAGCTG TATTTCCAAG ACAGTGGTAC AAGGTGACCC	1320
45	TTAATTACCC GTATCATGTT TCTTGACCAG CACATTCAAT CCTCCAACCT ACCCTACTGC	1380
	CATGACCTTC CGCACATCTC TAAGTTTTAT CTTTGCAATA CTCAGGTTT TCGGAAATTT	1440
	GCTAATGGTT GTGATAAACC ATACAGCTTG AGCCAGTGAG GCAGATTGGG CTGGTGCCTT	1500
50	CGTCTGAGTT TTCTGCTTT CCTGCCTCGT GCAGATTCTG AGGTATATCT GCTGCCTTGG	1560
	AAGACATAAG AAGCAGTGAT ACTCCCTGGC TCGGTTATTT TCTCCATACA ATGCACACAT	1620
55	GGTACAATGA TAGAAGGCAA AATTGCCACT GTCTTCTTTT TTTTCTCATA TATCTAAGGA	1680
	AGATATATCA GGTGTGCTT CATGTACCGC TTCTAGTGAA ATGTAGAGGA AGGCTCAAAG	1740
	GAGTCAACAT TTAGATCTGG AAGGACAAG TCATGCCTTG GGCCTAGAAT ACCCTGATGA	1800
60	GAAAAGAGAA GAGGAAGGGA GGCCATATCT ACAACANCAN CCTCTCGGCA CTGCTGCTCC	1860

TTATTTTAAC TTTGTCTTGC ATTGTCTGT ATTTATCACA GTTCTGTGTG AACAGCTTTT 1920
CAAGTATTTG GGGAGTTTAT CTGCCATCC TCCCCTTCTG GTTCTCTGCA CCCACCTGTC 1980
5 CCACTGCAGT TCCTTCCGTG CTCTGTGACT TTAAGAGAAG AAGGGGGGAG GGGTCCCGGA 2040
TTTTATGTTT GTTTGTTTTT TCTCCTTAGC AGTAGGACTT GATATTTTCA ATTTTGGAAG 2100
10 AACTAAAAGA TGAATAAACT GGGTTTTTTT TGTGTGTTGT TTTTGTA AAAA 2160
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2196

15

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 1945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCACAGAGTC GGGCGGACCG ACAGGGAGAG GAGGAGAGGG GGTCTGCGCG CGGCCGCTAC 60
CCAGAAGCCA GCGGACGGCA GCACGGAGTG GGCTGTCCCC GAGCCCAGCC CCGAGCGAGC 120
30 CCCCCCCCCG CCCCCGMAGG ACGCGCCTYC CAGCCAGCCC GACTYCTAGG AGGAGGGGAG 180
GCGGAAAGC AGCTCAAGCC TCACCCACCG CCCTGCCCCC AGCCCCGCCA CTCCCAGGCT 240
35 CCTCGGACT CGCGGGTCC TCCTGGGAGT CTCGGAGGGG ACCGGCTGTG CAGACGCCAT 300
GGAGTTGGTG CTGGTCTTCC TCTGCAGCCT GCTGGCCCCC ATGGTCTTGG CCAGTGAGC 360
TGAAAAGGAG AAGGAAATGG ACCCTTTTCA TTATGATTAC CAGACCTTGA GGATTGGGGG 420
40 ACTGGTGTTC GCTGTGGTCC TCTTCTCGGT TGGGATCCTC CTTATCCTAA GTCGCAGGTG 480
CAAGTGCACT TTCAATCAGA AGCCCCGGC CCCAGGAGAT GAGGAAGCCC AGGTGGAGAA 540
45 CCTCATCACC GCCAATGCAA CAGAGCCCCA GAAAGCAGAG AACTGAAGTG CAGCCATCAG 600
GTGGAAGCCT CTGGAACCTG AGGCGGCTGC TTGAACCTTT GGATGCAAAT GTCGATGCTT 660
AAGAAAACCG GCCACTTCAG CAACAGCCCT TTCCCAGGA GAAGCCAAGA ACTTGTGTGT 720
50 CCCCCACCCT ATCCCCCTA ACACCATTC TCCACCTGAT GATGCAACTA AACTTGCCT 780
CCCCACTGCA GCCTGCGGTC CTGCCCCCT CCCGTGATGT GTGTGTGTGT GTGTGTGTGT 840
55 GTGACTGTGT GTGTTTCTA ACTGTGGTCT TTGTGCTTAC TTGTTTGTG ATGTAATTGT 900
GTTTGTAGT GAACTGTGA CTCGCTTTC CAGGCAGGGG CTGAGCCACA TGGCCATCTG 960
CTCCTCCCTG CCCCCGTGGC CCTCCATCAC CTTCTGCTCC TAGGAGGCTG CTTGTTGCC 1020
60

	GAGACCAGCC CCTCCCCCTG ATTTAGGGAT GCGTAGGGTA AGAGCACGGG CAGTGGTCTT	1080
	CAGTCGTCTT GGGACCTGGG AAGGTTTGCA GCACTTTGTC ATCATTCTTC ATGGACTCCT	1140
5	TTCACCTCTT TAACAAAAAC CTGCTTCCT TATCCCACCT GATCCCAGTC TGAAGGTCTC	1200
	TTAGCAACTG GAGATACAAA GCAAGGAGCT GGTGAGCCCA GCGTTGACGT CAGGCAGGCT	1260
10	ATGCCCTTCC GTGGTTAATT TCTTCCCAGG GGCTTCCACG AGGAGTCCCC ATCTGCCCCG	1320
	CCCCTTACA GAGCGCCCGG GGATTCCAGG CCCAGGGCTT CTACTCTGCC CCTGGGGAAT	1380
	GTGTCCCCTG CATATCTTCT CAGCAATAAC TCCATGGGCT CTGGGACCCT ACCCCTTCCA	1440
15	ACCTTCCCTG CTTCTGAGAC TTCAATCTAC AGCCCAGCTC ATCCAGATGC AGACTACAGT	1500
	CCCTGCAATT GGTCTCTTGG CAGGCAATAG TTGAAGGACT CCTGTTCCGT TGGGGCCAGC	1560
20	ACACCGGGAT GGATGGAGGG AGAGCAGAGG CCTTTGCTTC TCTGCCTACG TCCCCTTAGA	1620
	TGGGCAGCAG AGGCAACTCC CGCATCCTTT GCTCTGCCTG TCRGTGGTCA GAGCGGTGAG	1680
	CGAGGTGGGT TGGAGACTCA GCAGGCTCCG TGCAGCCCTT GGAACAGTG AGAGGTTGAA	1740
25	GGTCATAACG AGAGTGGGAA CTCAACCCAG ATCCCGCCCC TCCTGTCTCTC TGTGTTCCCG	1800
	CGGAAACCAA CCAACCGTG CGCTGTGACC CATTGCTGTT CTCTGTATCG TGATCTATCC	1860
30	TCAACAACAA CAGAAAAAAG GAATAAATA TCCTTGTGTT CTTAGTGAAA AAAAAAAAAA	1920
	AAAAAAAAA AAAAAAAAAA CTCGA	1945

35

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

45

	GGGTCGACCC ACGCGTCCGG CAGCCGTCGT TTGAGTCGTT GCTGCCGCTG CCCCCTCCCG	60
	GATCAGGAGC CAGTGTATAC CGCCGCCCCA CCGCCTTGGT GCCGCTAGAG GAAACGAGAA	120
50	GGAGGCCGCC TCGGTTTGT CGCCGAGCT CGCCCMYGY CYGGRAGAGC CGAGCCCCGG	180
	CCCAGTCGGT CGCTGCCAC CSCTCGTAGC CGTTACCCGC GGGCCGCCAC AGCCGCCGGC	240
55	CGGGAGAGGC GCGGCCATG GCTCTGGAG CCGATTCAA AGGTGATGAC CTATCAACAG	300
	CCATCTCAA ACAGAAGAAC CGTCCCAATC GGTAAATTGT TGATGAAGCC ATCAATGAGG	360
	ACAACAGTGT GGTGTCTTG TCCAGCCCA AGATGGATGA ATTGCAGTTG TTCCGAGGTG	420
60	ACACAGTGT GCTGAAGGA AAGAAGAGAC GAGAAGCTGT TTGCATCGTC CTTTCTGATG	480

	ATACTTGTTT	TGATGAGAAG	ATTCCGGATGA	ATAGAGTTGT	TCGGAATAAC	CTTCGTGTAC	540
	GCCTAGGGGA	TGTCATCAGC	ATCCAGCCAT	GCCCTGATGT	GAAGTACGGC	AAACGTATCC	600
5	ATGTGCTGCC	CATTGATGAC	ACAGTGAAG	GCATTACTGG	TAATCTCTTC	GAGGTATACC	660
	TTAAGCCGTA	CTTCCTGGAA	GCGTATCGAC	CCATCCGGAA	AGGAGACATT	TTTCTTGTC	720
10	GTGGTGGAT	GCGTCTGTG	GAGTTCAAAG	TGGTGGAAAC	AGATCCTAGC	CCTTATMGCA	780
	TTGTTGCTCC	AGACACAGTG	ATCCACTGCG	AAGGGGAGCC	TATCAAACGA	GAGGATGAGG	840
	AAGAGTCCTT	GAATGAAGTA	GGGTATGATG	ACATTGGTGG	CTGCAGGAAG	CAGCTAGCTC	900
15	AGATAAAGGA	GATGGTGGAA	CTGCCCTGA	GACATCCTGC	CCTCTTTAAG	GCAATTGGTG	960
	TGAAGCCTCC	TAGAGGAATC	CTGCTTTACG	GACCTCCTGG	AACAGGAAAG	ACCCTGATTG	1020
20	CTCGAGCTGT	AGCAAATGAG	ACTGGAGCCT	TCTTCTTCTT	GATCAATGGT	CCTGAGATCA	1080
	TGAGCAAATT	GGCTGGTGAG	TCTGAGAGCA	ACCTTCGTAA	AGCCTTTGAG	GAGGCTGAGA	1140
	AGAATGCTCC	TGCCATCATC	TTCATTGATG	AGCTAGATGC	CATCGCTCCC	AAAAGAGAGA	1200
25	AAACTCATGG	CGAGGTGGAG	CGGCGCATTG	TATCACAGTT	GTTGACCCTC	ATGGATGGCC	1260
	TAAAGCAGAG	GGCAGATGTG	ATTGTTATGG	CAGCAACCAA	CAGACCCAAC	AGCATTGACC	1320
30	CAGCTCTACG	GCGATTTGGT	CGCTTTGACA	GGGAGGTAGA	TATTGGAATT	CCTGATGCTA	1380
	CAGGACGCTT	AGAGATTCTT	CAGATCCATA	CCAAGAACAT	GAAGCTGGCA	GATGATGTGG	1440
	ACCTGGAACA	GTAGCCAATG	AGACTCACGG	GCATGTGGGT	GCTGACTTAG	CAGCCCTGTG	1500
35	CTCAGAGGCT	GCTCTGCAAG	CCATCCGCAA	GAAGATGGAT	CTCATTGACC	TAGAGGATGA	1560
	GACCATTGAT	GCCGAGGTCA	TGAATCTCT	AGCAGTTACT	ATGGATGACT	TCCGGTGGGC	1620
40	CTTGAGCCAG	AGTAACCCAT	CAGCACTGCG	GGAAACCGTG	GTAGAGGTGC	CACAGGTAAC	1680
	CTGGGAAGAC	ATCGGGGGCC	TAGAGGATGT	CAAACGTGAG	CTACAGGAGC	TGGTCCAGTA	1740
	TCCTGTGGAG	CACCCAGACA	AATTCCTGAA	GTTTGGCATG	ACACCTTCCA	AGGGAGTTCT	1800
45	GTTCATGGA	CCTCCTGGCT	GTGGGAAAAC	TTTGTGTGGC	AAAGCCATTG	CTAATGAATG	1860
	CCAGGCCAAC	TTCATCTCCA	TCAAGGGTCC	TGAGCTGCTC	ACCATGTGGT	TTGGGGAGTC	1920
50	TGAGGCCAAT	GTCAGAGAAA	TCTTTGACAA	GGCCCCGCAA	GCTGCCCCCT	GTGTGCTATT	1980
	CTTTGATGAG	CTGGATTCTGA	TTGCCAAGGC	TCGTGGAGGT	AACATTGGAG	ATGGTGGTGG	2040
	GGCTGCTGAC	CGAGTCATCA	ACCAGATCCT	GACAGAAATG	GATGGCATGT	CCACAAAAAA	2100
55	AAATGTGTC	ATCATTTGCG	CTACCAACCG	GCCTGACATC	ATTGATCCTG	CCATCCTCAG	2160
	ACCTGGCCGT	CTTGATCAGC	TCATCTACAT	CCCACTTCCT	GATGAGAAGT	CCCGTGTTC	2220
60	CATCCTCAAG	GCTAACCTGC	GCAAGTCCCC	AGTTGCCAAG	GATGTGGACT	TGGAGTTCTT	2280

GGCTAAATG ACTAATGGCT TCTCTGGAGC TGACCTGACA GAGATTTGCC AGCGTGCTTG 2340
 CAAGCTGGCC ATCCGTGAAT CCATCGAGAG TGAGATTAGG CGAGAACGAG AGAGGCAGAC 2400
 5 AAACCCATCA GCCATGGAGG TAGAAGAGGA TGATCCAGTG CCTGAGATCC GTCGAGATCA 2460
 CTTTGAAGAA GCCATGCGCT TTGCGCGCCG TTCTGTCACT GACAATGACA TTCGGAAGTA 2520
 10 TGAGATGTTT GCCCAGACCC TTCAGCAGAG TCGGGGCTTT GGCAGCTTCA GATTCCCTTC 2580
 AGGAACCCAG GGTGGAGCTG GCCCCAGTCA GGCAGTGA GCGGCACAG GTGGCAGTGT 2640
 ATACACAGAA GACAATGATG ATGACCTGTA TGGCTAAGTG GTGGTGGCCA GCGTGCACTG 2700
 15 AGCTGGCCTG CCTGGACCTT GTTCCCTGGG GGTGGGGCGG CTTGCCACAG AGAGGGACCA 2760
 GGGGTGCGCC CACAGCCTGC TCCATCTCTC AGTCTGAACA GTTCAGCTAC AGTCTGACTC 2820
 20 TGGACAGGGG GTTCTCTGTG CAAAAATACA AAACAAAAGC GATAAAATAA AAGCGATTTT 2880
 CATTTGGTAA AAAAAAAAAA AAAAAAAAT CCGGGGGGGG GCCCGAACCA TTT 2933

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(2) INFORMATION FOR SEQ ID NO: 166:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TCGGAGAGCC GCGGGGCGNG CGCCTCTCGG CCAGGAAGCG CCTCTTGGAC GCGTGTNACC 60
 GATGCCCAGA AGTGGCCTTG GGCTGGGGAT CACCATAGCT TTTCTAGCTA CGCTGATCAC 120
 40 GCAGTTTCTC GTGTATAATG GTGTCTATCA GTATACATCC CCAGATTTCC TCTATATTCG 180
 TTCTTGGCTC CCTTGATAT TTTTCTCAGG AGGCGTCACG GTGGGAACA TAGGACGACA 240
 45 GTTAGCTATG GGTGTTCCTG AAAAGCCCCA TAGTGATTGA GTCTTCAAAA CCACCGATTC 300
 TGAGAGCAAG GAAGATTTTG GAAGAAAATC TGAAGTGTGA TTATGACAAA GATTATCTTT 360
 TTTCTTAAGT AATCTATTTA GATCGGGCTG ACTGTACAAA TGAAGTCTGG AAAAACTCT 420
 50 TCACCTAGTC TAGAATAGGG AGGTGGAGAA TGATGACTTA CCCTGAAGTC TTCCCTTGAC 480
 TGCCCGCACT GCGCCTGTC TGTCCCTGG AGCATCTGC CCAGGCTACG TGGGTTGAGG 540
 55 CAGGTGGCAG CTTCCTAAGT ATTCGATTTT ATTCATGTGA TTAACAACAG TTGCCATATT 600
 TCAAGCCTT GAACCTAAGAC TCAATTACCA ACCCGCAGTT TTGTGTCACT GCCCAAAGGA 660
 60 GGTAGGTGA TGGTGCTTAA CAAACATGAA GTATGGTGA ATAGGAATAA TATTTATCCA 720

	AAAGATTTTT AAAAATAGGG CTGTGTTTAA AAAAAAAAC AAAACARGAA AAGCAGCAGT	780
	GATTATAGAG AGGTCACACT CTAAGTGGGG TCGCGGCGTG GCCACGCTTC ACGGTCACGC	840
5	TCGTCCGTCC TGCAGTGGCG TGTTTACATG GTCACACGTG TGTGTATCAC CAGTGGGTCA	900
	ACTGCTTGTC ATTCTCCCG TGGCAGTTTG TGTAGACAAT CTTACTGAGC AAAAGGCAAT	960
10	GAAAAGTCTT GGTCCCACA CTGCATATA TTGGAATTTT CACCTCAGTT TATGAAGTTT	1020
	ATTTGGAAT CCATAGTCAT CTAAGAATGA ATACCTGTCT GCCATGTATT TCAATCTTAG	1080
	TGAGCCAAAA TTGTTTGT TTACTACAG AATAGAGATG ACTGTTTTTT GCCACAGCCC	1140
15	TATGGRATTT GCAATCTGTG ATTGCCTTGT AAAAAGGAGA GTGCATATGG CACTGCATTA	1200
	AACGTGTGGT GTTCTAGTC AATGATATG GTGAGCACA TGTATTCAAT TAATGCATA	1260
20	GACCATACCA GACCTAATTT GCAAGTATG GGTCTTAAAC TTCAAGTGCA ATGTATATGA	1320
	AAACCAATCT GAGCCTGTG TCTCTTAAAT ATTTATTTTT TTTAACGTGT GAGATGTTCTG	1380
	AGAGAAGGTT CTCCATTCAT TTCAGTGTG CCTGGAGGAA ACTCGGCAAT GATTTCTTTC	1440
25	AGTTGTGAAG TTCCTTTCGT GTTACACCCT CCACTGAACC CTCAACCTTC GAAATACTCC	1500
	AGTTTGTGG GTTTGGTCAT TTTACTTAT AAATTTACCT TTTGTATTT TGCAATTTAC	1560
30	ATGTGTTGG TTGTTTAA ATTCTGTGAA AGTGGCTTGA TTAAAAGACT CCTTTTAAAT	1620
	GGAAGCCACC AGTCAGCAGA ATGGAAGCTT AGAGGAACTT GCCTGTGAGC GCTGGTCTTT	1680
	GTGTTTGGTT TTGTGATGTA ACGATCTTTG CTGGGGTTTT TTGCTTTGTT TTGAGGGAAA	1740
35	TGTCTTGGAG TAAATTTTAA GTTCTTGGAG TTAATTTGTT TTACAGGAAT TTTGTTTTTT	1800
	AAAAAATAG GATCATCTG AACTTTGGAA TGACCCCTT ATATATTTTC TGAAAAATGAA	1860
40	AACAGTTACA TGAAAAAAT TTCCAATGAA GATGTCAGCA TTTTATGAAA AACCAGAAGT	1920
	TATTAGATGA AAGCAGCGAG TGAATCTTTA AAACAGACTT GATCAGCAC ACACAATAAG	1980
	TCTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG AAATAATGTA GCCAAAAGAA	2040
45	TGTAAATTTG AGGATTTTTT TGCCAATAGT TTATAGAAAA TATATGAACC AAAGTGATTT	2100
	GAGTTTGTA AAATGTAAAA TAGTATGAAC AAAATTTGCA CTCTACCAGA TTTGAACATC	2160
50	TAGTGAGGTT CACATTCATA CTAAGTTTTC AACATTGTGT TCTTTTGTCA TTCATTTTTT	2220
	ACTTTTATTA AAGGTCAAA ACC	2243

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(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

5	GGTGGGNAGC TTTNAATTTT CCCTTACWGG GCGCTNTAA GGGGAAACCT TCCCGGAATT	60
	TTCTGGGTCGA CCCACGCGTC CGGCCAGCCT AGGAGAAGAA GTTCGTAGTC CCAGAGGTGA	120
10	GGCAGGAGGC GGCAGTTTCT GCGGGGTGAG GCGGGAGCTG AAGTGACAGC GGAGCGGAA	180
	GCAACGGTCG GTGGGGCGGA GAAGGGGGCT GCGCCAGGA GGAGGAGGAA ACCCTTCCGA	240
	GAAAACAGCA ACAAGCTGAG CTGCTGTGAC AGAGGGGAAC AAGATGGCGG CGCCGAAGGG	300
15	GAGCCTCTGG GTGAGGACCC AACTGGGGCT CCCGCCGCTG CTGCTGCTGA CCATGGCCTT	360
	GGCCGGAGGT TCGGGGACCG CTTGGGCTGA AGCATTTGAC TCGGTCTTGG GTGATACGGC	420
20	GTCTTGCCAC CGGGCCTGTC AGTTGACCTA CCCCTTGAC ACCTACCCTA AGGAAGAAGA	480
	GTGTACGCA TGTACAGAG GTTGCAGGCT GTTTTCAATT TGTAGTTTG TGGATGATGG	540
	AATGACTTA AATCGAACTA AATTGGAATG TGAATCTGCA TGTACAGAAG CATATTCCCA	600
25	ATCTGATGAG CAATATGCTT GCCATCTTGG KTGCCAGAAT CAGCTGCCAT TCGCTGAACT	660
	GAGACAAGAA CAACTTATGT CCTGATGCC AAAATGCAC CTACTCTTTC CTCTAACTCT	720
30	GGTGAGGTCA TTCTGGAGTG ACATGATGGA CTCCGCACAG AGCTTCATAA CCTCTTCATG	780
	GACTTTTAT CTTCAAGCCG ATGACGGAAA AATAGTTATA TTCCRGCTTA AGCCAGRAA	840
	TCCCAGGTAC GCACCACATT TGGAGCCAGG AGCCCTACCA AATTTGRGRG RAWMTCTCT	900
35	AAGCAAAATG TCCNCAKMT CGSMAATGAG AAATTCACAA GCGCACAGGA ATTTTCTTGA	960
	AGATGGAGAA AGTGATGGCT TTTAAGATG CCTCTCTCTT AACTCTGGGT GGATTTTAAC	1020
40	TACAACTCTT GTCCTCTCGG TGATGGTATT GCTTTGGATT TGTGTGCAA CTGTGTGCTA	1080
	CACGCTGTTG GACGAGTAT AGTTTCCCTC TGAGAAGCTG AGTATCTATG GTGACTTGA	1140
	GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTGTGG TTGTTAGATC	1200
45	TAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC TTGCTCATTC	1260
	TGAAATTTAA GCATTTTCT TTTAAAAGAC AAGTGAATA GACATCTAAA ATTCCACTCC	1320
50	TCATAGAGCT TTTAAATGG TTTCATGGA TATAGGCCCT AAGAAATCAC TATAAAATGC	1380
	AAATAAAGTT ACTCAAATCT GTGAAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG	1440
	GCCCGTTACC AAKTCGCCCT ATWGTGADTB GTATMTTAT TTTACTAATA TCTGTAGCTA	1500
55	TTTTGTTTTT KGCTTKGGTT ATKGTTTTTY TCCCTTYTCT WAGCTATRAG CTGATCATKG	1560
	CYSCTTCTCA CCTCTGCCA TGATACTGTC AGTTACCTTA GTTACAAGC TGAATATTTA	1620
60	GTAGAAATGA TGCTTCTGCT CAGGAATGGC CCACAAATCT GTAATTTGAA ATTTAGCAGG	1680

AAATGACCTT TAATGACACT ACATTTTCAG GAACTGAAAT CATTAAAATT TTATTGAAAT 1740
AATTATGTGC TGAAAAAAA AAAAAAAAAA AMWMRARASK RRWWACTCGA GGGGGGGCCC 1800
5 GGTACCCNAT TCGCCG 1816

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(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AGAAACCGTT GATGGGACTG AGAAACCAGA GTTAAACCT CTMTGGAGCT TCTGAGGACT 60
CAGCTGGAAC CAACGGGCAC AGTTGGCAAC ACCATCAACT TCTCCCAAGC AGAGAAACCC 120
25 GAACCCACCA ACCAGGGGCA GGATAGCCTG AAGAAACATC TACACGCAGA AATCAAAGTT 180
ATTGGGACTA TCCAGATCTT GTGTGGCATG ATGGTATTGA GCTTGGGGAT CATTTTGGCA 240
TCTGCTTCCT TCTCTCCAAA TTTTACCCAA GTGACTTCTA CACTGTTGAA CTCTGCTTAC 300
30 CCATTCATAG GACCCCTTTT TTTTATCATC TCTGGCTCTC TATCAATCGC CACAGAGAAA 360
AGGTTRACCA AGCTTTTGGT GCATAGCAGC CTGGTTGGAA GCATTCTGAG TGCTCTGTCT 420
35 GCCCTGGTGG GTTTCATTAT CCTGTCTGTC AAACAGGCCA CCTTAAATCC TGCCTCACTG 480
CAGTGTGAGT TGGACAAAAA TAATATACCA ACAAGAAGTT ATGTTTCTTA CTMTTATCAT 540
GATTCACTTT ATACCACGGA CTGCTATACA GCCAAAGCCA GTCTGGCTGG AWCTCTCTCT 600
40 CTGATGCTGA TTTGCACTCT GCTGGAATTC TGCCTAGCTG TGCTCACTGC TGTGCTGCGG 660
TGGAACAGG CTTACTCTGA CTTCCTGGG AGTGTACTTT TCCTGCCTCA CAGTTACATT 720
45 GGTAATTCTG GCATGTCCTC AAAAATGACT CATGACTGTG GATATGAAGA ACTATTGACT 780
TCTTAAGAAA AAAGGGAGAA ATATTAATCA GAAAGTTGAT TCTTATGATA ATATGAAAAA 840
GTTAACCATT ATAGAAAAGC AAAGCTTGAG TTTCCCTAAAT GTAAGCTTTT AAAGTAATGA 900
50 ACATTAAAAA AAACCATTTAT TTCACTGTCA TTAAAGATA ATGTG 945

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(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 GGCAGAGCCA CAGGAAGGAT GAGGAAGACC AGGCTCTGGG GGCTGCTGTG GATGCTCTTT 60
 GTCTCAGAAC TCCGAGCTGC AACTAAATTA ACTGAGGAAA AGTATGAACT GAAAGAGGGG 120
 10 CAGACCCCTGG ATGTGAAATG TGACTACACG CTAGAGAAGT TTGCCAGCAG CCAGAAAGCT 180
 TGGCAGATAA TAAGGGACGG AGAGATGCCC AAGACCCTGG CATGCACAGA GAGGCCTTCA 240
 AAGAATTCCC ATCCAGTCCA AGTGGGGAGG ATCATACTAG AAGACTACCA TGATCATGGT 300
 15 TTAGTGGCGG TCCGAATGGT CAACCTTCAA GTGGAAGATT CTGGACTGTA TCAGTGTGTG 360
 ATCTACCAGC CTCCCAAGGA GCCTCACATG CTGTTTCGATC GCATCCGCTT GGTGGTGACC 420
 20 AAGGGTTTTT CAGGGACCCC TGGCTCCAAT GAGAATTCTA CCCAGAATGT GTATAAGATT 480
 CCTCTACCA CCACTAAGGC CTTGTGCCA CTCTATACCA GCCCCAGAAC TGTGACCCAA 540
 GCTCCACCCA AGTCAACTGC CGATGTCTCC ACTCCTGACT CTGAAATCAA CCTTACAAAT 600
 25 GTGACAGATA TCATCAGGGT TCCGGTGTTC AACATTGTCA TTCTCCTGGC TGGTGGATTC 660
 CTGAGTAAGA GCCTGGTCTT CTCTGTCTG TTTGCTGTCA CGCTGAGGTC ATTTGTACCC 720
 30 TAGGCCCACG AAGCCACGAG AATGTCCTCT GACTTCCAGC CACATCCATC TGGCAGTTGT 780
 GCCAAGGGAG GAGGGAGGAG GTAAAAGGCA GGGAGTTAAT AACATGAATT AAATCTGTAA 840
 TCACCRGCTA AAAAAAAAAA AAAAAAACN CGANCCTNGG TTTTCAGCTC CATCAGCTCC 900
 35 TT 902

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1883 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

50 AGAAAACAAC TGAAAACCA CATTTTCTA CATACAGCTG GGGAGGTAGC TGAGAACTTG 60
 GCACTGCGCA CACATACTAG GTTGAAAGAG AGTTGAGGAA ACCAGAAGGC CAAGTGATC 120
 55 TGCTGGCAAA CCCTGAACCT GTCTCCTGCG CTTGCTCTAC AGTTCTGAAG TTGAAAATCC 180
 TTTTCATGCC TAGCATCTGC TTGAGTTATA AACCCCAAGG CAGCCATGTC ATAGACTAGT 240
 GTTTACTCTT GTTTTACTT TGTTTAATG CTTCTAAGA CCCAAGTGCC TCCTGCTGTT 300
 60

	TCCTCCTTTG TGGTAGCCTC TGGCCATCTG GGACCTCAAT CCCAGCTTT CCCACTTTCA	360
	GCAGTCCTTT GCTCTCTTTG CTTCTACCTC AAATAGCCCC AGGAGTGGGC TTTAGTCTCC	420
5	AATATGGAGC ATYTCAAGCT TCTCCTGGGG GATGGGGATT GGGATGGGCA GAATCTGTTT	480
	TGGWCTCTCCG GGTATTTCCT AGTGGGTGTA AAAGCAGAGC TGGGCCTTTC CCTCTCTTAT	540
10	CCCTGAGGGT GGGTAAGAAG GACTGTATCT ACACCTGTTT TTCCCTACCT TCTCTTTTGT	600
	TAGGGAGGCC TCATTCTAAG TTCCTCAAGA GAGTCCTTGG CTTAAAGCTG TAGCAAGGGT	660
	GTGCTAGGTG GGGGATTGG AGCAAAACCG TCGAGTAGGC ATGATACTGG TATGGAGTGG	720
15	GCCTGCAAAA TCAGACAGAA ATGGCTTGAG AAGCCGCAGG GGAGCATGCC TGTCTCTCAG	780
	TGATAGAGTA TGGGAGGGAC CTCCTAGCT TGGAAAATGA GAATTGAAGG GGTATGAAC	840
20	AAATAGGATG CCTAGTTGAG GATGTTCCCA AAGTTTGTG CAATCTTATC ATTAGTAGAT	900
	TTTATAAGCC ACAGAGACAA ACCAGAAACG GAATAATGTT ACTTTGGATG CTTTATTTTT	960
	TTGTCTAGG TGTGGCTTTG TACATGCAGA AGAATGCTAT ATGCTGCACA TTTTGCCTTT	1020
25	AAAGTCTTAC GACTTTCCCC ATTTTAGTCT AATGGGAAGA TACAGATGTG CAAGTCTGCT	1080
	TTTTTGT TTTTATTAT TTTTTTTTT TTGCTCTGTG TTATGGACAT TTTCAGACAT	1140
30	GCACAGAAGT GGAGAGGATG GTCCTTGAC CCCATGTGTC CATCACCTAG CTGCATCACT	1200
	TATCAGCTAT GGTCAACCTG GTTTCATCTG TATCTCTCTC TTTTCACCTG TATTGTTTTAT	1260
	TGAAAAATCCA AGACACTATG CCAATGCAAC CGTGACTACT TTGGGAGATT GGTAGTCTCT	1320
35	TTTGATGGTG ATAGTGATGG GGTGCACTAT CATAATCACA TCAGGTCTGC TTTTTCCTTT	1380
	TAATGTTAAC TAATGAAGTT CCAGAGATGG GCCTTAGAAA TGTGTTTTAA GAATTAACAA	1440
40	GGAGTCTCAA AAAGAAATGA GAGGATGCT TCCTTTCCCC TTGCATCTAC AAAACAAGAG	1500
	AGAGACTGTT CTGTTGTAAA ACTCTTTCAA AAATCTGAT ATGGTAAGGT ACTTGAGACC	1560
	CTTCACCAGA ATGTCAATCT TTTTCTCTGT GTAACATGGA AACTTGTGTG ACCATTAGCA	1620
45	TTGTATCAG CTTGTACTGG TCTCATAACT CTGGTTTGG AAGAATAATT TGGAAATTGT	1680
	TGCTGTGTTT TGTGAAAATA ACCTCCCCAA AATAATTAGT AACTGGTTGT TCTACTTGGT	1740
50	AATTTGACAC CTTGTTAATA ACGCAATTAT TTCTGTGTTT TTAACAGTA TAAATAGTTG	1800
	TAAGTTTGCA TGCATGATGG AAAAAATAAA ACCTGTATCT CTGTTAAAAA AAAAAAAAAA	1860
	AAAAAAAAAA AAAAAAAAAA AAA	1883
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(2) INFORMATION FOR SEQ ID NO: 171:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	TACTTTTAGA TTTACTGCCT TCAAAAAGTG CCTATTCTGA GCAACATAAA CGTTATTCCCT	60
10	TACATATGTA TGTACACACG GTACCCAGAG TCGTACTGTG GCAGCCTTCA AAAACATACC	120
	ATCAGAAAGA GTAGGTGCTG AGATAAGGNA ACTTTGCCAA ATGNAAGAAA GTCACCTACT	180
15	TCCAATATCC CCTCTTCAAG CGGCTACCGT GRAASGGGCT GCAAACACAT TCCCTGAGCA	240
	TCCCTTGCTG ATACAGCTTC TTTATATTTA TATCCTACTG GATGGTAGCA TATTGCTAAG	300
	GTTTCTGTGA CTCTGCTTCA AGGGAATGTA AGYTTTATGG CATTGAAACA TTTAGGAAAA	360
20	AAAAAGATGT TTAAGAGAAT TAATAGAGCC GTAGTCTGTA TTAGGATGTG TGTCAATATG	420
	GTGTTCTATA AACTAAGCAT CGGTGGGTTT AGAGTGTAA AGTGTACGCA CATTCCTTCT	480
25	CCTTTTGTCT CTCAGGCTAA CATGAGAGAA AATAGAAAAG TCTTGCTGTG GGGGATTGGA	540
	AGCTCAGGGG GCCAAATGTC CTTGCCAGAT CCTTAGAGCA TTAATTGAC TCCTAAAAAT	600
	AGTAGTGTAT GTTATTGTAT GGCTTTTGTT TCCATAGTTC CATCACTGAC AAAACTGTCA	660
30	ATACTGTTGA TGGAGCAGCA GCATAGCCTA GAGTGATGCA TTCTTACCCA GAGGTGGCAA	720
	TAGGAGAGGG TCCATGTAAA TAGGACGAGG TAGACAGTGC ATGATTGTAG GAGAAGGGTT	780
35	GAAGGGAGGA CATGATTCCA AAAAAGATCG TTCTCAATGT GTCGTCTGAC TCAACCAGCT	840
	GGCAGATTAC ACTTGCCAAG TCGTTCCTTT TCCTTCTAAG TCAGTTGGCT CCATATTAC	900
	TTGAATATGC CTCTGTTTGG GCAAAGCAAG ATACCTCCAC TTAACCTTTA TCCAAGGAAG	960
40	CTCTTGGTGT CCTCTGGTC ATAAAGTTGT CTCCTACCTA ACCCAGTTTT ACCAAATGGA	1020
	AGTAAAAGGG GACAAACTAT GGAAGATGGA CTCCATGCCA TTGCAGTCAG CCACCATTTCT	1080
45	CTTTTCCATA TAAGGAGCCC CATTACATAA GCTACGGGTG AGGTGGAAC AGCTATGTTT	1140
	CATAATTTC AAGAGTGTGAC CACCCTGCTC TAGTCATCAT CATGGATGA ATCCAGTTGA	1200
	CTCTTTGGCA AAAGGGTGAT ACTTTTCACT AAAAATGCCT ACTCTTCCTG TTGATGTTCC	1260
50	TTTTCTGTTT TTACCTTGTC CAATTCCAC ACTAGTCATT TTTTATTATT TTTAGAGGAT	1320
	CAGATTTTAG CGCTGGAAAA TGAGTTCAAA AATTTCAGTG TAATGTCATA AGGATGTTGG	1380
55	GATACAGAGA TTTTTTTTTT CCTTGGAAC AAATGGACTG GGAAGAAACA CAGCATGGCT	1440
	TTGCTCTGAG TTTCAATCTG ATGATTATGA CCATGGAAGA TAGTCTTATG TAAAGGTTAA	1500
	ATGGTGTTTA CAAGTGATA GATAAGCGG AGATGGTGAG AAGCCGGGTT TTCTCTATGC	1560
60	TAAATGTGTC TACTAAGAGC AGCACTTCCT ACTAGCTAAG CACAATCATA GCCCCACCGT	1620

5 GATGAGCTGC TAGTCTGAAT AACATTCCT GACTTAGGGA AAGGCACACA AAAACATATA 1680
AAGAATATGT CTATTTTCAT ATGTGTGATA CTGACAGAGC CATGGTATTC CTAAAATATA 1740
GGTTTCTCIT TTTTCTTGTA TTCTTAGCAA ATTGCATTTA TTCACTACAT TACAAACCAT 1800
CACTGATGTA TCCAAAATAG CACACATAGT TCAGTATGAA AATAAGAGAA TAAAATCTGT 1860
10 TATAAGCAAG TGATTAGGT ATTTCTTTT GTGTTTATGC ATTATCTGAC TATATTAAAA 1920
CCTGTTTTTC TATTTACCTT CTATCAGTTT TCTCTACCAA TTATGTTTTT TCAATGCTCT 1980
ATAAGAATGA ATATGGAAAT TATATTCTT TTTTCTGTAA AAGAGTTGCA ACTACTTTAT 2040
15 TATATTTAGA AATCCAATAA ACTTCTTATT ACATTTAAAA AAAAAAAAAA AAAACTCGAA 2100

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(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 1930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

30 CCTTTGANTG TGGTCCCGGG TGCNGATTGG CAGCGCCTCC GCCGCGGCTC GTGGTTGTCC 60
CGCCATGGCA CTGTCCGGGG GGCTGCCCGG GGAGCTGGCT GAGGCGGTGG CCGGGGGCCG 120
35 GTGCTGGTG GTGGGGGCGG GCGGCATCGG CTGCGAGCTC CTCAAGAATC TCGTGTCTAC 180
CGGTTTCTCC CACATCGACC TGATTGATCT GGATACTATT GATGTAAGCA ACCTCAACAG 240
ACAGTTTTTG TTTCAAAAGA AACATGTTGG AAGATCAAAG GCACAGGTTG CCAAGGAAAG 300
40 TGTAATGTCAG TTTTACCCGA AAGCTAATAT CGTTGCCTAC CATGACAGCA TCATGAACCC 360
TGACTATAAT GTGGAATTTT TCCGACAGTT TATACTGGTT ATGAATGCTT TAGATAACAG 420
45 AGCTGCCCGA AACCATGTTA ATAGAATGTG CCTGGCAGCT GATGTTCTTC TTATTGAAAG 480
TGGAACAGCT GGGTATCTTG GACAAGTAAC TACTATCAAA AAGGGTGTGA CCGAGTGTTA 540
TGAGTGTCAT CCTAAGCCGA CCCAGAGAAC CTTTCCTGGC TGTACAATTC GTAACACACC 600
50 TTCAGAACCT ATACATTGCA TCGTTTGGGC AAAGTACTTG TTCAACCACT TGTTTGGGGA 660
AGAAGATGCT GATCAAGAAG TATCTCCTGA CAGAGCTGAC CCTGAAGCTG CCTGGGAACC 720
55 AACGGAAGCC GAAGCCAGAG CTAGAGCATC TAATGAAGAT GGTGACATTA AACGTATTTT 780
TACTAAGGAA TGGGCTAAAT CAACTGGATA TGATCCAGTT AAACTTTTTA CCAAGCTTTT 840
TAAAGATGAC ATCAGGTATC TGTGACAAT GGACAACTA TGGCGGAAAA GGAAACCTCC 900
60

	AGTTCGGTTG GACTGGGCTG AAGTACAAAG TCAAGGAGAA GAAACGAATG CATCAGATCA	960
	ACAGAATGAA CCCAGTTAG GCCTGAAAGA CCAGCAGGTT CTAGATGTAA AGAGCTATGC	1020
5	ACGTCCTTTT TCAAAGAGCA TCGAGACTTT GAGAGTTCAT TTAGCAGAAA AGGGGGATGG	1080
	AGCTGAGCTC ATATGGGATA AGGATGACCC ATCTGCAATG GATTTTGTC CCTCTGCTGC	1140
10	AAACCTCAGG ATGCATATTT TCAGTATGAA TATGAAGAGT AGATTTGATA TCAAATCAAT	1200
	GGCAGGGAAC ATTATTCCTG CTATTGCTAC TACTAATGCA GTAATTGCTG GGTGTAGATG	1260
	ATTGGAAGGA TTGAAGATTT TATCAGGAAA AATAGACCAG TGCAGAACAA TTTTTTIGAA	1320
15	TAAACAACCA AACCCAAGAA AGAAGCTTCT TGTGCCTTGT GCACTGGATC CTCCCAACCC	1380
	CAATTGTTAT GTATGTGCCA GCAAGCCAGA GGTGACTGTG CGGCTGAATG TCCATAAAGT	1440
20	GACTGTCTC ACCTTACAAG ACAAGATAGT GAAAGAAAAA TTTGCTATGG TAGCACCAGA	1500
	TGTCCAAATT GAAGATGGGA AACGAACAAT CCTAATATCT TCCGAAGAGG GAGAGACGGA	1560
	AGCTAATAAT CACAAGAAGT TGTGAGAATT TGAATTAGA AATGGCAGCC GGCTTCAAGC	1620
25	AGATGACTTC CTCCAGGACT ATACTTTATT GATCAACATC CTTCATAGTG AAGACCTAGG	1680
	AAAGGACGTT GAATTTGAAG TGTGTGGTGA TGCCCCGAA AAAGTGGGGS CCAAACAAGC	1740
30	TGAAGATGCT GCCAAAAGCA TAACCAATGG GCAGTGATGA TGGGAGCTTC AGCCCTCCAC	1800
	CTYCACAGCT TCAAGGAGGC AAGATGGACG TYTCYCATAG TTGATYCGGR TGAAGAAGRT	1860
	TCTCCAATAA TTGCCCGACG TTCATTGAAG GAAGGAGGAG GAGGCCCGCC AAGAGGGGAA	1920
35	TTTAGGNTTG	1930

40 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

50	GGCCCTGGCC TCTGGGCTGA GGCTTGCTAG GGACTCGGG TGGCTCTAAG GGGCAGGGAT	60
	AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG ACCAGCCCCT TCTCGTGCRG GTTCCACCCC	120
55	GATGCAGGTG GTCACGTGCT TGACGCGGGA CAGCTACCTG ACGCACTGCT TCCTCCAGCA	180
	CCTCATGGTC GTGCTGTCTT CTCTGGAACG CACGCCCTCG CCGGAGCCTG TTGACAAGGA	240
	CTTCTACTCC GAGTTTGGGA ACAAGACCAC AGGGAAGATG GAGAACTACG AGCTGATCCA	300
60	CTCTAGTCGC GTCAAGTTTA CCTACCCAG TGAGGAGGAG ATTGGGGACC TGACGTTTAC	360

	TGTGGCCCAA AAGATGGCTG AGCCAGAGAA GGCCCCAGCC CTCAGCATCC TGCTGTACGT	420
5	GCAGGCCTTC CAGGTGGGCA TGCCACCCCC TGGGTGCTGC AGGGGCCCCC TGCGCCCCAA	480
	GACACTCCTG CTCACCAGCT CCGAGATCTT CCTCCTGGAT GAGGACTGTG TCCACTACCC	540
	ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA GAGAGACAGG TACCGGCTGG ACGATGGCCG	600
10	CCGCGTCCGG GACCTGGACC GAGTGCTCAT GGGCTACCAG ACCTACCCGC AGCCCTCACC	660
	CTCGTCTTCG ATGACGTGCA AGGTCATGAC CTCATGGGCA GTGTCACCCT GGACCACTTT	720
	GGGGAAGTGC CAGGTGGCCC GGCTAGAGCC AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG	780
15	TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG CTCATCTCGC TGTGTGGCTCG CCAGTGGGAG	840
	GGCCTGTGTG GCCGTGAGCT GCCTGTCGAG CTCACCGGCT AGCCCAGGCC ACAGCCAGCC	900
20	TGTCGTGTCC AGCCTGACGC CTACTGGGGC AGGGCAGCAG GCTTTTGTGT TCTCTAAAAA	960
	TGTTTTATCC TCCCTTTGGT ACCTTAATTT GACTGTCTC GCAGAGAATG TGAACATGTG	1020
	TGTGTGTTGT GTTAATTCTT TCTCATGTTG GGAGTGAGAA TGCCGGGCC CTCAGGGCTG	1080
25	TCGGTGTGCT GTCAGCCTCC CACAGGTGGT ACAGCCGTGC ACACCAAGTGT CGTGTCTGCT	1140
	GTGTGTTGGAC CGTGTGTAAC ACGTGACACT GTGGGTCTGA CTTTCTCTTC TACACGTCTT	1200
30	TTCTTGAAGT GTCAGTCCA GTCCTTTGTT GCTGTGCTG TTGCTGTGTC TGTGCTGTT	1260
	GGCATCTTGC TGCTAATCCT GAGGCTGGTA GCAGAATGCA CATTTGGAAGC TCCCACCCCA	1320
	TATTGTTCTT CAAAGTGAG GTCTCCCCTG ATCCAGACAA GTGGGAGAGC CCGTGGGGGC	1380
35	AGGGGACCTG GAGCTGCCAG CACCAAGCGT GATTCTGCT GCCTGTATTC TCTATTCCAA	1440
	TAAAGCAGAG TTTGACCCG TCAAAAAAAA AAAAAAAAAA AAAAAAAAAA ATTNCTGCGG	1500
40	CCTCAAGGG	1509

45 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 3173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

55	TCGACCCAS GCGTCCGTGC TTTCCACAG AAGGTTAGAC CCTGAAAGAG ATGGCTCAGC	60
	ACCACCTATG GATCTTGCTC CTTGCTGTC AAACCTGGCC GGAAGCAGCT GGAAAGACT	120
60	CAGAAATCTT CACAGTGAAT GGGATTCTGG GAGAGTCAGT CACTTTCCTT GTAAATATCC	180

	AAGAACCACG GCAAGTTAAA ATCATTGCTT GGACTTCTAA AACATCTGTT GCTTATGTAA	240
	CACCAGGAGA CTCAGAAACA GCACCCGTAG TTAGTGTGAC CCACAGAAAT TATTATGAAC	300
5	GGATACATGC CTTAGGTCCG AACTACAATC TGGTCATTAG CGATCTGAGG ATGGAAGACG	360
	CAGGAGACTA CAAAGCAGAC ATAAATACAC AGGCTGATCC CTACACCACC ACCAAGCGCT	420
10	ACAACCTGCA AATCTATCGT CGGCTTGGGA AACCAAAAAT TACACAGAGT TTAATGGCAT	480
	CTGTGAACAG CACCTGTAAT GTCACACTGA CATGCTCTGT AGAGAAAGAA GAAAAGAATG	540
	TGACATACAA TTGGAGTCCC CTGGGAGAAG AGGGTAATGT CCTTCAAATC TTCCAGACTC	600
15	CTGAGGACCA AGAGCTGACT TACACGTGTA CAGCCCAGAA CCTGTTCAGC AACAAATTCTG	660
	ACTCCATCTC TGCCCCGGCAG CTCTGTGCAG ACATCGCAAT GGGCTTCCGT ACTCACCACA	720
20	CCGGGTGCT GAGCGTGCTG GCTATGTTCT TTCTGCTTGT TCTCATTTCTG TCTTCAGTGT	780
	TTTTGTTCGG TTGTGTCAAG AGAAGACAAG ATGCTGCCTC AAAGAAAACC ATATACACAT	840
	ATATCATGGC TTCAAGGAAC ACCCAGCCAG CAGAGTCCAG AATCTATGAT GAAATCCTGC	900
25	AGTCCAAGGT GCTTCCCTCC AAGGAAGAGC CAGTGAACAC AGTTTATTCC GAAGTGCAGT	960
	TTGCTGATAA GATGGGGAAA GCCAGCACAC AGGACAGTAA ACCTCCTGGG ACTTCAAGCT	1020
30	ATGAAATGTT GATCTAGGCT GCTGGGCTGA ATTCTCCCTC TGGAACTGA GTTACAACCA	1080
	CCAATACTGG CAGGTTCCCT GGATCCAGAT CTTCTCTGCC CAACTCTTAC TGGGAGATTG	1140
	CAAAGTCCA CATCTCAGCC TGTAAAGCAA GCAGGAAACC TTCTGCTGGG CATAGCTTGT	1200
35	GCCTAAATGG ACAAATGGAT GCATACCCTT CCTGAAATGA CTCCCTTCTG AATGAATGAC	1260
	AAAGCAGGTT ACCTAGTATA GTTTTCCCAA ACTTCTTCCC ATCATAGCAC ATGTAGAAAA	1320
40	TAATATTTTT ATGGCACACT GGGATAAACA AGCAAGATTG CTCACTTCTG GAAGCTGCAT	1380
	ATGACTAGAG GCCTCTTGTG ACTGGAGGTA ACAACCTGC CCAGTAACTG TGGGAGAAGG	1440
	GGATCAATAT TTTGCACACC TGTAAATAGC CATGGCACAC CAGCCAAGAT GCTCTGCTCA	1500
45	CAGTCAGTAT GTGTGAAGAT CCCTGGTGCG TGGCCTTCAC CACGCATCTT GAGCAAATTA	1560
	GGAAAAATGA CCCTTCGCTT GAGGCAGATG CAGCCCTTCC CCCGAGTGCA TGGCTTGGAG	1620
50	AGCAGAATGT GGGCTGCATA TAAGCACACT CATCCCTTTG TCTGGGAATC TTTGTGCAGG	1680
	GCATAACAGG CTTAGTAAGT CCAAACACAG ATGACAGTGC TGTGTGGGTC TCTGTCAGAG	1740
	TTGTGGCTCT CAGCCATGTA GACACACTCT CCAAATGGAG TGTGGAAAA GTTCTTTCT	1800
55	GCAGGGTCTA GAGACTGCTG GGACACTTTT CTGGAGTGC TACTTCAGAA GCCTTATAGG	1860
	ATTTTCTTTC TGGCCAAGAT TTCCTTCTGT ATCACTCCAA GCAGCCTCAG CAGAAGAAGC	1920
60	AGCCATGCCC AGTATPCCCA CTCTCCAAA GGAAGTGACC AGCTTATATT TCTCACACTT	1980

	CTGGGGA	ACT	GGGTATAATC	CAACCATCAA	AATAGAAGAC	CTTGCAAGAA	GCAGAGTCAT	2040
	TCTCCAGAAG	GA	ACTTGGGA	GATGATGGTG	CAGATGATGA	AACTGGGTTC	ATCCCAGTTC	2100
5	CAAAGACTCA	GAGAACTAGA	GT	TTAAGCTG	AGGCAGAGTG	CCGCCACCCCT	GGCATGCCCC	2160
	ACAAACAGAT	CACCAGCCAG	CTTACACAGG	CATTA	ACTCT	CCTCAATGAG	GAAGAATCAT	2220
	TCACAACTGA	GCAAGACATT	CATATGATCA	TTTAAGGAAG	TGTTTCCCTT	ATGTGTTAGC		2280
10	AAGTATAATC	GGCTAACTCC	TAAATCCCAA	TGAATAGTCC	TAGGCTGGAC	AGCAATGGGC		2340
	TGCAATTAGG	CAGATAAAGA	CATCAGTCCC	AGTAAATGAA	TCCATAGACT	CATCTAGCAC		2400
15	CAACTACCAT	TAGCACTATG	TTAGGAGCTG	CAAGGCCCCA	AAGTAGAAGA	TGTGCATAAT		2460
	GTCTGCTCTT	GTGTAGCTCA	GGAGACAATT	CCAGCACAGA	CACTACAGTT	AACGCTGAAC		2520
	TGCAGCTGCA	AGTAATAGCA	TGAACAGTCA	GAAAAATACC	TTATGAGGGG	GCAGGGCTGA		2580
20	AGCTGGCCCT	TGAAGGATGG	ATGAAATTTG	GATAGAGAAT	GAGGAAGACA	GAGGGCCTCC		2640
	AAGTGAGAGA	AGCATGAAAA	ATGAGCAGGG	GCCTGGATCA	GTGGGGTGTA	TTCAGAGCAC		2700
25	CTCTCCAGAT	GCACCATGCA	TGCTCACAGT	CCCTTGCCTA	TGTGTGGCAG	AGTGTCCCAG		2760
	CCAGATGTGT	GGCCCCACCC	CATGTCCATT	TACATGTCTT	TCAATGCCCA	CCTCAAAAGG		2820
	TACCTCTTCT	GTAAAGCTTT	CCCTGGTATC	AGGAATCAAA	ATTAATCAGG	GATCTTTTCA		2880
30	CACTGCTGTT	TTTTCCTCTT	TGGTCCTTCT	ATCACTAAAA	CTCATCTCAT	TCAGCCTTAC		2940
	AGCATAACTA	ATTATTGTGT	TTCCTCACTA	CATTGTACAT	GTGGGAATTA	CAGATAAAGC		3000
35	GAAGCCKGCT	GGGGTGGTGG	CTCACGCCTG	TAATCCCAAC	ACTTTGGGAG	GCCAAGGCAG		3060
	GCGGATCACC	TGAGGTCAGG	ARTTCGAGAT	TARTCTGGCC	AACATGGTGA	AACCCCATMT		3120
40	NTACTAAAAA	TACGAAATTA	GCCAGGTGTG	GTGGCACACA	TCTGTAGTCC	CAG		3173

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 991 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

	AAATTCGGCA	CAGCTGAGAG	GAGACACAAG	GAGCAGCCCG	CAAGCACCAA	GTGAGAGGCA	60
55	TGAAGTTACA	GTGTGTTTCC	CTTTGGCTCC	TGGGTACAAT	ACTGATATTG	TGCTCAGTAG	120
	ACAACCACGG	TCTCAGGAGA	TGTCTGATTT	CCACAGACAT	GCACCATATA	GAAGAGAGTT	180
60	TCCAAGAAAT	CAAAAGAGCC	ATCCAAGCTA	AGGACACCTT	CCCAAATGTC	ACTATCCTGT	240

CCACATGGGA GACTCTGCAG ATCATTAAAGC CCTTAGATGT GTGCTGCGTG ACCAAGAACC 300
5 TCCTGGCGTT CTACGTGGAC AGGGTGTTC AAGGATCATCA GGAGCCAAAC CCCAAAATCT 360
TGAGAAAAAT CAGCAGCATT GCCAACTCTT TCCTCTACAT GCAGAAAAC CTGCGGCAAT 420
GTCAGGAACA GAGGCAGTGT CACTGCAGGC AGGAAGCCAC CAATGCCACC AGAGTCATCC 480
10 ATGACAACTA TGATCAGCTG GAGGTCCACG CTGCTGCCAT TAAATCCCTG GGAGAGCTCG 540
ACGTCTTTCT AGCCTGGATT AATAAGAAATC ATGAAGTAAT GTCCTCAGCT TGATGACAAG 600
GAACCTGTAT AGTGATCCAG GGATGAACAC CCCCTGTGCG GTTTACTGTG GGAGACAGCC 660
15 CACCTTGAAG GGGGAAGGAGA TGGGAAGGC CCCTTGACG TGAAAGTCCC ACTGGCTGGC 720
CTCAGGCGTG CITATTCGCG TTGAAAATAG CAAAAAGTC TACTGTGGTA TTTGTAATAA 780
20 ACTCTATCTG CTGAAAGGGC CTGCAGGCCA TCCTGGGAGT AAAGGGCTGC CTTCCCATCT 840
AATTATATGT GAAGTCATAT AGTCCATGTC TGTGATGTGA GCCAAGTGAT ATCCTGTAGT 900
ACACATTGTA CTGAGTGGTT TTTCTGAATA AATTCATAT TTTACCTAAA AAAAAAAAAA 960
25 AAAAACTCGA GGGGGGGCCC GTACCCAATT T 991

30

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ACAGCCCTCT TCGGAGCCTG AGCCCGGCTC TCCTCACTCA CCTCAACCCC CAGGCGGCCC 60
CTCCACAGGG CCCCTCTCCT GCCTGGACGG CTCTGCTGGT CTCCCGTCC CCTGGAGAAG 120
45 AACAAAGCCA TGGGTGGGCC CTTGCTGCTG CCCCTCTGTC YCCTGCTGCW GCCGCCAGCA 180
TTTCTGCAGC CTRGTGGCTC CACAGGATCT GGTCCAAGCT ACCTTTATGG GTCACTCAA 240
50 CCAAAACACC TCTACGCTC CATGGGTGGC TCTGTGAAA TCCCCTTCTC CTTCTATTAC 300
CCCTGGGAGT TAGCCAYAGY TCCCRACGTG AGAATATCCT GGAGACGGGG CCACTTCCAC 360
GGGCAGTCCT TCTACAGCAC AAGGCCGCTT TCCATTCACT AGGATTATGT GAACCGGCTC 420
55 TTTCTGAACT GGACAGAGGG TCAGGAGAGC GGCTTCCTCA GGATCTCAAA CCTGCGGAAG 480
GAGGACCACT CTGTGTATTT CTGCCGAGTC GAGCTGGACA CCCGAGATC AGGGAGGCAG 540
CAGTTGCAGT CCATCAAGGG GACCAAACTC ACCATCACCC AGGCTGTAC AACCACCACC 600

	ACCTGGAGGC CCAGCAGCAC AACCACCATA GCCGGCCTCA GGGTCACAGA AAGCAAAGGG	660
	CACTCAGAAT CATGGCACCT AAGTCTGGAC ACTGCCATCA GGGTTGCATT GGCTGTCGCT	720
5	GTGCTCAAAA CTGTCATTTT GGGACTGCTG TGCCTCCTCC TCTGTGGTGG AGGAGAAGGA	780
	AAGGTAGCAG GGCGCCAAGC AGTGACTTCT GACCAACAGA GTGTGGGGAG AAGGGATGTG	840
10	TATTAGCCCC GGAGGACGTG ATGTGAGACC CGCTTGIGAG TCCTCCACAC TCGTTCCCCA	900
	TTGGCAAGAT ACATGGAGAG CACCCTGAGG ACCTTTAAAA GGCAAAGCCG CAAGGCAGAA	960
	GGAGGCTGGG TCCCTGAATC ACCGACTGGA GGAGAGTTAC CTACAAGAGC CTTCATCCAG	1020
15	GAGCATCCAC ACTGCAATGA TATAGGAATG AGGTCTGAAC TCCACTGAAT TAAACCACTG	1080
	GCATTTGGGG GCTGTTYATT ATAGCAGTGC AAAGAGTTCC TTTATCTCC CCAAGGATGG	1140
20	AAAATACAAT TTATTTTGCT TACCATACAC CCCTTTTCTC CTCGTCCACA TTITCCAATC	1200
	TGTATGGTGG CTGTCTTCTA TGGCAGAAGG TTTTGGGGAA TAAATAGCGT GANATGNTNC	1260
	TGACTNAAAA AAAAAAAAAA AAAAATCTGA	1290
25		

(2) INFORMATION FOR SEQ ID NO: 177:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

	TGGGGCCCCCT TTTGGATGCT CTGGGTGTTT TTGCCAAGAG TTACAGGATG TCAAGTGTGG	60
40	GGAGCTCAGC ACCCTTGCTG TGGACCAAGT AAGGCTGTTC CAGACCAGGT GCTTCCAGAC	120
	ATTTCCAGGC TCCAGGAGAG AGGCTGGGAG CCCCCACAGA AAGCACAGGA AAATGCAAAA	180
45	AAAAAACAGT CTTTTTTTTT TTTTGTCTT TTATTATGAA AACAAAACAA ATGCCCCAGG	240
	AGAAGGGTCC ATGATTACCA GAAACATCAA AGAGTACTTT CTACCATTTT TATTCTGTG	300
	TGTTGAGGCC AGCATTGCAA TAAACAAGCT AACTACTTA CATTTGACTC ATTTTCAGTA	360
50	ACTGACATTT ACAGGAATAT ACTAGAAACG GCACTAAAAA GTTTAAGAAA AGTTACGGTA	420
	AACTTGCATG CACATCATAC AGAAAAGTAA CATTTTAAAT ATAAAAAGA AAAACTTCCT	480
55	GGAAGCATTG TGCCAGTATT AAGGAACAGT GCTACTCTGG ATGTGACAAA TTCTGTATGT	540
	GGGTGTTACT CTTTCCCAA AGACTGTCAG AGGCGTGAGT GCTGCAAAAG AACAACAACA	600
	AAAACAAACA CAAAAAAA TGTGTCTTAC AGTTTGTAAAG CAAGATGACA CTGCCCAACA	660
60	CAAAGAGGGG TCTGGAGTTC AGTTACCGCC CGAAGCCTGC CCCCTCGGCC TCCAGGGGTC	720

	ATTCAGAGTG TTCTCAAATC CAATTCGGAC ACACGACTTG TCACTACTCC TCTCCCTTG	780
5	AAAAAGCAT GTTAGAAGCT GCCCTACAGG TCTCAGCAGT GGGACAATCT AATTGAATCA	840
	CCGCAGCCTT CTAATACAGA AGAAACGGAC GTGACTGTCA CCTCAGCCC GCCAGCAAGG	900
	GCGCTGAGGA AGTCATTAAT CCTTCGAAAC TCTGAAAAGA AACCAGTGTT GAAGTCTGGA	960
10	CAGAAAGCCT TAAAAAAGTG ACAGCACCAA TGCAGCTGCT CAGTGTACCC NCCGTGGGCT	1020
	GTCAGGGTCA GTGGCTTCTT TCTAGATGAA AGGAGCAGAG GCGAGCCGAC GCCACCGTCA	1080
15	CAGAGAACCA GCCGAGAAGG AAAGGCCCCA CGATGCTCCC TGTGCGCTGC CCCACAGCC	1140
	GGCCGCTCCC CCGACGGCTC ACACAGGCAG CACCTCACTG CCTGTGGCT GGAGGGGCAT	1200
	TGCAAGGAGC GCGCCCGACG CCCAGGCACC CCGGGCTTAG GGTGTACGTA TCACCCAGCC	1260
20	CTGTGCTGGC AGCACGTTAC CAACCAGCCT GCGTGAAGAC CTGTCAACTG TCGTGTGTGA	1320
	ATTCCCTAAA TTCGGTTTAA ATAGTCCATT AAAGATCTGT TTAGAAAATA CCTTTGAAAA	1380
25	CGAGGGTAAC TTTAAAAAAT GGAACCTTTC AAATCCATTT ATATTTTAT TATAAACAAA	1440
	ACTTAATTAA AAGTTTAAAC AACTGGCTGA AAACTCACCA AGTGTACAGC TCACCAGCAA	1500
	TTTAAAAAAT GATAATTTAC CAGCATCTCC TCATCAGAGT TCCCTCTCCA GTAAGGGTAT	1560
30	ACCTACATCT GTAAGGGTCA GTGGACTCTG AATCAATTTT ATGGTTGTTT TAAAATCACC	1620
	GTGTATTAGG ATACTAATGA TAGTCCCTAT ATCCATCCAG AAATGCTGGC AGAAAGCACT	1680
35	GGCCACCATA CAGGACAGAC CACACCACAG CTCCATACCC AGCGTCTGCC TGGAGGCTCC	1740
	CCCACGCTGA GGTCCGGGAG AATGCCTGGT TTCAGTCATT TCCGACTAA CTGTGACAAC	1800
	GCGTGAGCAG GGAGCACCGT GCGAGTCTCC GGGAGGGAAT CCTCCTGGGG CCCAGAGACT	1860
40	CCTCCACCCC TGGGGAGGGC AGACAGGCTC GGGARGGCCT GGCCAGGCCA CTGGAGGCTG	1920
	GCAGGGAGCA GGCATGTCCA CCCGCAAGCC TGGGAGGCTA ACTCTGGCAT TCCTGGCCCG	1980
45	AGCCGCCATG CTCATTGGTG GGCCAGTTTG GGACATCCCC GTACTCAAAG ACCATATGGC	2040
	AGCCTCTGGG AAAACAAAAC CAAAACATCA CCTTCTATTA AACTCTGTAT ATTATATTTT	2100
	TTTACAATAG AAAGTTAAAA ATCAAGACTT AGATTTACTA TACATTTTTT CTCTCAGATT	2160
50	ACAAAGTTTA TATTATATAA CTGGGGTTCC CTAAATGAT TTCTTTTAAA ACAGTCTTAA	2220
	AGAGACCAGA AGTGAATACA AAAGAACTAA ACAAAT'AAA AAATTAGAAT GTGCTGTAGC	2280
55	TGAAAGCTGT	2290

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

10 GGCACGAGCC ATGCCTGGCC TCTCCTTGAT TCTTACAGTC ACTTGTGTGG CTGTTTCTGA 60
 CTCAGCAGCT ACCTGCATTG TGGCCAAAGG ATGACCTATT CCTTCTCAGG AGGGCAAAAA 120
 TGTGGAATAG TGTCTGTCCA TGCCTCTCCT CATGGGCTAC CACCTCTGCC ACCGTGGTTA 180
 15 ATCAGTAACA ACCAGGAGAG AAGCTGCTGG AACTGACCTC TGGGAACTCC CTGGGATGGT 240
 TTGGTGCAGG AATGTAGTAG GCATACACGT GGTTCGTGG ATCTGGGCCC TCCTGATGTG 300
 AGTAGAGAGG TAAAAGGCCA CCATCTCCTT GACCTCTGGG GAACTCATCC ACAAAGAAGA 360
 20 TGTTTCCAAG ATGCTTCTGA AGATTCCTA AAAATAGCCG GTTCCACCC CCGTGAATGC 420
 ATCCATTCTA GAATGCTCCT TCACCAGGAC CAGAGAACTG ATTTACAGAA GTGACATGAA 480
 25 AACATTCCAT CCCAGAATTT GCAGTAGCTC AAATTAAGTT TCTAGCTATT AAAAAGAAAA 540
 AAAAAAAA 549

30

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGCACGAGGG CTCATTCAAT CCGCGCCGGG CCTGCCAGAC ACCTGCGCCC TTCTGCAGCC 60
 45 GCCCGCCGCA TCCGCGCCG CAGCCCCAG CATGTCGGGC CCAGACGTCG AGACGCGTC 120
 CGCCATCCAG ATCTGCCGGA TCATGCGGCC AGATGATGCC AACGTGGCCG GCAATGTCCA 180
 CGGGGGGACC ATCCTGAAGA TGATCGAGGA GGCAGGCGCC ATCATCAGCA CCCGGCATTG 240
 50 CAACAGCCAG AACGGGAGC GCTGTGTGGC CGCCTGGCT CGTGTGAGC GCACCGACTT 300
 CCTGTCTCCC ATGTGCATCG GTGAGGTGGC GCATGTCAGC GCGGAGATCA CCTACACCTC 360
 CAAGCACTCT GTGAGGTGC AGGTCAACGT GATGTCCGAA AACATCCTCA CAGGTGCCAA 420
 55 AAAGCTGACC AATAAGGCCA CCCTGTGGTA TGTGCCCCTG TCGTGAAGA ATGTGGACAA 480
 GGTCTCTGAG GTGCCTCTG TTGTGTATC CCGGCANGAG CAGGAGGAGG AGGGCCGGAA 540
 60 GCGGTATGAA GCCCAGAAGC TGGAGCGCAT GGAGACCAAG TGGAGGAACG GGGACATCGT 600

CCAGCCAGTC CTCAACCCAG AGCCGAACAC TGTCAGCTAC AGCCAGTCCA GCTTGATCCA 660
5 CCTGGTGGGG CCTTCAGACT GCACCCTGCA CGGCTTTGTG CACGGAGGTG TGACCATGAA 720
GCTCATGGAT GAGGTCGCCG GGATCGTGGC TGCACGCCAC TGCAAGACCA ACATCGTCAC 780
AGCTTCCGTG GACGCCATTA ATTTTCATGA CAAGATCAGA AAAGGCTGCG TCATCACCAT 840
10 CTCGGGACGC ATGACCTTCA CGAGCAATAA GTCCATGGAG ATCGAGGTGT TGGTGGACGC 900
CGACCCTGTT GTGGACAGCT CTCAGAAGCG CTACCGGGCC GCCAGTGCCT TCTTCACCTA 960
CGTGTGCTG AGCCAGGAAG GCAGGTCGCT GCCTGTGCCC CAGCTGGTGC CCGAGACCGA 1020
15 GGACGAGAAG AAGCGCTTTG AGGAAGGCAA AGGGCGGTAC CTGCAGATGA AGGCGAAGCR 1080
ACAGGGCCAC GCGGASCYTC AGCCCTAGAC TCCCTCCTCC TGCCACTGGT GCCTCGAGTA 1140
20 GCCATGGCAA CGGCCCCAGT GTCCAGTCAC TTAGAAGTTC CCCCCTTGGC CAAAAACCCA 1200
ATTCACATG AGAGCTGGTG TTGTCTGAAG TTTTCGTATC ACAGTGTAA CCTGTACTCT 1260
CTCCTGCAAA CCTACACACC AAAGCTTTAT TTATATCATC CCAGTATCAA TGCTACACAG 1320
25 TGTGTGTCCTG AGCGCCGGGA GCGCTTGGGC AGAAACCCTC GGAATGCTT CCGAGCACGC 1380
TGTAGGTAT GGAAGAACC CAGCACCCT AATAAAGCTG CTGCTTGGCT GGAAAAAAA 1440
30 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
AGAAAAAAN 1509

35

(2) INFORMATION FOR SEQ ID NO: 180:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

AGCTGTATCA TAGGAAAGAT GGCCACACCG GCGGTACCAG TAAGTGCTCC TCCGGCCACG 60
CCAACCCAG TCCCGGCGGC GGGCCAGCC TCAGTTCAG CGCCAACGCC AGCACCGGCT 120
50 GCGGCTCCGG TTCCCGCTGC GGCTCCAGCC TGCATCCTCA GACCTGCGG CAGCAGCGGC 180
TGCAACTGCG GCTCCTGGCC AGACCCCGGC CTCAGCGCAA NTCCAGCGCA GACCCAGCG 240
55 CCCGCTCTGC CTGGTCTGCT TCTTCCAGGG CCTTCCCCG GCGGCCGCGT GGTGAGGCTG 300
CACCCAGTCA TTTTGGCTC CATGTGGAC AGCTACGAGA GACGCAACGA GGGTGCTGCC 360
CGAGTTATCG GGACCCTGTT GGGAACTGTC GACAAACACT CAGTGGAGGT CACCAATTGC 420
60

TTTTCAGTGC CGCACAATGA GTCAGAAGAT GAAGTGGCTG TTGACATGGA ATTTGCTAAG 480
 AATATGTATG AACTGCATAA AAAAGTTTCT CCAATGAGC TCATCCTGGG CTGGTACGCT 540
 5 ACGGGCCATG ACATCACAGA GCACTCTGTG CTGNATCCAT GAGTACTACA GCCGAGAGGC 600
 CCCCACCCC ATCCACCTCA CTGTGGACAC AAGTCTCCAG AACGGCCGCA TGAGCATCAA 660
 10 AGCCTACGTC AGCACTTTAA TGGGAGTCCC TGGGAGGACC ATGGGAGTGA TGTTCACGCC 720
 TCTGACAGTG AAATACGCGT ACTACGACAC TGAACGCATC GGAGTTGACC TGATCATGAA 780
 GACCTGCTTT AGCCCCAACA GAGTGATTGG ACTCTCAAGT GACTTGCAGC AAGTAGGAGG 840
 15 GGCATCAGCT CGCATCCAGG ATGCCCTGAG TACAGTGTG CAATATGCAG AGGATGTACT 900
 GTCTGGAAAG GTGTCAGCTG ACAATACTGT GGGCCGCTC CTGATGAGCC TGGTTAACCA 960
 AGTACCGAAA ATAGTTCCTG ATGACTTTGA GACCATGCTC AACAGCAACA TCAATGACCT 1020
 20 TTGATGGTG ACCTACCTGG CCAACCTCAC ACAGTCACAG ATTGCACTCA ATGAAAACT 1080
 TGTAAACCTG TGAATGGACC CCAAGCAGTA CACTTGCTGG TCTAGGTATT AACCCCAGGA 1140
 25 CTCAGAAGTG AAGGAGAAAT GGGTTTTTTG TGGTCTGAG TCACACTGAG ATAGTCAGTT 1200
 GTGTGTGACT CTAATAAAG GAGCCTACCT TTTGTAAAT AAAAAAAAAA AAAAAAACCN 1260
 SGRGGGGGG CCCGGTCCCA TTSSCCCTTT NGTAATTCGT NITACAATCC CCNGGC 1316
 30

(2) INFORMATION FOR SEQ ID NO: 181:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GGCATGWKCA GACATGACTT CTATTGCCAG GCTGGTCAAG TGGCAGGGTC ATGAGGGAGA 60
 45 CATCGATAAG GGTGCTCCTT ATGCTCCCTG CTCTGGAATC CACCAGCGGG CTATCTGCGT 120
 TTATGGGGCT GGGGACTAGA ATTGGATGCT TCAAAACCAT CACCTGTTGG CCAACAAGTT 180
 50 TGACCCAAAG GTAGATGATA ATGCTCTTCA GTGCTTAGAA GAATACCTAC GTTATAAGGG 240
 CCATTCTATT GGGACCTGAA CTTTGAAGAC CACAMTATG AAGAGGCGTT GCTTACCYGT 300
 TGGGGGCCAA GAGGCATGTT ACCAAACATG GYYCARGAAM YTTGGYKGGG AMCARKKKKG 360
 55 GKKGGAARRM CMRGGGYTTG SCAAWTCSK KGGCMWCCYT TTAGGGTAAR RGGGCKGTW 420
 ATTAGATGTG GGGTAAAGTA GGATCTTTTG CCCTTGCAAA TTTGCTGCCT GGGTGAATGY 480
 60 TGCTTGTTCC TTCTCMACCC CTAACCCTAG TAGTTCCTCC ACTAACTTTC TCACTAAGTG 540

AGAATGAGAA CTGCTGTGAT AGGGAGAGTG AAGGAGGGAT ATGTGGTAGA GCACTTGATT 600
 TCAGTTGAAT GCCTGCTGGT AGCTTTTCCA TTCTGTGGAG CTGCCGTTCC TAATAATTCC 660
 5 AGGTTTGTA GCGTGGAGGA GAACTTTGAT GGAAAGAGAA CCTTCCCTTC TGTACTGTTA 720
 ACTTAAAAAT AAATAGCTCC TGATTCAAAG TAAAAA AAAA AAAA 777

10

(2) INFORMATION FOR SEQ ID NO: 182:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GGCACAGATA ACTATGTACA TGTATTCCTT AAATGTTTTT TTAAGTTTTA TATTCTTGGC 60
 25 ACTGGTCTTC AAATGTGTAC ATGTGTGCCA GGGAGCAAAT GCCTTCTTGT TTCTGAAATT 120
 GGTCTTTTAG ACTGTCTTTT TTTCCTATCT TCTCACCTCC TGCCCTCCTC TCAGGGTACT 180
 TCCGTGGCCA GAACCCCTCC AGGTCAGAGG CAGAAGAGAA GCCTCATGGG TCACAGCAGC 240
 30 AGATGTGGGC TGGAGATCTA TTCAITTTGGT TTTGGCTTGA ATTTTCTGRA TGGTTTACTT 300
 GATCYTGGGA AAGANATATC TTGCCAGGAA AAATGATAGN CCTTGACAAT GTTGAATGAT 360
 35 CCTGCACCAC CTTGAAAGAC ATTTCTAATA TGGTTTGTCA GGCAAAGTGG TTAGTAGTCA 420
 TTTGTGGCCT GAGGTAGAAG TCCTCAGAAA TCACGAGACT TCACTGATAA AATGCTGACT 480
 TGCCCTTGA CTGGGCTCTG TGAGAGTGGC CTCTGCACT GTGCACAGTA GGTGTGAACA 540
 40 CACCACACCT ACAGGGACCA CGTGGTGGGC TGTGGACTAG CGGCCAAGCT CCCTGCAGGC 600
 CCACTAATAG AATTCAGCTT TTAGCATGGG CTGTTTCATA CTGTTCTGAT GAAACTGATT 660
 45 TGGTTTCTTT CCTCCATACC CCTTCTGCAT TTCAGTGTMT TTGTTTAGTT TTCCTGGTTT 720
 TTAATTATAA CTACAAAATA AAATCTTTAG GCTATTCACC TTAGCTTAGT AAAAAAAAAA 780
 AAAAAAACT C 791

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(2) INFORMATION FOR SEQ ID NO: 183:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

5	AAATTGATTA ACAGCTTGAA AGAAGGCTCT GGTTTTGAAG GCCTAGATAG CAGCACTGCC	60
	AGTAGCATGG AGCTGGAAGA ACTTCGGCAT GAGAAAGAGA TGCAGAGGGA GGAAATACAG	120
	AAGCTGATGG GCCAGATACA TCAGCTCAGA TCCGAATTAC AGGATATGGA GGCACAGCAA	180
10	GTTAATGAAG CAGAATCAGC AAGAGAACAG TTACAGGWTG TGCATGACCA AATAGCTGGG	240
	CAGAAAGCAT CCAAACAAGA ACTAGAGACA GAACTGGAGC GACTGAAGCA GGAGTCCAC	300
	TATATAGAAG AAGATCTTTA TCGAACAAAG AACACATTGC AAAGCAGAAT TAAAGATCGA	360
15	GACGAAGAAA TTCAAAACT CAGGAATCAG CTACCAATA AAACTTTAAG CAATAGCAGT	420
	CAGTCTGAGT TAGAAAATCG ACTCCATCAG CTAACAGAGA CTCTCATCCA GAAACAGACC	480
20	ATGCTGGAGA GTCTCAGCAC AGAAAAGAAC TCCCTGGTCT TTCAACTGGA GCGCCTCGAA	540
	CAGCAGATGA ACTCCGCCTC TGGAAGTAGT AGTAATGGGT CTTGATTAA TATGTCTGGA	600
	ATTGACAATG GTGAAGGCAC TCGTCTGCGA AATGTTCTTG TTCTTTTAA TGACACAGAA	660
25	ACTAATCTGG CAGGAATGTA CGGAAAAGTT CGCAAAGCTG CTAGTTCAAT TGATCAGTTT	720
	AGTATTCGCC TGGGAATTTT TCTCCGAAGA TACCCCATAG CCGGAGTTTT TGTAATTATA	780
30	TATATGGCTT TGCTTCACCT CTGGGTCATG ATTGTTCTGT TGAATTACAC ACCAGAAATG	840
	CACCACGACC AACCATATGG CAAATGAACC AAGCCCAGTT GTTCAGTGA TTGGTTGTCT	900
	TTTTCTAGAC TTGGGATCTG CAAGAAGGCC AATTGCCTAA AATTCTGAG AACAGTGCAC	960
35	AAGATTATTT TATCACTACA AGCTTTTAAC TTTTAAAGTT ATTGTACAAG TATTCTACCT	1020
	AAATCTCCA ATTTCCTTTA AATGGTAAGA GTTCTTAAAA CAGACAATAA TTTAACAAGC	1080
40	TCAGCTCTGC TTTATCTGAG TTTAGTGGTC CTAATATATA TGTAAGAGAA GATGGTGGGG	1140
	TTGTTACCT CTGTACAGAC CATCTGTATG TTAGGTGACA TTGATTATGG GTTATAATCA	1200
	GGGAAACTAA TTGTATTTAG TGACAAAAAT AAAAAGTTTT TTTTATATAA TTCAGTCTGC	1260
45	TTTGGATTT TCATATATTT AACTTTGCAA AAAGATTAC TTTGTACATG TTACAGGCTT	1320
	GATTGGTGTA AATCTTTTAA TAAATACATA AATAAAAGNA AAATATGCAT TTTCTTTTC	1380
50	TAAAAAATAA AAAAAAATAA CTCGA	1405

55 (2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

5	GTCATGCAGT GCGCCGGAGA ACTGTGCTCT TTGAGGCCGA CGCTAGGGGC CCGGAAGGGA	60
	AACTGCGAGG CGAAGGTGAC CGGGGACCGA GCATTTTCTG TCTGCTCGGT AGACCTGGTG	120
	CACCACCACC ATGTTGGCTG CAAGGCTGGT GTGTCTCCGG AACTACCTT CTAGGGTTTT	180
10	CCACCCAGCT TTCACCAAGG CCTCCCTGT TGTGAAGAAT TCCATCACGA AGAATCAATG	240
	GCTGTTAACA CCTAGCAGGG AATATGCCAC CAAAACAAGA ATTGGGATCC GCGTGCGGAG	300
15	AACTGGCCAA GAACTCAAAG AGGCAGCATT GGAACCATCG ATGGAAAAA TATTTAAAT	360
	TGATCAGATG GGAAGATGGT TTGTTGCTGG AGGGGCTGCT GTTGGTCTTG GAGCATTGTG	420
	CTACTATGGC TTGGGACTGT CTAATGAGAT TGGAGCTATT GAAAAGGCTG TAATTGGCC	480
20	TCAGTATGTC AAGGATAGAA TTCATTCCAC CTATATGTAC TTAGCAGGA GTATTGGTTT	540
	AACAGCTTGG TCTGCCATAG CAATCAGCAG AACGCCTGTT CTCATGAAT TCATGATGAG	600
25	AGGCTCTTGG GTGACAATG GTGTGACCTT TGCAGCCATG GTTGGAGCTG GAATGCTGGT	660
	ACGATCAATA CCATATGACC AGAGCCCAGG CCCAAAGCAT CTTGCTTGGT TGCTACATTC	720
	TGGTGTGATG GGTGCAGTGG TGGCTCCTCT GACAATATTA GGGGCTCCTC TTCTCATCAG	780
30	AGCTGCATGG TACACAGCTG GCATTGTGGG AGGCCTCTCC ACTGTGGCCA TGTGTGCGCC	840
	CAGTGAAAAG TTTCTGAACA TGGGTGCACC CCTGGGAGTG GGCCTGGGTC TCGTCTTTGT	900
35	GTCTCTATTG GGATCTATGT TTCTTCCACC TACCACCGTG GCTGGTGCCA CTCTTACTC	960
	AGTGGCAATG TACGGTGGAT TAGTTCTTTT CAGCATGTTT CTTCTGTATG ATACCCAGAA	1020
	AGTAATCAAG CGTGCAGAAG TATCACC AAT GTATGGAGTT CAAAAATATG ATCCCATTA	1080
40	CTCGATGCTG AGTATCTACA TGGATACATT AAATATATTT ATGCGAGPTG CAACTATGCT	1140
	GGCAACTGGA GGCAACAGAA AGAAATGAAG TGAATCAGCT TCTGGCTTCT CTGCTACATC	1200
45	AAATATCTTG TTAAATGGG CAGATATGCA TTAAATAGTT TGTACAAGCA GCTTTCGTTG	1260
	AAGTTTAGAA GATAAGAAAC ATGTCATCAT ATTTAAATGT TCCGGTAATG TGATGCCTCA	1320
	GGTCTGCCCT TTTTCTGGA GAATAAATGC AGTAATCCTC TCCCAAATAA GCACACACAT	1380
50	TTTCAATTCT CATGTTGAG TGATTTTAAA ATGTTTGGT GAATGTGAAA ACTAAAGTTT	1440
	GTGTCATGAG AATGTAAGTC TTTTCTTAC TTTAAATTT AGTAGGTTCA CTGAGTAACT	1500
55	AAAATTTAGC AAACCTGTGT TTGCATATTT TTTKGGAGTG CAGMMTAWTG TAATTARAGC	1560
	ATTCCAGTAA NAGTGTNTTT AAGTTGNTC TATATN	1596

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

10 GCGCAGAGCC CGYACGAGCA GGACGACGAC GACAAGGGCG ACTCCAAGGA AACGCGGCTG 60
15 ACCCTGATGG AGGAAGTGCT CCTGCTGGGC CTCAAGGACC GCGARGGTTA CACATCATTT 120
TGGAATGACT GTATATCATC TGGATTACGT GGCTGTATGT TAATTGAATT AGCATTGAGA 180
GGAAGGTTAC AACTAGAGGC TTGTGGAATG AGACGTAAAA GTCTATTAAAC AAGAAAGGTA 240
20 ATCTGTAAGT CAGATGCTCC AACAGGGGAT GTTCTTCTTG ATGAAGCTCT GAAGCATGTT 300
AAGGAACTC AGCCTCCAGA AACGCTCCAG AACTGGATG AATTACTTAG TGGTGAGACA 360
25 TGGAATCCAT TAAAATTGCA TTATCAGTTA AGAAATGTAC GGAACGATT AGCTAAAAAC 420
CTGGTGAAA AGGGTGTATT GACAACAGAG AACAGAACT TCCTACTTTT TGACATGACA 480
ACACATCCCC TCACCAATAA CAACATTAAG CAGCGCCTCA TCAAGAAAGT ACAGGAAGCC 540
30 GTTCTTGACA AATGGGTGAA TGACCCTCAC CGCATGGACA GGCGCTTGCT GCCCTCATT 600
TACCTGGCTC ATGCCTCGGA CGTCTGGAG AATGCTTTTG CTCCTCTTCT GGACGAGCAG 660
35 TATGATTMTG CTACCAAGAG AGTGCGGCAG CTTCTCGACT TAGACCCTGA AGTGGAATGT 720
CTGAAGGCCA ACACCAATGA GGTCTGTGG GCGGTGGTGG CGGCGTTCAC CAAGTAACTC 780
TGCTCGGGGT GAACCATTTCT CCTTCTCTC AAGTAAACCA GTAGTTTTTC TTCTGTGAC 840
40 TTCTGGTTTT CTGTAATTG TACTTTCCCA CACTATAATT GGCTTCTGTT TTACAAAATG 900
GTGGGTGGCT TTTTCTTTTT TGTACGTGTA CAGGATTCTG CTGGTACGAG AGGCCTTCCT 960
CTTCTGTTTT TAAAAAAG TTTTACTGCC ATATTGGCAT TCCATTCCCT GTTGCCATCC 1020
45 TCACTGTTAC CTGTTTTGGG TTTCTGGTCT ACTTTGACTT TCAAAGTACC TCCAGCCTCC 1080
TCATACGCAC AGCTTTTGA TGACCTCAGC TTGAGTTTCT CCATATGTGC ATGTACATCT 1140
50 AGCATTCTGC CTACAGTTCA GACAGAAGTC ACAAAAAGGC CTTCAACTCA CCAAAGGTAA 1200
ATATCTGTAT CTATTAGGAC ATTTTITACA TAGACTTCAG TTGAGATGTA TACTTAGCAA 1260
AATTATTTTT AAATTGAAAC AGCACAGTAA ATACTTAATA TAAATGTCC CTTGGATTTT 1320
55 GCTTCCCATG TAAATCTATT GTATTATTAC ACTTGTATA ATTTTAACTA TAAAGGTCCA 1380
ATTGTTTCAC AGAGCCAGTT TGGATGGGC TGCATTCCAT TTATGCTGTA TATAGTTTGA 1440
60 ATTATATATA AATTACCCCT TCTCTGGCC ACCCTGCTC CCATCTTAGT ATTTTGCAAG 1500

ATCTAATCAG TTGTACACCT GGTGCCCCCTC GCTTGCTTCA ATCATGGTTA TTTGATGGCA 1560
 5 AAATCGACCT CTGTGCGCTG AAGGAGAGAG AAAAGATGTG TGTCTGATTG GTCCTGGGAT 1620
 TTTTGTAGCT GTGCCATTTA TGGTACTCTT TGCCTATGCA TCCCCTTTTT AGATTTTTTTT 1680
 TAAATTTTAT CTTACTGTTT TTATAATTTT TATTGGGAAG AGGCTTGTGA CCAGTACCAA 1740
 10 TCTTGAGTTT CTTTTTCTGT CCACAAGTAA ATTAATATCT GCTCTGAAAT GTCATTTATC 1800
 TACTCACACA TTCTTGGGGA AAAAAATCAA ATGTCAGTCC TAGCAGATGT TGCATGTAAA 1860
 15 TTGGTAGCAA GTAATGATTA CAACCCAGAG GATTAAGAAT TTTGTAACAG AAAGCTCTAT 1920
 GTTTTAATTT TTTATATACA ATTAGGATAA TTAGCATTGT CAGACTATAA ACCTTTGCTT 1980
 TTTAAAGTTT ATTTTACTA TTTCTTTATC ACTTTATGT ATCATCACCA TTGGTTTCAT 2040
 20 AATGTAAATA CTATATGTTG AACAAATTAA ATGTCAAAT TTTTATTAC CATAGTCCAT 2100
 GTTAATAGTG GGGCTTTCAG GTGTTTAGAG ATTTTTTTTG TTGTTGTAA CATTCAATGC 2160
 25 AAAAGTACTA GATGGTGTAT AACTCTAGAG TTGAATTTTA AGGGATTCCC TAATATGTAT 2220
 ACTATCTTTT TATCTGAAGT AATAAATAAA CAATGATCTT GAAAGTGCCY RAAAMAAAAA 2280
 AAAAAAAAAA AAA 2293

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(2) INFORMATION FOR SEQ ID NO: 186:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GGCACGAGGC GAGCCGGCGC ACCGTACGCT GGGACGTGTG GTTTCAGCTC GTGCGCCTCC 60
 45 CCGTGGGTTT GCGACGTTTA GCGACTATTG CGCCTGCGCC ACGCCGGCTG CGAGACTGGG 120
 GCGGTGGCTG CTGGTCCCGG GTGATGCTAG GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG 180
 GTGTAGGTGG GAGTCACGGA CGGTTCCGGG CCCGAGGTGT CCGCGAAGGT GCGGCACATG 240
 50 GGCGGCAGGG GAGAGCATGG CTCAGCGGAT GGTCTGGGTG GACCTGGAGA TGACAGGATT 300
 GGACATTGAG AAGGACCAGA TTATTGAGAT GGCTGTCTG ATAAGTACT CTGATCTCAA 360
 55 CATTTTGGCT GAAGTCTTA ACCTGATTAT AAAACAACCA GATGAGTTGC TGGACAGCAT 420
 GTCAGATTGG TGTAAGGAGC ATCACGGGAA GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG 480
 60 TACAATTACA TTGCAGCAGG CAGAGTATGA ATTTCTGTCC TTTGTACGAC AGCAGACTCC 540

	TCCAGGGCTC TGTCCACTTG CAGGAAATTC AGTTCATGAA GATAAGAACT TTCTTGACAA	600
	ATACATGCCC CAGTTCATGA AACATCTTCA TTATAGAATA ATTGATGTGA GCACTGTAA	660
5	AGAACTGTGC AGACGCTGGT ATCCAGAAGA ATATGAATTT GCACCAAAGA AGGCTGCTTC	720
	TCATAGGGCA CTTGATGACA TTAGTGAAAG CATCAAAGAG CTTCACTTTT ACCGAAATAA	780
10	CATCTTCAAG AAAAAAATAG ATGAAAAGAA GAGGAAAATT ATAGAAAATG GGGAAAATGA	840
	GAAGACCGTG AGTTGATGCC AGTTATCATG CTGCCACTAC ATCGTTATCT GGAGGCAACT	900
	TCTGGTGGTT TTTTTCCTC ACGCTGATGG CTTGGCAGAG CACCTTCGGT TAACTTGCAT	960
15	CTCCAGATTG ATTACTCAAG CAGACAGCAC ACGAAATACT ATTTTCTCC TAATATGCTG	1020
	TTTCCATTAT GACACAGCAG CTCCTTTGTA AGTACCAGGT CATGTCCATC CCTTGGTACA	1080
	TATATGCATT TGCTTTTAAA CCATTTCTTT TGTTTAAATA AATAAATAAG TAAATAAAGC	1140
20	TAGTTCTATT GAAATGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1200
	AAAAAAAAAA AN	1212

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(2) INFORMATION FOR SEQ ID NO: 187:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

	GCTTCGGGAA GTTGCTTTTG TCCAAACATC CGGGCTTCTC CTTTTGTGT TCCGGCCGAT	60
40	CCCACCTCTC CTCGACCCTG GACGTCTACC TTCCGGAGGC CCACATCTTG CCCACTCCGC	120
	GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA GGGACATGGC AACTACAGCG	180
45	GCGCGGGCGG GCGGCGCCCG AAATGGAGCT GGCCCGGAAT GGGGAGGGTT CGAAGAAAAC	240
	ATCCAGGGCG GAGGCTCAGC TGTGATTGAC ATGGAGAACA TGGATGATAC CTCAGGCTCT	300
	AGCTTCGAGG ATATGGGTGA GCTGCATCAG CGCCTGCGG AGGAAGAAGT AGACGCTGAT	360
50	GCAGCTGATG CAGCTGCTGC TGAAGAGGAG GATGGAGAGT TCCTGGGCAT GAAGGGCTTT	420
	AAGGGACAGC TGAGCCGCA GGTGGCAGAT CAGATGTGGC AGGCTGGGAA AAGACAAGCC	480
55	TCCAGGGCCT TCAGCTTGTA CGCCAACATC GACATCCTCA GACCCTACTT TGATGTGGAG	540
	CCTGCTCAGG TGCGAACAGG GCTCCTGGAG TCCATGATCC CTATCAAGAT GGTCAACTTC	600
	CCCCAGAAAA TTGCAGGTGA ACTCTATGGA CCTCTCATGC TGGTCTTCAC TCTGGTTGCT	660
60	ATCCTACTCC ATGGGATGAA GACGTCTGAC ACTATTATCC GGGAGGGCAC CCTGATGGGC	720

	ACAGCCATTG GCACCTGCTT CGGCTACTGG CTGGGAGTCT CATCCTTCAT TTACTTCCTT	780
5	GCCTACCTGT GCAACGCCCA GATCACCATG CTGCAGATGT TGGCACTGCT GGGCTATGGC	840
	CTCTTTGGGC ATTGCATTGT CTTGTTTCATC ACCTATAATA TCCACCTCCA CGCCCTCTTC	900
	TACCTCTTCT GGCTGTTGGT GGGTGGACTG TCCACACTGC GCATGGTAGC AGTGTGTTGGTG	960
10	TCTCGGACCG TGGGCCCCAC ACAGCGGCTG CTCCTCTGTG GCACCCTGGC TGCCCTACAC	1020
	ATGCTCTTCC TGCTCTATCT GCATTTTGCC TACCACAAAG TGGTAGAGGG GATCCTGGAC	1080
15	AACTGGAGG GCCCAACAT CCCGCCCATC CAGAGGGTCC CCAGAGACAT CCCTGCCATG	1140
	CTCCCTGCTG CTCGGCTTCC CACCACGCTC CTCAACGCCA CAGCCAAAGC TGTGCGGTG	1200
	ACCTGCACT CACACTGACC CCACCTGAAA TTCTTGCCA GTCTCTTTC CCGCAGCTGC	1260
20	AGAGAGGAGG AAGACTATTA AAGGACAGTC CTGATGACAT GTTTCGTAGA TGGGGTTTGC	1320
	AGCTGCCACT GAGCTGTAGC TGGCTAAGTA CCTCCTTGAT GCNTGTCGGC ACTTCTGAAA	1380
25	GGCACAAGGC CAAGAACTCC TGGCCAGGAC TGCAAGGCTC TGCAGCCAAT GCAGAAAATG	1440
	GGTCAGCTCC TTTGAGAACC CCTCCCACCC TACCCCTTCC TTCTCTTTTA TCTCTCCAC	1500
	ATTGTCTTGC TAAATATAGA CTTGTAATT AAAATGTTGA TTGAAGTCTG GAAAAAATAA	1560
30	AAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATC TCGAG	1605

35 (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

45	ATTCCGCATG AGGGGGTCAC GTGGTGGCTG GGCCGGGGAA ATGGCGGCTT CAGGAGAGAG	60
	CGGGACTTCA GCGGCGGAG GCAGCACC GAAGCATT ATGACCTTCT ACAGTGAGGT	120
50	GAAACAAATA GAGAAGAGAG ACTCGTTTCT AACTTCGAAA AATCAGATTG AAAGACTGAC	180
	CCGTCTGGT TCCTCTTACT TCAATTGAA CCCATTGAG GTTCTTCAGA TAGATCCTGA	240
	AGTTACAGAT GAAGAAATAA AAAAGAGGTT TCGGCAGTTA TCCATCTTGG TGCATCCTGA	300
55	CAAAAATCAA GATGATGCTG ACAGAGCACA AAAGGCTTTT GAAGCTGTGG ACAAAGCTTA	360
	CAAGTTGCTA CTGGATCAGG AGCAAAAGAA GAGGGCCCTG GATGTAATTC AGGCAGGAAA	420
60	AGAATACGTG GAACACACTG TGAAAGAGCG AAAAAACAA TTAAAGAAGG AAGGAAAACC	480

	TACAATTGTA GAGGAGGATG ATCCTGAGCT GTTCAAACAA GCTGTATATA AACAGACAAT	540
	GAAACTCTTT GCAGAGCTGG AAATTAAAAG GAAAGAGAGA GAAGCCAAAG AGATGCATGA	600
5	AAGGAAACGA CAAAGGGAAG AAGAGATTGA AGCTCAAGAA AAAGCCAAAC GGGAAAGAGA	660
	GTGGCAGAAA AACTTTGAGG AAAGTCGAGA TGGTCGTGTG GACAGCTGGC GAAACTTCCA	720
	AGCCAATACG AAGGGGAAGA AAGAGAAGAA AAATCGGACC TTCCTGAGAC CACCGAAAGT	780
10	AAAAATGGAG CAACGTGAGT GACCGCCCAA GGTACAGGC ACAGAACCTT TCCCCTGCTA	840
	TCTCCCTTCC TGCTTCGAAG GACTCATTCT TTCTCCAC TTCCACCCA ACATAGAGTA	900
15	GTATTGCTT TTTAGTCCAT TTTGTTTTCA ATACGATTTA ATATCGATCA GAGTAATTCT	960
	TTGTACATT GAAATGAGG GCTTGGTTTA AAAAAAGACC TTTCCTCTC CCTGCCCTTA	1020
	GAACAACCAG TATTAGAAGG TGCCACCATT GGTGCTGCCT TCTCTTCCA CAGCCTGTAA	1080
20	CTCAGTGTG TGTACTTCAC TGAATTGTGA TGGTTAGAAA CTTCGTGGAT AGTTTGTGGA	1140
	AATCATCCAA TTAAACATAC TGCTTAAAC AGTGTGCTG TGACTTCAGA GACAAGCCTG	1200
25	GAAGGGGCAC CTTAGGAAGC CCCTTCGCTT CAGTTGCTCG CTTCGCGTG TGCTCCCTTC	1260
	GAAGGGCCAG ATAAGACAGG GAACACTTGT GAGCACACAG AGCAGCATCT GATGCCCTGT	1320
	GGTGTTCGGC ATGTGCCCC TGTCTACTGA CCAATCAGTG TGGCATGAGG CCCACGCCAC	1380
30	CCAAACCTTT CACTTTCCAA AGAGCTAGCC GTCCTCCACC CAGTACCATG TCCTAGCCTG	1440
	TCTGCATTG TTAGTGGTAA TATTCTTTAT GTATAATAAA TTTTATACC CAAAAAAAAA	1500
35	AAAAAAAAA ACTCGA	1516

40 (2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50	GCTCCCATGT TGCTGGCTGT CCGTACATCA CCCTGTCCCC TGCAGGAGGG GGCTACAGGC	60
	CATCTCCCTC CTGTAGGCCT CTGACTCCCC TCCACTTTTG GGGCTCAGC TTATCTCGGG	120
	CAGGGGACCA TTGCAGCATC CTCCCCTCCT CNGGACTCAA GGTGCTGAGG TATAAGCCCT	180
55	GGGCCCCAGA TCCCTGRTKA CACCTTCCTG GAGAAGACTC TCAAAAGTGA CTGTATATTT	240
	GAGTTCACCA GCAATAACTC CCCACACTCG AAGCAGGTCC AAACCCMAGG ATCCCAGGGT	300
60	CCTTGGGCTC TGTGGCACTG TCTTCCCAAG ATCCTTCCTG TTGCACAATG GGAAACCTAA	360

GAGGAAAAAG ACAGGGGCCT GCTTGCCCAG CCATGCGAGG GATTCCATGC CCACCTGCCC 420
 TCTGYCTGCC TCGCTGGAAT GTGGGCCCCCT GCTCCCCGTC AGGTTGTGCT GTCTCTGACC 480
 5 TATGTTTACA TCCCGGAGGG GTTCTCTGCCT CCTCCCCACC CAGGTCAGGG TGTGGTCCAG 540
 CAGCTTGCTG TGGGGTGCTG ACATGTGTCA CCACTGCCCC CCTTGCCCCC GGGGGGTCA 600
 10 TGGTCTCCTC CTGGATGCTG CTCCTTGAAT YTTTTTYYT GAWAAACCYT TTAMAATTAA 660
 AAAAAAAAAA AAAAAACTCG A 681

15

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GCCTCAAGCC ACGCATATGA TAATTTTCTG GAACATTCAA ATTCAGTGTT TCTACAGCCA 60
 GTTAGTCTAC AAACCATTCG AGCAGCACCA TCAAACCAGA GTCTGCCACT TTTGTGTCATC 120
 30 GCTGGATGAT TGCTGGGCAA AGGTGGCCTT TTAGAGCTCT TAAAAGCCCA CAAAAGGCT 180
 ATTCGTAGAG CCACAGTCAA CACATTTGGT TATATTGCAA AGGCCATTGG CCTCATGATG 240
 35 TATTGCTAC ACTTCTGAAC AACCTCAAAG TTCAAGAAAG GCAGAACAGA GTTTGTACCA 300
 CTGTAGCAAT AGCTATTGTT GCAGAAACAT GTTACCCTT TACAGTACTC CCTGCCTTAA 360
 TGAATGAATA CAGAGTTTCT GAACGAATG TTCAAAATGG AGTGTTAAAA TCGCTTCTCT 420
 40 TCTTGTTTGA ATATATTGGT GAAATGGGAA AAGACTACAT TTATGCCGTA ACACCGTTAC 480
 TTGAAGATGC TTTAATGGAT AGAGACCTTG TACACAGACA GACGGCTAGT GCAGTGGTAC 540
 45 AGCACATGTC ACTTGGGGTT TATGGATTGG GTTGTGAAGA TTCGCTGAAT CACTTGTGTA 600
 ACTATGTATG GCCCAATGTR TTTGAGACAT CTCCTCATGT AATTCAGGCA GTTATGGGAG 660
 CCTAGAGGG CCTGAGAGTT GCTATTGGAC CATGTAGAAT GTTGAATAT TGTTTACAGG 720
 50 GTCTGTTTCA CCCAGCCCGG AAAGTCAGAG ATGTATATTG GAAAATTTAC AACTCCATCT 780
 ACATTGGTTC CCAGGACGCT CTCATAGCAC ATTACCCAAG AATCTACCAA CGATGATAAG 840
 55 RACACCTATA TTCGTTATGA ACTTGACTAT ATCTTATAAT TTTATTGTTW ATTTKGTGKT 900
 TAATGCACAS TACTTCACAC CTTAACTTG CTTTGATTGG GTGATGTAAA CTTTAAACA 960
 TTGCAGATCA GTGTAGGACT GGTCCATAGG GGAAGAGCTA GGAANTCCAT AGGC 1014
 60

(2) INFORMATION FOR SEQ ID NO: 191:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

15	TCGCAGCAGG GTGTGTCCAG ATGGTCAGTC TCTGGTGGCT AGCCTGTCCT GACAGGGGAG	60
	AGTTAAGCTC CCGYTCTCCA CCGTGCCGGC TGGCCAGGTG GGCTGAGGGT GACCGAGAGA	120
	CCAGAACCTG CTTGCTGGAG CTTAGTGCTC AGAGCTGGGG AGGGAGGTTC CGCCGCTCCT	180
20	CTGCTGTCTAG CGCCGGCAGC CCCTCCCGGC TTCACTTCCT CCCGAGCCC CTGCTACTGA	240
	GAAGCTCCGG GATCCAGCA GCCGCCACGC CCTGGCTCA GCCTGCGGG CTCCAGTCAG	300
	GCCAAACCCG ACGCGCANTG GGAGGAAGAC AGGACCCTTG ACATCTCCAT CTGCACAGAG	360
25	GTCTTGCTG GACCGAGCAG CCTCCTCCTC CTAGGATGAC CTCACCTCC AGCTCTCCAG	420
	TTTTCAGGTT GGAGACATTA GATGGAGGCC AAGAAGATGG CTCTGAGCG GACAGAGGAA	480
30	AGCTGGATTT TGGGAGCGGG CTGCCTCCCA TGGAGTCACA GTTCCAGGGC GAGGACCGGA	540
	AATTGCCCC TCAGATAAGA GTCAACCTCA ACTACCGAAA GGAACAGGT GCCAGTCAGC	600
	CGGATCCAAA CCGATTGAC CGAGATCGGC TCTTCAATGC GTCTCCCGG GGTGTCCCCG	660
35	AGGATCTGGC TGGACTTCCA GAGTACCTGA GCAAGACCAG CAAGTACCTC ACCGACTCGG	720
	AATACACAGA GGGCTCCACA GGTAAAGAGT GCCTGATGAA GGCTGTGCTG AACCTTAAGG	780
40	ACGGGGTCAA TGCTTGCATT CTGCCACTGC TGCAGATCGA CCGGGACTCT GGCAATCCTC	840
	AGCCCTGGT AAATGCCCAG TGCACAGATG ACTATTACCG AGGCCACAGC GCTCTGCACA	900
	TGCCCATTTGA GAAGAGGAGW CTGCAGTGTG TGAAGCTCCT GGTGGAGAAT GGGGCCAATG	960
45	TGCATGCCCG GGTCTGCGGC GCTTCTTCCA GAAGGGCCAA GGGACTTGCT TTTATTTCCG	1020
	TGAGCTACCC CTCTYTTTGG CCGCTTGAC CAAGCAGTGG GATGTGGTAA GCTACCTCCT	1080
50	GGAGAACCCA CACCAGCCCG CCAGCTGCA GGCAGTACT CCCAGGGCAA CACAGTCCTG	1140
	CATGCCCTAG TGATGATCTC GGACAACTCA GCTGAGAACA TTGCACTGGT GACCAGCATG	1200
	TATGATGGGC TCCTCCAAGC TGGGGCCCGC CTCTGCCCTA CCGTGAGCT TGAGGACATC	1260
55	CGCAACCTGC AGGATCTCAC GCCTCTGAAG CTGGCCGCCA AGGAGGGCAA GATCGAGATT	1320
	TTCAGGCACA TCCTGCAGCG GGAGTTTCA GGAAGTGAAG ACCTTTCCCG AAAGTTCACC	1380
60	GAGTGGTGCT ATGGGCCTGT CCGGGTGTG CTGTATGACC TGGCTTCTGT GGACAGCTGT	1440

5 GAGGAGAACT CAGTGCTGGA GATCATTGCC TTTCATTGCA AGAGCCCGCA CCGACACCGA 1500
ATGGTCGTTT TGGAGCCCTT GAACAAACTG CTGCAGGCGA AATGGGATCT GCTCATCCCC 1560
AAGTTCCTCT TAAACTTCCT GTGTAATCTG ATCTACATGT TCATCTTCAC CGCTGTGACC 1620
TACCATCAGC CTACCCTGAA GAAGCAGGCC GCCCCTCACC TGAAAGCGGA GGTGGAAC 1680
10 TCCATGCTGC TGACGGGCCA CATCCTTATC CTGCTAGGGG GGATCTACCT CCTCGTGGGC 1740
CAGCTGTGGT ACTTCTGGCG GCGCCACGTG TTCATCTGGA TCTCGTTCAT AGACAGCTAC 1800
TTTGAAATCC TCTTCCTGTT CCARGCCCTG CTCACAGTGG TGTCCCARGT GCTGTGTTTC 1860
15 CTGGSCATCG AGTGGTACCT GCCCCTGCTT GTGTCTGCGC TGGTCTGGG CTGGCTGAAC 1920
CTGCTTTACT ATACACGTGG CTTCAGCAC ACAGGCATCT ACAGTGTCTAT GATCCAGAAG 1980
20 CCCTGGTGAG CCTGAGCCAG GANNITGGCG CCCCAGAGCT CCTACAGGCC CCAATGCCAC 2040
AGAGTCAGTG CAGCCCATGG AGGGACAGGA KGACGAKGGC AACGGGGCCC AGTACAGGGG 2100
TATCCTGGAA GCCTCCTTGG AGCTCTTCAA ATTCACCATC GGCATGGGCG AGCTGGCCTT 2160
25 CCAGGARCAG CTGCACCTCC GCGGCATGGT GCTGCTGCTG CTGCTGGSCT ACGTGTGCT 2220
CACCTACATC CTGCTGTCTA ACATGCTCAT CGCCCTCATG AGCGAGACCG TCAACAGTGT 2280
30 CGCCACTGAC AGCTGGAGCA TCTGGAAGCT GCAGAAAGCC ATCTCTGTCC TGGAGATGGA 2340
GAATGGCTAT TGGTGGTGCA GGAAGAAGCA GCGGGCAGGT GTGATGCTGA CCGTTGGCAC 2400
TAAGCCAGAT GGCAGCCCSG ATGAGCGCTG GTGCTTCAGG GTGGAGGAGG TGAAGTGGC 2460
35 TTCTATGGAG CAGACGCTGC CTACGCTGTG TGAGGACCCG TCAGGGGCAG GTGTCCCTCG 2520
AACTCTCGAG AACCTGTGCC TGGCTTCCCC TCCCAAGGAG GATGAGGATG GTGCCCTCTGA 2580
40 GGAAACTAT GTGCCCGTCC AGCTCCTCCA GTCCAACTGA TGGCCAGAT GCAGCAGGAG 2640
GCCAGAGGAC AGAGCAGAGG ATCTTTCCAA CCACATCTGC TGGCTCTGGG GTCCCACTGA 2700
ATTCTGGTGG CAAATATATA TTTTCACTAA CTCAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
45 AAAAAAAAAA AAAAAAGGC 2779

50

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

	ACCCGCTCCG CTCCGCTCCG CTGGGCCCG CGCCGCCCGT CAACATGATC CGCTGCGGCC	60
	TGGCCTGCGA GCGCTGCCGC TGGATCCTGC CCCTGCTCCT ACTCAGCGCC ATCGCCTTCG	120
5	ACATCATCGC GCTGGCCGGC CGCGGCTGGT TGCAGTCTAG CGACCACGGC CAGACGTCCT	180
	CGCTGTGGTG GAAATGCTCC CAAGAGGGCG GCGGCAGCGG GTCCTACGAG GAGGGCTGTC	240
10	AGAGCCTCAT GGAGTACGCG TGGGGTAGAG CAGCGGCTGC CATGCTCTTC TGTGGCTTCA	300
	TCATCCTGGT GATCTGTTTC ATCCTCTCCT TCTTCGCCCT CTGTGGACCC CAGATGCTTG	360
	TCTTCCTGAG AGTGATTGGA GGTCTCCTTG CCTTGGCTGC TGTGTTCCAG ATCATCTCCC	420
15	TGGAATTTA CCCCCTGAAG TACACCCAGA CCTCACCCCT TCATGCCAAC CSTGCTGTCA	480
	CTTACATCTA TAACTGGGCC TACGGCTTTG GGTGGGCAGC CACGATTATC CTGATYGGCT	540
20	GTGCCTTCTT CTTCTGCTGC CTCCCCAACT ACGAAGATGA CCTTCTGGGC AATGCCAAGC	600
	CCAGGTACTT CTACACATCT GCCTAACTTG GGAATGAATG TGGGAGAAAA TCGCTGCTGC	660
	TGAGATGGAC TCCAGAAGAA GAAACTGTTT CTCACGGCGA CTTTGAACCC ATTTTMTGGC	720
25	AGTGTTTATA TTATTAACT AGTCAAAAAT GCTAAAATAA TTTGGGAGAA AATATTTTTT	780
	AAGTAGTGT ATAGTTTCAT GTTTATCTTT TATTATGTTT TGTGAAGTTG TGTCTTTTCA	840
30	CTAATTACCT ATACTATGCC AATATTTCTT TATATCTATC CATAACATTT ATACTACATT	900
	TGTAAGAGAA TATGCACGTG AAACCTAACA CTTTATAAGG TAAAAATGAG GTTTCCAAGA	960
	TTTAATAATC TGATCAAGTT CTGTGTATTT CCAAATAGAA TGGACTCGGT CTGTTAAGGG	1020
35	CTAAGGAGAA GAGGAAGATA AGGTTAAAAG TTGTTAATGA CCAAACATTC TAAAAGAAAT	1080
	GCAAAAAAAA AGTTTATTTT CAAGCCTTCG AACTATTTAA GGAAAGCAA ATCATTTCTCT	1140
40	AAATGCATAT CATTTGTGAG AATTTCTCAT TAATATCCTG AATCATTCAT TTCAGCTAAG	1200
	GCTTCATGTT GACTCGATAT GTCATCTAGG AAAGTACTAT TTCATGGTCC AAACCTGTTG	1260
	CCATAGTTGG TAAGGCTTTC CTTTAAGTGT GAAATATTTA GATGAAATTT TCTCTTTTAA	1320
45	AGTTCMTTAT AGGGTTAGGG TGTGGGAAAA TGCTATATTA ATAAATCTGT AGTGTMTTGT	1380
	GTATATATGT TCAGAACCAG AGTAGACTGG ATTGAAAGAT GGACTGGGTC TAATTTATCA	1440
50	TGACTGATAG ATCTGGTTAA GTTGTGTAGT AAAGCATTAG GAGGGTCATT CTGTGCACAA	1500
	AAGTGCCACT AAAACAGCCT CAGGAGAATA AATGACTTGC TTTTCTAAAT CTCAGGTTTA	1560
	TCTGGGCTCT ATCATATAGA CAGGCTTCTG ATAGTTTGCA ACTGTAAGCA GAAACCTACA	1620
55	TATAGTTAAA ATCCTGGTCT TTCTTGGTAA ACAGATTITA AATGTCTGAT ATAAAACATG	1680
	CCACAGGAGA ATTGCGGGAT TTGAGTTTCT CTGAATAGCA TATATATGAT GCATCGGATA	1740
60	GGTCATTATG ATTTTTTACC ATTTGACTT ACATAATGAA AACCAATTCA TTTTAAATAT	1800

	CAGATTATTA TTTTGTAAGT TGTGGAAAAA GCTAATGTGA GTTTTCATTA TGAAGTTTTC	1860
	CCAATAAACC AGGTATTCTA AAAAAAAAAA AAAAAAACTN GAGGGGGGGC CCGGTACCCA	1920
5	ATT	1923
10	(2) INFORMATION FOR SEQ ID NO: 193:.	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2346 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:	
20	AGGCTCAGGG GGACACTCTC AAAATTACAC AGCTTTTAAC AGGTGGCAGA ATTGGGGTTC	60
	AGACCCAGAT CTGGGTTCAA GTCACCTCATG GTGTGATTGC GGCAATTCCTT CCCGCATCTG	120
	GGCCTTGCCA TCTCTCTCTC CGAGTGGACA TGGAGAGGAC GGGGGCCCAG CAGCTGGAIG	180
25	GCTGCAGGGG ATCAAGTCTT CTCTGGGGCT GGGCACGTAN AAGAGCATGT GGCTGGTGGA	240
	CGGCATGCCT GGCTCCTCAC CTGGCAGTCT GCCTGCCCTG CTAACCGGCT GTCTCTTGTT	300
30	CCCCTAGTGC CCTCGGCTAG CATGACCCGC CTGATGCGWT SCCGCACAGC CTCTGGTTCC	360
	AGCGTCATTG TCTGGATGGC ACCCGCAGCC GCTCCACAC CAGCGAGGGC ACCCGAAGCC	420
	GCTCCACAC CAGCGAGGGC ACCCGCAGCC GCTCGCACAC CAGCGAGGGG GCCCACCTGG	480
35	ACATCACCCC CAACTCGGGT GCTGCTGGGA ACAGNGCCGG GCCCAAGTCC ATGGAGGTCT	540
	CCTGCTAGGC GGCCTGCCCA GCTGCGGCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC	600
40	CTCCCCGGCC CCTTTTCGCC CCCTGCCTGC CATACTGCGC CTAACTCGGT ATTAATCCAA	660
	AGCTTATTTT GTAAGAGTGA GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC	720
	TCTCCAAAGG CGGGGTGGCG GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC	780
45	CTCTTCCATT AACCACTGGC CGGTGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAC	840
	GCCAAAACA AGACCGGTAC AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC	900
50	ATCCTGGTTC AAACGGGTGC CTGGTCAGAA GGCCAGCCGC CCACITCCCG TITCCTCTTT	960
	AACTGAGGAG AAGCTGATCC AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG	1020
	GGTAATAGTG ACATGCAGGC ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGGTG	1080
55	GGATTCATGT CGAGGCTAGA GGCAATTGGA ACAACAAATC TACGTAGTGA ACTTGAAGAA	1140
	ACCGATTTTT AAAGTGGTG CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT	1200
60	TTTTCTAGCA TCCTCTTAAT GTGCAGCAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG	1260

	ACAAAAATAT TTCAGCAAAC GTTGGGCATC ATGGTTTTTG AAGGCTTTAG TTCTGCTTTC	1320
	TGCCTCTCCT CCACAGCCCC AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG	1380
5	TTCAGGGAGA AGATCATTTA GATTTGTTTT GCATTCCCTA GAATGGAGGG CAACATTCCA	1440
	CAGCTGCCCT GGCTGTGATG AGTGTCTTG CAGGGGCCG AGTAGGAGCA CTGGGGTGGG	1500
10	GGCGGAATTG GGGTTACTCG ATGTAAGGA TTCCTTGTG TTGTGTGAG ATCCAGTGCA	1560
	GTTGTGATTT CTGTGGATCC CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC	1620
	AGTTTTCAAT CTTGACAGC TGGGCTGGAA CGTGAATCA GTAGCTGAAC CTGTCTGACC	1680
15	CGGTACGTT CTGTGATCCT CAGAACTCTT TGCTCTTGTC GGGGTGGGG TGGGAATCA	1740
	CGTGGGAGC GGTGGCTGAG AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT	1800
20	CCTTCCCTCT CTGTCTTCCT CTTTCTCTGC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC	1860
	CACTGACGTT TCTGGGCGGC CAGTCCGGCT GCCAGGTTC TGTACTACTG CCTGTACTTT	1920
	TTCATTTTGG CTCACCGTGG ATTTTCTCAT AGGAAGTTTG GTCAGAGTGA ATTGAATATT	1980
25	GTAAGTCAGC CACTGGGACC CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG	2040
	TCCAGCCTTC CAGGTGGCGT GAGAGGCAAT GACTCGTTAC CTGCCGCCCA TCACCTTGGA	2100
30	GGCCTTCCCT GGCCTTGAGT AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGACTACGGA	2160
	TGGGAAACTA TTGTGCACAA GTCTTTCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA	2220
	TTTCCAGACC AATAAATTG TAACCTTGCA AAAAAAAAA AAAAAAAAA AAAAAAAAA	2280
35	AAAAAAAAA AAAAAAACT CGAGGGGGC CCGTACCCAA TTGCCCGTAT ATGATCGTAA	2340
	ACAATC	2346
40		

(2) INFORMATION FOR SEQ ID NO: 194:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	TATCTGAACC ACCCTTTATT CTACATATGA TAGGCAGCAC TGAAATATCC TAACCCCTTA	60
55	AGCTCMAGGT GCCCTGTGGN ACGAGCAACT GGACTATAGC AGGGCTGGGC TCTGTCTTCC	120
	TGGTCATAGG CTCACTCTTT CCCCCAAATC TTCCTCTGGA GCTTTGCAGC CAAGGTGCTA	180
60	AAAGGAATAG GTAGGAGACC TCTTCTATCT AATCCTTAAA AGCATAATGT TGAACATTCA	240

	TTCAACAGCT GATGCCCTAT AACCCCTGCC TGGATTCTT CCTATTAGGC TATAAGAAGT	300
	AGCAAGATCT TTACATAATT CAGAGTGGTT TCATTGCCTT CCTACCCCTCT CTAATGGCCC	360
5	CTCCATTAT TTGACTAAAG CATCACACAG TGGCACTAGC ATTATACCAA GAGTATGAGA	420
	AATACAGTGC TTTATGGCTC TAACATTACT GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG	480
10	GATGGCAGCC TCAGGGCTTC CTTATGTCCT CCACCACAAG AGCTCCTTGA TGAAGGTCAT	540
	CTTTTCCCC TATCCTGPTC TTCCCCTCCC CGCTCCTAAT GGTACGTGGG TACCCAGGCT	600
	GGTCTTGGG CTAGGTAGTG GGGACCAAGT TCATTACCTC CCTATCAGTT CTAGCATAGT	660
15	AAACTACGGT ACCAGTGTTA GTGGGAAGAG CTGGGTTTTC CTAGTATACC CACTGCATCC	720
	TACTCCTACC TGGTCAACCC GCTGCTTCCA GGTATGGGAC CTGCTAAGTG TGGAATTACC	780
20	TGATAAGGGA GAGGGAATA CAAGGAGGGC CTCGTGTGTT CCTGGCCTCA GCCAGCTGCC	840
	CACAAGCCAT AAACCAATAA AACAAGAATA CTGAGTCAGT TTTTATCTG GGTCTCTTC	900
	ATTCCCACTG CACTTGGTGC TGCTTTGGCT GACTGGGAAC ACCCCATAAC TACAGAGTCT	960
25	GACAGGAAGA CTGGAGACTG*TCCACTTCTA GCTCGGAACT TACTGTGTAA ATAAACTTTC	1020
	AGAACTGCTA CCATGAAGTG AAAATGCCAC ATTTTGCTTT ATAATTTCTA CCCATGTTGG	1080
30	GAAAACTGG CTTTTTCCCA GCCCTTTCCA GGGCATAAAA CTCAACCCCT TCGATAGCAA	1140
	GTCCCATCAG CCTATTATT TTTTAAAGAA AACTTGCACT TGTTTTTCTT TTTACAGTTA	1200
	CTTCTTCTT GCCCAAAAT TATAAATCTT AAGTGTAATA AAAAGTCTTA ACAACAGCTT	1260
35	CTTGCTTGTA AAAATATGTA TTATACATCT GTATTTTAA ATTCGTCTCC TGAAAAATGA	1320
	CTGTCCCAT CTCCACTCAC TGCAATTGGG GCCTTTCCCA TTGGTCTGCA TGTCTTTTAT	1380
40	CATTGCAGGC CAGTGGACAG AGGGAGAAGG GAGAACAGG GTCGCCAACA CTGTGTGTGC	1440
	TTTCTGACTG ATCCTGAACA AGAAAGAGTA AACTGAGGC GCTCGCTCCC ATGCACAACT	1500
	CTCCAAAACA CTTATCCTCC TGCAAGAGTG GGCTTTCCAG GGTCTTTACT GGAAGCAGT	1560
45	TAAGCCCCCT CCTCACCCT TCCTTTTTC TTTCTTTACT CCTTTGGCTT CAAAGGATTT	1620
	TGGAAAAGAA ACAATATGCT TTCACTCAT TTTCAATTTC TAAATTGCA GGGGATACTG	1680
50	AAAAATACGG CAGGTGGCCT AAGGCTGCTG TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT	1740
	TACAAGATAA AAAACGAATC CCCTAAACAA AAAGAACAAT AGAACTGGTC TTCCATTTTG	1800
	CCACCTTTCC TGTTCAATGAC AGCTACTAAC CTGGAGACAG TAACATTTCA TTAACCAAAG	1860
55	AAAGTGGGTC ACCTGACCTC TGAAGAGCTG AGTACTCAG CCACTCCAAT CACCCTACAA	1920
	GATGCCAAGG AGTCCAGG AAGTCCAGCT CCTTAACTG ACGCTAGNCA ATAAACCTGG	1980
60	GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT CCATCTGTGA GGTGACAGGC AAGGATGAAA	2040

	GACAAAGAAG GAAAAGAGTA TCAAAGGCAG AAAGGAGATC ATTTAGTTGG GTCTGAAAGG	2100
	AAAAGTCTTT GCTATCCGAC ATGTACTGCT AGTACCTGTA AGCATTTTAG GTCCCAGAAT	2160
5	GGAAAAAAA ATCAGCTATT GGTAATATAA TAATGTCCTT TCCCTGGAGT CAGTTTTTTT	2220
	AAAAAGTTAA CTCTTAGTTT TTAATTGTTT AATTCTAAAA GAGAAGGGAG CTGAGGCCAT	2280
	TCCCTGTAGG AGTAAAGATA AAAGGATAGG AAAAGATTCA AAGCTCTAAT AGAGTCACAG	2340
10	CTTTCCCGG TATAAACCT AAAATTAAGA AGTACAATAA GCAGAGGTGG AAAATGATCT	2400
	AGTTCTGAT AGCTACCCAC AGAGCAAGTG ATTTATAAAT TTGAAATCCA AACTACTTTC	2460
15	TTAATATCAC TTGGTCTCC ATTTTCCCA GGACAGGAAA TATGTCCCCC CCTAACTTTC	2520
	TTGCTTCAAA AATTAAATC CAGCATCCCA AGATCATTCT ACAAGTAATT TTGCACAGAC	2580
	ATCTCTCAC CCCAGTGCCT GTCTGGAGCT CACCCAAGGT CACCAAACAA CTGGTTGTG	2640
20	AACCNACTG CCTTAACCTT CTGGGGGAGG GGGATTAGCT AGACTAGGAG ACCAGAAGTG	2700
	AATGGGAAAG GGTGAGGACT TCACAATGTT GGCCTGTCAG AGCTTGATTA GAAGCCAAGA	2760
25	CAGTGGCAGC AAAGGAAGAC TTGGCCCAGG AAAAACCTGT GGGTTGTGCT AATTTCTGTC	2820
	CAGAAATAG GGTGGACAGA AGCTTGTGGG GTGCATGGAG GAATTGGGAC CTGGTTATGT	2880
	TGTTATCTC GGAAGTGAA TTTTGGTGAT GTAAAACAGA ATATTCTGTA AACCTAATGT	2940
30	CTGTATAAAT AATGAGCGTT AACACAGTAA AATATTCAAT AAGAAGTCAA AAAAAAAAAA	3000
	AAAAAACTCG AGGGGGGGCC CGGTACCCAA TTTNCCAAAT AGAGATNGTA TTAC	3054
35		

(2) INFORMATION FOR SEQ ID NO: 195:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GGCAGAGCTC GTGGCCGNAA CTTTCTCTGC TCCTGGCTGC CACCTACTGG CTGGCCGCGG	60
50	CCCTGGCCTG GGCCTGCACC AGCCTGCGNG CGGGCTCCCA CAGCAGCCCC CTTCCAAGCA	120
	CGCTCCCCAC ACCGCGCACC TTCTGCGGGA ACGTGCTCGC CGTGCCGGGG ACCATATGGA	180
55	CGGAAGGCTT TGTGCTCACC TACAAGCTGG GTGAGCAGGG TGCCAGCAGC CTGTTGATCC	240
	TCTTGGCTCC TGCTGGAGCA CGAGCGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG	300
	TGTGGGTGCT GTGGTCTGCT CCATCGCTGG CTCCTCCCTG GGTGGGACCT TGCTGGCCAA	360
60	GCACTGGAAA CTGCTGCCTC TGTGAGGTCG GTGCTGCGCT TCCGCTCGG GGGCCTAGCC	420

5 TGTCTAGACTG CCTTGGTCTT CCACCTTGGA CACCTTGGG GCCAGCATGG ACGCTGGCAC 480
AATCTTGAGA GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GARGCCTGGT 540
CACCACAGTC ACCTTCACTG GGAATGATGC GCTGCAGCCA GCTGGCCCCC AGGGCCTTGC 600
AGGCCACACA CTACAGCCTT CTGGCCACGC TGGAGCTGCT GGGGAAGCTG CTGCTGGGCA 660
10 CTYTGGSCGG AGGGCCTGGC TGATGGGTG GGGCCACATC CCTGCTTCTT GCTCCTGCTC 720
ATCCTCTCTG CCTTTCCTG TCTGTACCTG GACCTAGCAC CCAGCACCTT TCTCTGAGCT 780
GAGTGGCTGG AGTGGTCAAT AAAGCCACAT GTGCCTGTGG CCCAAAAAA AAAAAAAAAA 840
15 AAAAAAAAAA AAAAAAAGT GAGGGGGGGC CCGGTACCCA AATCGCCGGA TATGATCGTA 900
AACAATC 907
20

(2) INFORMATION FOR SEQ ID NO: 196:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GGCACGAGGA GGGACAGGGA GTGGGCAAGG GGAAGAAGCA GCTTATTTGA CTAACCAGCC 60
35 CCTCTGTGGT CCACCAGCGT CTTGGCTTGG TGGGAGGGCT CTCAATCAGC AGGGCCCCAG 120
KAGGGCAAGA AGAAGTGGGG CAAAGCCTGG CGCTCGGCCG CGGTGCGGCG AGCTTTGCGA 180
TCTGGAGCCA CGCCTCCTCC AGGCCATGCT CCTTGAACCT GGAATGTCA ACCGGAGCCC 240
40 TTAACACCAG CCCTCCAGCA TCTAATAGAC TTGAATCTAC TCTAAACGAA TATTTAATCC 300
AACCTCAACT ACATTGTAGC TCAGTCCAAC GACTAACCCT GAAATGGGGG TGTTCAGCC 360
45 TTCAGCGAGA TGGCCAAGCG GTCCCTGGG GGCTGTGGCA GCGGGCTTAT CCTTCTCTGT 420
TGCCAACCTT GCCGTCCGAC CTCCTCCGCC CCCATGCGGT GACCCCGTCC GTGTCTGTGT 480
CTGTCCATAC GTGTGAGTCC AGCTAAAAG ACAAACAGA ACCCGTGGGC CCAGCTCGGA 540
50 AGGTGCGTGG AGAAGGCTCC GACGTCTCCG AAGTGCAGCC CTTGGGATGG CATTCCGTTG 600
TGTGCCTTAT TCCTGGAGAA TCTGTATACG GCTCGCCTAT AAGAAATATA GCCTCTTCAT 660
55 GCTGTATTAA AAGGACTTTT AAAAGCAAAA AAAAAAAAAA AAAAAGTGA GGGGGGGCCC 720
GGTACCCAAT TCGCCCAATA GTGAGTCGTA TTACAATTCA CTGGGCCGTC STTTTAACAA 780
CGTCGTGAAC TGGGAAAACC CTGGCGTTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC 840
60

CTTTGCGCAG CTGGCGTTAA TAGCGAAAAA NGCCCGCACC CGAATCGCCC TTCCCAACAG 900
TTTGCGCAGC CCTGAATGGC GAAATGGCAA ATGTGAAGCG TTTAATATTT TKKTAAAAAT 960
5 TCCNCGTTWA AWTTTTTGTT TAAATCARCT CAATTTTTTT AACCCAATAA GSCCGAAATC 1020
CGGCAAATCC CCYTTATTAA TTCCAAAAAA ATAAACCSAA AAWGGGTTTG AATTTTTTCT 1080
TTCCCCAYTT TTGGAACAA AWTYCCCCCT TTTTAAAAAA GTTGAACCC CCAMCCYTCC 1140
10 AAAGGGGAAA AAACSYTTTT YTGCGGGGNA ANGGGGCCCC CNTACTTTNA ACAYCCCCCC 1200
CCAAMCAATT TTTTGGGGG GTCCCNAAAG GTCCCCCTAA AANCTTTTTT CGGAACCCNA 1260
15 AGGGGANCCC CCCATTAAAA ATTTTNGGTN 1290

20 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

30 GGTGTCCTG GATGTCGTG TAGGTGAGTT TTACCAAGGA TTATGGTAAC AAATGAGTGA 60
GACCTCTATG GAGAAAATAT TGAAGNNCAT TAAAGAAGAC CTCATANTAG GAGAGAATGT 120
SCTTTGGAGG ATTTGTATTG AGCTTTTACA GTATTCATTT TTCAACTCAA GGCAATGGCT 180
35 TTCTACACCA ACTCTAATCC ATAAACGGGT CTTATGACAT CTATGAAGTA GTAGCAAGAC 240
ATGCTTAGTG TGTATTTCTC TCTTTGAGAC ACTGTAATTT CTACCAGAAA TTTCAGAGC 300
40 ATTATGTAGG TAGAAAAAAA TGCAAGCAAG CTGTTAAAGA TCTTGATCC CATTATATAG 360
TATGTATAGC TGAAATCTGT AATTCAATCA CTTTCTCT TTTATCCTCT AACCAGAAAA 420
45 TTGTTTAATT TTGCATCCCA AATGTTTTTA ATCTTTGTAT ATTTTTTAAA AAYCCTTTTC 480
TCCTCATCAT TGCCTTTTTT GTGGTGTAA ATAGACTTAC TTGCACTTTG AAGATGAGTT 540
ACTCCTTGTC ATCTTACAAA TATGTGATAT GGTAAATTTT ATAACAGATG TCAGTTTTGA 600
50 ACCAAGAATT GGTGATTTGT TTATAAGAAA AAAACTGGCT TCATTTCTGT GAAATTGCTC 660
TTTGAAAATT TCTTTTTTACA CGTGAAGCC AACTGAGATA CCGTGATGGT GTTGATTTCT 720
TTCAATGATG CTTACCATCT ATTTTAGCCA CTGAGCCTTT TATTATTTGT CTATTTGTAA 780
55 AGTTTATTTG TCTTAACTCA TTAAATAAAT ATACTGTTTA TCTGTTTCTG AATGGGGACT 840
GAACTTTTTG GATATTGATA TTGATTTGAA AATATTTTGG AATTTTTTCT ACTTGAAATT 900
60 TTAGAAATCT AATKGAAAAT TCTATAATGT ACTGAAAGTA WGGTTGTGTA CAGTGAKCAC 960

TCTCTAATAA TATGATGNCT TGCCCTAAAN GAGGNGGGAC ATGTCCCACT TTCCACCACG 1020

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(2) INFORMATION FOR SEQ ID NO: 198:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AATTCCCGAA GCTGAGGGTT GTGTGCCNTC GGGCGAGCCA AGTCTTTTGA CCGGACCCCTT 60
CCCCGCGCAG AAGANCTGAA GTTGATTGTA GAGCCTGTKT TTGGGGTTTRA GCCGAGCTGC 120
20 TGCGGGCTTY GTGCCCGGCC AGGACACAAG YTACTTGCAA CGGGGCGGCG CCTGGCTTAT 180
GATGTTCCCTC AACCCAGGGG CGGCCTCTGC CCTCTACTCG TGCCAGGCCC ACTTGCCAGG 240
25 CAGGAGCCCT CCCCAAGCCT TCAGGGCTGC TCGGAGTCAC CTGTTGGAAT GGACTAAAAG 300
GACCCTTGTC TGGGAACAGG TGCTCCAAAC ACCCTGCTGC TGGCTGCCAG GCAGGCCCTC 360
TGGAAGGGAA GGGGCAGGAC TCATCAGGAC CTCCTGGAC CCTGCAGGCG AGGCAGTTGG 420
30 CCCGAGCCCA AGCATTGGC TCTGCTGCC CCAAGGGGAC AGGAAGCCTC TTGGGCCTCT 480
TCCCTTCCTG GACAAGGCCC CCTGCCTTTG CCTCACATAA ACTG 524

35

(2) INFORMATION FOR SEQ ID NO: 199:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGATACAAG GAAGGGTGAT CATCATCTGT CACCATGCAA TTCTGCTCA CAGCCTTTCT 60
50 GTTGGTGCCA CTTCTGGCTC TTTGIGATGT CCCCATATCC CTAGGCTTCT CCCCTCCTA 120
GAAGGGCTTC TTGATAGATT AGAAAATAAG AATGAGTGAC ATTTCCTATG TGCATATAAG 180
AAGGAGCCAC AAGACATGTC TTTTAAATAA AAGGACAGTG TCCATCCTTT TAGCTGCCGA 240
55 ATAGAACCTT GGTCTCATCC TCCTGGAGCT AGGSCTTAAA ACAGCTTCTG TGTTTCTSAT 300
TKGTCTCART GTTTTGCCAA GGTTTTATTC GG 332

60

(2) INFORMATION FOR SEQ ID NO: 200:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

CCAGGGAAGC CCCARGCCTG TCCTGAATTG ACATCAGTGC TTCCTGAAC TGCCTCCCC 60
15 ACCCCTGGGC ATTATCCAG GAAACTTATG TTTTCTAGAA GCTAAGCAGC TGCTGGGACT 120
CAGGGACTGG TGCAGGTAGG CTGAGTGCCA GCTCAGTCTC AGAAGGTCTC TGAAGATCTG 180
GACTGAGGAC CYTGCTACTC CCCAAGCCAG AGCCCATCAG CCAGGCCTGC TGTGAGCCAC 240
20 CTGCCTGTGG AGTGCTGAGC TCAACCAAAG GCTGGCAAGC TCTGGGCCTC ATTTAAGGGA 300
TTCTGATGAG CCGATGGGCC CTGGAGCCAG CCCATTAAAG CATCTGGCTC GTTTMTGGAA 360
25 AAAAAAAAAA AAAAAG 376

30 (2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1192 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 CCCAGTATAT TTCTATAACA TTTATTTTAG TGAACCTATA ATGTTTCTTT GTATTAAATT 60
ATTAGATTAT ATCTTTAGAT AATATTGTTA CTNAATTAGT AGGTAATATA TATTTTATTC 120
AAAAATAAAT TGTGCATCTA ATGTCTACCA ATTAATGTAC TTGTAGATGT ATCTTATCTT 180
45 AACTTGAGTC TTTGCTGCCC CTAATGAGGT GTGAAGGACT CTTCTCCCCT GGGGAAGTTT 240
TTCTTTTTC A GGAGGGAGGA GGGCTTTCCC AGGTAATGTG TCTAGAGTGT TGGCAGAAR 300
50 AATCTGGGAC CACACCACAC CAGTTCTCTC CTTAATCCAC GTCATTTGCC TTCTATCCCA 360
GCTATGTTTC CAGTGTCTC TGGGTGTTTC CAAGAGCAAC AAGAAAYGAA TAAATCTCTG 420
KTGAGTTGTT TATTTGTTCT TCACTTGTTT TTACACTGTA WTTTCTGAGT TTATGGGTGT 480
55 CTGTGAATTA AAAAGGAAA GTRGAAATAA GTAAAACTCA GGTGAAGGA AATATACATA 540
AATAAGATAA AGCTGACCTG TAGATATARR CAGGTTATAA RAGCTTAGAG TTGTCTAAGT 600
60 TGRGTGCAAA KTTTCCTCTG ATCTTTCTGA TGCCGARACA AAAAAGGCAG TCATGTTTGT 660

5 WATGTGATTG GAATGGAACC CGARAAGAGA GCAYGCTGTG TTCTTGGGGA CAGGAAAGCT 720
 TGYGTGCACC AAGTCTKAAC CACCACCTTC ATGGGACATA GRITATGTGC TGGAACATAT 780
 TTCACACCGG CTGGGCAGTA AACACTTGTA GTGTTGTGCA GTGGAACGG TCATCTCCG 840
 CTAAAGCAG GCGTGTGTG CAGCGGAAAT GGTCACTGTC TGCTAAAACA CAGCTTCCAT 900
 10 CGTAATGTAT GCTCCTTACT CAAAGAGTGT GGTCCCAAAC AGCCTTGGG AGGTCCCTCT 960
 TGATTTCATG ATGAAACCTG GAACATCTTG AGGACTGAGT TAACCATAGG TCCTTAAATA 1020
 ACTCTCCACA CGTTTTTCTT AGTTTATCTC TACATGCAGG GTGTGCAGCA GCCTGTTCAA 1080
 15 AGTCATATTT TCTGGGAAAT ATTTCCAGTG TTTATTTGCA CTMTAGCCCA CTCGTGTGTAG 1140
 CCTTATTTCT TCTAAACTCA CCATTAATCT GAATAATAGT CAAATTTAGG GG 1192
 20

(2) INFORMATION FOR SEQ ID NO: 202:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

ATCTTGGGCT ATCTTTGACA GGGGATTCTT GCAAGTTGAT GCTTTCTACA AGTGAATATA 60
 35 GTCAGTCCCC AAAGATGGAG AGCTTGAGTT CTCACAGAAT TGATGAAGAT GGAGAAAACA 120
 CACAGATTGA GGATACGGAA CCCATGTCTC CAGTTCTCAA TTCTAAATTT GTTCCTGCTG 180
 AAAATGATAG TATCCTGATG AATCCAGCAC AGGATGGTGA AGTACAACG AGTCAGAATG 240
 40 ATGACAAAAC AAAGGAGAT GATACAGACA CCMGGATGA CATTAGTATT TTAGCCACTG 300
 GTTGCAAGGG CAGAGAAGAA ACGGTAGCAG AAGATGTTTG TATTGATCTC ACTTGTGATT 360
 45 CGGGGAGTCA GGCAGTCCG TCACCAGCTA CTCGATCTGA GGCACTTTCT AGTGTGTTAG 420
 ATCAGGAGGA AGCTATGGAA ATTAAGAAC ACCATCCAGA GGAGGGGTCT TCAGGGTCTG 480
 AGGTGGAAGA AATCCCTGAG ACACCTGTG AAAGTCAAGG AGAGGAACTC AAAGAAGAAA 540
 50 ATATGGAGAG TGTTCGTTG CACCTTCTC TGAAGTAAAC TCAGTCCCA 589

55

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 847 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5
GGCAGGAGCG CAAGCTGCTG GCCGCCATCA ACGCGTTCCG CCAGGTGCGG CTGAAACACC 60
GGAAGCTCCG GGAACAAGTG AACTCCATGG TGGACATCTC CAAGATGCAC ATGATCCTGT 120
10 ATGACCTGCA GCAGAATCTG AGCAGCTCAC ACCGGGCCCT GGAGAAACAG ATTGACACGC 180
TGGCGGGGAA GCTGGATGCC CTGACTGAGC TGCTTAGCAC TGCCCTGGGG CCGAGCAGCT 240
TCCAGAACCC AGCCAGCAGT CCAAGTAGCT GGACCCACGA GGAGGAACCA GGCTACTTTC 300
15 CCCAGTACTG AGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCAGCCTGAA CAAAGCACCT 360
CAAGTGCAAG GACCAAAGGG GGCCTGGCTT GGATGGGTG GCTTGCTGAT GGCTGCTGGA 420
20 GGGGACGCTG GCTAAAGTGG GGAGGCCTTG GCCCACCTGA GCGCCAGGT GGGAACATGG 480
TCACCCCCAC TCTGCATACC CTCATCAAAA AACTCTCAC TATGCTGCTA TGGACGACCT 540
CCAGCTCTCA GTTACAAGTG CAGGCGACTG GAGGCAGGAC TCTTGGGTCC CTGGGAAAGA 600
25 GGGTACTAGG GCGCCGGATC CAGGATTCTG GGAGGCTTCA GTTACCGCTG GCCGAGCTGA 660
AGAACTGGGT ATGAGGCTGG GCGGGGGCTG GAGGTGGCGC CCCCTGGTGG GACAACAAAG 720
30 AGGACACCAT TTTTCCAGAG CTGCAGAGAG CACCTGGTGG GGAGGAAGAA GTGTAATCA 780
CCAGCCTCTG CTCTTATCTT TGTAAATAAT GTTAAAGCCA GAAAAAAAAA AAAAAAAAAA 840
AAAAAAAA 847
35

(2) INFORMATION FOR SEQ ID NO: 204:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

ACAAACATAC TCGCAGGAAG GAGTCTCATG CTGCCCGCAG CATCAGCGCA ACNCNTGGCC 60
50 GCCATCAACG CGTTCCGCCA GGTGCGGCTG AAACACCGGA AGCTCCGGGA ACAAGTGAAC 120
TCCATGGTGG ACATCTCCAA GATGCACATG ATCCTGTATG ACCTGCAGCA GAATCTGAGC 180
55 AGCTCACACC GGGCCCTGGA GAAACAGATT GACACGCTGG CGGGGAAGCT GGATGCCCTG 240
ACTGAGCTGC TTAGCACTGC CCTGGGGCCG AGGCAGCTTC CAGAACCCAG CCAGCAGTCC 300
AAGTAGCTGG ACCCACGNAG GAGGAACCAG GCTACTTTCC CCAGTACTGA GGTGGTGGAC 360
60

ATNCGTCTCT TGCCACTCCN TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC 420
 AAAGGGGGCC CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC 480
 5 TAAAGTGGGK AGGCCTTGGC CCACCTGAGG CCCCAGGTGG GAACATGGTC ACCCCCACTC 540
 TGCATACCCT CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT 600
 TACAAGTGCA GCGCACTGGA GGCAGGACTC CTGGGTCCCT GGGAAAGAGG GTACTAGGGG 660
 10 CCCGGATCCA GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT 720
 GAGGCTGGG CGGGCYGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATT 780
 15 TTCCAGAGCT GCAGAGAGCA CCTGGTGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT 840
 CTTATCTTTG TA 852

20

(2) INFORMATION FOR SEQ ID NO: 205:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GATTGGGCAC GAGGCTTGCT GGAGCAGGAG AAGTCTCTRG CCGGTGGGC ACTGGTGCTG 60
 GCASGARCTG GCATTGGACT CATGGTGCTG CATGCAGAGA TGCTGTGGTT CGGGGGGTGC 120
 35 TCGGCTGTCA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 180
 CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGCAAGAT CGTYTGCTG 240
 40 TGCACTGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGCCCGTGGT GGCCCGGAAG 300
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACCTCA TGATGGATAT CCAGTATACC 360
 AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 420
 45 ACTCGCAGGA AGGAGTCTCA TGCTGCCCGC AGGCATCAGC GCAANCTGCT GGCCGCCATC 480
 AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 540
 50 GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 600
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 660
 CTGCTTAGCA CTGCCCTGGG GCCGAGGAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 720
 55 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 780
 CTGCCACTCC TGANCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC AAAGGGGGCC 840
 60 CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC TAAAGTGGGK 900

AGGCCTTGGC CCACCTGAGG CCCCAGGTGG GAACATGGTC ACCCCCACTC TGCATACCCT 960
CATCAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT TACAAGTGCA 1020
5 GCGGACTGGA GGCAGGACTC YTGCGTCCCT GGGAAAGAGG GYACTAGGGG CCCGGATCCA 1080
GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT GAGGCTGGGG 1140
10 CGGGGCTGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT TTCCAGAGCT 1200
GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACTCACC AGCCTCTGCT CTTATCTTTG 1260
TAATAAATGT TAAAGCCAGA AAAAAATAAA AAAAAAAAAA AAAAACTCG AGGGGGGCCC 1320
15 AGACCCAATC TCCCTATAGT AAGNCGCCNN ANAN 1354

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(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

30

TCCCCAGGTG CACAGCCAGG GCCCTCCTGT CTGCAGGAGA ATTCACAGCT GGTGTGGGAC 60
TCAGCCCTTA GNCATTCAA AGCCTTAATG TTGTAATCAT ATCTTACGTG TTGAAGACCT 120
35 GACTGGAGAA ACAAATGTG CAATAACGYG AATTTTATCT TAGAGATCTG TGCAGCCTAT 180
TTCTGTCAACA AAAGTTATAT TGTCTAATAA GAGAAGTCTT AATGGCCTCT GTGAATAATG 240
TAACTCCAGT TACACGGTGA CTTTAAATAG CATACAGTGA TTTGATGAAA GGACGTCAAA 300
40 CAATGTGGCG ATGTCGTGGA AAGTTATCTT TCCCGCTCTT TGCTGTGGTC ATTGTGTCTT 360
GCAGAAAGGA TGGCCCTGAT GCAGCAGCAG CGCCAGCTGT ANATAAAAAA TAATTCACAC 420
45 TATCAGACTA GCAAGGCACT AGAACTGGAA AAGACCACAG AAAACAAAGA ATCCAACCTT 480
TTCATCTTAC AGGTGAACAA ACTGTGATGA TGCACATGTA TGTGTTTGT AAGCTGTGAG 540
CACCGTAACA AAATGTAAAT TTGCCATTAT TAGGAAGTCC TGGTGGCAGT GAAGAAGCAC 600
50 CCAGGCCACT TGACTCCAG TCTGGTGCCC TGCTACACC AGACAACACA GGAGCTGGGT 660
CAGATTCCCC TCAGCTGCTT AACAAAGTTC CTCGAACAGA AAGTGCTTAC AAAGCTGCCT 720
55 TCTCGGATAC TGAAAGGTCG AGTTTCTGA ACTGCACTGA TTTTATTGCA GTTGAAAAA 780
AAAAAAGCT ATTCCAAAGA TTCAAGCTG TTCTGAGACA TCTTCTGATG GCTTTACTTC 840
CTGAGAGGCA ATGTTTTTAC TTTATGCATA ATTCATGTGT GCCAAGGAAT AAAGTGAAGA 900
60

AACAGCACCT TTTAATATAT AGGTCTCTCT GGAAGAGACC TAAATTAGAA AGAGAAAAC 960
GTGACAATTT TCATATTCTC ATTCTTAAAA AACACTAATC TTAAC TAACA AAAGTTCTTT 1020
5 TGAGAA TAAG TTACACACAA TGGCCACAGC AGTTTGCTCT TAATAGTATA GTGCCTATAC 1080
TCATGTAATC GGT TACTCAC TACTGCCTTT AAAAAAAAA ACCAGCATAT TTATTGAAAA 1140
CATGAGACAG GATTATAGTG CCTTAACCGA TATATTTTGT GACTTAAAA ATACATTTAA 1200
10 AACTGCTCTT CTGCTCTAGT ACCATGCTTA GTGCAATGA TTATTTCTAT GTACAACTGA 1260
TGCTGTCTT TATTTTAATA AATTTATCAG AGTGAAAAA AAAAAAAAAA AAAAAAAAAA 1320
15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGAA NAAAAANA 1378

20 (2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

30 AANCCACTGC ANMTTAAACC CCCTCCCTC CAAGAAAGTT CACAACCGGC CATGGATGAC 60
CCTCATTTTA GATGGGCCNC AATATTTAAG ATGGACTGRG GMCCCARAG ACTGACCTT 120
GAAAGGGGGA CTCAGAAGAA AGATCCTGA CATTGCCMAA CATGCTGGGC TTGTCCAACA 180
35 CAGTGATGCG GCTCATCGAG AARCGGGCTT TCCMAGGACA AGTACTTTAT GATAGGTGGG 240
ATGCTGCTGA CCGTGTGGT CATGTTCTC GTGGTGCACT ACCTGACATG AGCCAGCCAC 300
40 GCTCAGTGGC TGAACAGCAT TCCCACAGCC TGCAAGTGTG TGTGTGTGTG AAAGAGAGAG 360
GGGGCCAGA GGCCGCTTT TGAATGTTT GCCTGTCTGA ACTGTGAAGA CACTTGGGAG 420
TGATTGTGGT CTAATTTCCA ACCTGCTCTG TTTTCTGTGA CATCTTGAG GGGAGCTAG 480
45 TGCCAMCACC ATGCGCGGTG CTTAGGAAAT GAAAGAAGTC CCGGTCTGT CTCTCTCACT 540
CTCGCTCTCA MTGGGGGAGG GAAAGAATGG CTTTGGTGGC TTTGTTTACA CAGCTGATGC 600
50 GTGSCCTGGG AAGGTGTCCA CAGTGAGCCC TGTGTGCAGG ACTGTCCACN ACGGTTTACA 660
CCTGTTCACC ATCAGGCCTT TCTGGCTCCT GATAGGTGG AGCAAAAGTG GAAAGGAAAG 720
GAAAGAGGCY TTTTCTTACA GCCATTATAT TAAATAGTAG GTCGATTAC ATCYTCGTGC 780
55 TCCTGGCCAC CCTCCCTGT GCCTCAGTGA CATGTAGATG ACTGACTGCC AATACTTGTC 840
ACCATTCCTT GGAAGCAGCT ACCTAGGGGA AACAAGATGT AGTGCTATTG CCGATAACAA 900
60 GTAAGATTTT CCACACTACA GCTGGGTGTT TCTCTTTTCT AAAGTGAGGC CAGTGTATT 960

5 TCCCGGGAGT GTTCAGTCTT GACCCTAGTC ACTGATTTTT TCTAGTTGTT AATAGAGTGG 1020
TTGGGCTTTT AAGGTTTCAGA GACTGTGGGC TTGGGCACCT GCGCCCAGGG STTTTGTTGG 1080
GGCCTTTGCC CCTTAGRAAA GTAGCTTTTA GGGGCAAAGA TTTGTTGATT TTCCCCATTA 1140
CAGTCTTCAG CTCNAGGGTT TTAAAA 1166

10

(2) INFORMATION FOR SEQ ID NO: 208:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TACTTCTAGG ATTATAAGGA ATTAACATTG AGATGACATT TCCATTGAG AAGGAAAATA 60
25 GTTGCTTTCA GTGCCTTTA TTTGATTCTT GGAGAGAGCA GACTCGCACS AACATTCAAC 120
CCCAGCGCTG ATATGACAGT AATCCTCAGA GGCAGAGCCC AGCACAAAAC AGCAATGCTA 180
GAAAGTTACA ATTGGAAAGT TTCCTGCCAG CTTCGGGAAT GACACTGCAA AGCTGATGCC 240
30 AGAAACTGCC AGRGTAATTC TCCTCATTAC TGCTCTACCC ACCCACTTTC AGCTCCCCAA 300
ATTAAGTAGT GCAGTTGACT AATTCTCTTT ACCTTTATCA TTTARGGTGA RGCATTGCAC 360
35 AAAAAGTCTC GACTTTGCCA TATAAGGGCT GTGGTTCTCT GTGTTCCCTT GGATAAGAGG 420
CATCACCATT ATCTGGAAAC ATGCAGTAAA TGCAGATTNT TCATCTTCTC CCCAGACCTC 480
CTGAGTTAGA AATTCACAAG TTCTCCAGGT GATCTCATAC ATGCTAAAGT TTGAGAACCA 540
40 TTGAGTAAAG TTAATGCATT AAGAAGAGAT TAGATAGGGA TGGTGGCGTA TCTTCCTACA 600
GTTTCCCTGT TAACAAGAAA GTCAGAGGTC AGTTGATCAG ACATTAGATT ATTTATTGCT 660
45 AAAACTAAAA AAAATTAAAA AAAACTGGAG GGGGGCC 697

50 (2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 932 base pairs
55 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

60 CGTGAGTCAC CTCTCTATAG TGGGCGTGGC CGAGGCCGGG GTGACCCTGC CGAAGCCTCC 60

	GCTGCCAGAA ACCATGTICA AGGTAATTAA AAGGTCOCTG GGGCCAGCCA GCCTGAGCTT	120
	GCTCACCTTC AAAGTCTATG CAGCACCAAA AAAGGACTCA CCTCCCAAAA ATTCCGTGAA	180
5	GGTTGATGAG CTTTCACTCT ACTCAGTTCC TGAGGGTCAA TCGAAGTATG TGGAGGAGGC	240
	AAGGAGCCAG CTTGAAGAAA GCATCTCACA GCTCCGACAC TATTGCGAGC CATAACAAC	300
10	CTGGTGTGAG GAAACGTACT CCCAACTAA GCCCAAGATG CAAAGTTTGG TTCAATGGGG	360
	GTTAGACAGC TATGACTATC TCCAAAATGC ACCTCCTGGA TTTTTCCTGA GACTTGGTGT	420
	TATTGGTTTT GCTGGCCTTA TTGGACTCCT TTGGCTAGA GGTTCAAAAA TAAAGAAGCT	480
15	AGTGTATCCG CCTGGTTTCA TGGGATTAGC TGCTCCCTC TATTATCCAC AACAGCCAT	540
	CGTGTTCGCC CAGGTCAGTG GGGAGAGATT ATATGACTGG GGTTTACGAG GATATATAGT	600
20	CATAGAAGAT TTGTGGAAGG AGAACTTTCA AAAGCCAGGA AATGTGAAGA ATTCACCTGG	660
	AACTAAGTAG AAAACTYCAT GYTCTGCCAT CTTAATCAGT TATRGGTAAA CATTGGAAC	720
	TCCATAGAAT AAATCAGTAT TTCTACAGAA AAATGGCATA GAAGTCAGTA TTGAATGTAT	780
25	TAAATTGGCT TTCTTCTTCA GGAAAACTA GACCAGACCT CTGTTATCTT CTGTGAAATC	840
	ATCCTACAAG CAACTAACC TGAATCCCT TCACCTAGAG ATAATGTACA AGCCTTAGAA	900
30	CTCCTCATTC TCATGTTGCT ATTTATGTAC CT	932

35 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

45	GTCATTCTTT AAATAAAGC TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA	60
	AGATTCCTCC TAGGGTTGAT ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTTCA	120
	TTTTAAAGCT TTGGCTATAT AGTCAGAAAT GTCTTAAATA ACAAACTATT TTGTATTTAA	180
50	TTTAGGGAAG ACTAAGGGA AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT	240
	ATTAGGGCTT AAAGGGCTTT TCTAGTTTTA TGAGAAATTTG TACTACTGAT TTTTATATAT	300
55	TCCTGTTTTT GAGATGAACA GATCTCTGGG GAAATTGTTG AGTTACAATG GCATTTCACT	360
	GTGATCCCTC TCAAGCTCAG ATCAGTTCTA TAACCAATG ACAACCTGTC TCTTTGGTTT	420
60	ACTGTCTGT GAAATGTCAG CTCAAGTTTC CCAGAAGTCG TGTGTTTATG ATGAGTCAGA	480

GTGCTTTTCC TCGGTGGGAC AGTTGCTGGC CCTCTTAATT TTGGTGTATG TGCTTCCAAG 540
TATCTAAACC TCCAGTCTGA TCTGTATATG CTATCCTAAC TGTTAATTGT ATTATTGATT 600
5 ATGTTGATTA TCTTGCTTGA AGGTCATAC TTTTCAATTT GATAGAAATA AAGTTTTTTT 660
C 661

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(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GAAACTGACA TTGTTAAACA CACTAAAACA GAAGTACTTA CCTCTGAAG ATTAAATATA 60
TAATGGTTGA CATGATACAT GTACATGAAT GGAATGACCA GATGCTTATG GTCTACATTT 120
25 TCCTTTATCC TGTTAGTATT ACCTTCCTTA ATCTTTGTC CTTAACATGC TAAATCCCTC 180
TTCAGTGTIT ATTTTCTAGT GACAGAATGC TAACATTTCT TACACCCTGG CAGAAGGGAG 240
30 AGAAATGTGT TTTGGGTGG GTAACATAAT TTTTGAGTGA AATATCATAA GATGAGAATG 300
GAAAGAGGGA GACACAAAGA GTTATAACAA AAAACAATG GTTTTTTTAG CCATTTGACT 360
GGCTCTTTAA ATAGTCTACA AGACATTCAC GTTNAACATC ACTTTTAGTG AAATAAAATG 420
35 TGCCATACTA GTATGTGCTT CAAAAGGGCA AATGTGCTTT AGTGCCCTAA GGCTAAATTT 480
TGGTCATTTG ACATCAGAGA TGTGTAAAGT ATTGCACTTA ATACGCACCT ATTTCTCAAT 540
40 AGTGNATTTT TTTTGGCTAG CATTNCTTT ACCACTAACC TTGTTGATA GC 592

45 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 938 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

55 TGGAGTGGCT TTCCAGCTGA ATGAATCCTA TGTCTCGCGT GCAGGTGGTT GGTTTTCAAT 60
GTTCTTSCAT ATTTTTTCC TATTGGCTCT TGGGAGTTT CTTTGTTCG TCCTGTGTTT 120
GCCCAGCTTT AATAAAACCA GGCGCAAACA AAAACCATAG CATCTGAAA CAATAGGGGG 180
60

CCCACATTGG ACCCAGTATG TCACTTTAAT GGACTTCAAG AAAAAATCTG AATGGGAAAA 240
 TGACACTAGG AATGTATACT CCACACATTT TATGCCATAT AATGGTGTGT TTTCTTAATT 300
 5 TTGTTTCTTG TGGCGAAATG TGGCTTTCAA ATTAAATGM CCTTTTCTTC TTKGAAACTT 360
 TTTGTTTKGA CTKGATAAT TAAGGGTTTG GAAAGATTCA TAATTMTGAG AGAGGTTTGC 420
 AACCAGGAGA TACAAAGAAG TCTCAGTAGT AATCTGTTC ATGTGCTTTT ACAGCCAGCT 480
 10 ACATTTAAGR ATGTATTAGT TACAGAAATT ATATGTCTGT GTATGTGTCT CTACTCAATA 540
 AAGTACATGC CTCACATAA TGGGTGCTG TCCATCTCG CAAATACTGG CCAAGTCCCT 600
 15 TTATGACAGG CACACAGAAA CCATAGCATG GTCTGGCTTT CAGAAAATGC CTCTCATCTT 660
 TCCTGGAACC TTATTTTGCT AAATGTCTGT TTTCTGTGA TTTGTGTAC CTCACAGCAC 720
 CATTGTGACC ATGGTGATGC CTCATTTGCA TGATATGTAC CTGTGTGTTA ATGTGAAATA 780
 20 CATTTTCATT GAAGAGTCTG ATGACTTGCT AGCGTTTTAT TTTTCTGTA AGCTCAATGT 840
 GCTGAAACCA AACCAGGCTT TTAACAACT GTGTAGAAGA AAACCAAAAA ATCCTGTGTG 900
 25 GGTGTCCTTT CCCTGTCAA CTCATTAAAA ATTCCTTT 938

30 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

40 AGCCTGCCGG GAGAGTGGTG GCATCTRARA GGCTGGTCGT GGACTGTGGT TGGGGGAGGT 60
 GGGAGCTGTT TTAACCGTGT GCCCCCTCTC CTGTGCKKGC GTGGGCATCC CCCGGGGCAG 120
 TGGAAACGGG GCGCTCCTCC AGCTTCCGAG TCCAGCCAGC CTGGGCGCGG GGCGCGCCCC 180
 45 CGAGACACCC GAGGAGTCCG TTCCTCCCTG GTTACGTGGA CTGTGGAGCT GGTCTCTTGT 240
 GGCTCAGCGC CGTGCGGAGG TTGAAGCGTA CCTGCGGAGG TCGCACCAGG GGCCTGAGGA 300
 50 GGAGGAGGAA GGGCATGAGC CGAGCTTGAG GAATCCGTGY TCCAAACTCT AACTCAAGG 360
 RTGCMCTGCG CAACTCTGGT GCGCATGGGC TGGGGCAGAT GTCCTTGAG TTCTACCAGA 420
 AGAAGAAGTC TCGCTGGCCA TTCTCAGACG AGTGCATCCC ATGGGAAGTG TGGACGGTCA 480
 55 AGGTGCATGT GGTAGCCCTG GCCACGAGC AGGAGCGGCA GATCTGCCGG GAGAAGGTGG 540
 GTGAGAACT CTGCGAGAAG ATCATCAACA TCGTGGAGGT GATGAATCGG CATGAGTACT 600
 60 TGCCCAAGAT GCCACACAG TCGAGGTGG ATAACGTGTT TGACACAGGC TTGCGGGACG 660

TGCAGCCCTA CCTGTACAAG ATCTCCTTCC AGATCACTGA TGCCTGGGC ACCTCAGTCA 720
 CCACCACCAT GCGCAGGCTC ATCAAAGACA CCCTTGCCCT CTGAGCGTCG CTGGATCTCT 780
 5 GGGAGCTCCT TGATGGCTCC CAGACCTTGG CTTTGGGAA TTGCACTTTT GGGCCTTTGG 840
 GCTCTGGAAC CTGCTCTGGG TCATTGGTGA GACTTGAAG GGGCAGCCCC CGCTGGCTTC 900
 10 TTGGTMTTGT GGTTGCCAGC CTCAGGTCAT CCTTTTAATC TTGCTGACG GTTCAGTCCT 960
 GCCTCTACTG TCTCTCCATA GCCCTGGTGG GGTCCCCCTT CTTTCTCCAC TGTACAGAAG 1020
 AGCCACCACT GGGATGGGA ATAAAGTTGA GAACATGAGT TTGGGCTGAA AAAAAAAAAA 1079
 15

(2) INFORMATION FOR SEQ ID NO: 214:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TGAAGCAGGC GCTCTTGGCT CGGCGCGGCC CGCTGCAATC CGTGGAGGAA CGCGCCGCCG 60
 30 AGCCACCATC ATGCTTGGC ACTTACAGGA AGGCTTCGGC TGCCTGGTCA CCAACCGATT 120
 CGACCAGTTA TTTGACGACG AATCGGACCC CTTCGAGGTG CTGAAGGCAG CAGAGAACAA 180
 35 GAAAAAGAA GCCGCGGGG GCGGCGTTGG GGGCCCTGGG GCCAAGAGCG CATCAGGGCC 240
 GCGGCCGAGA CCAACTCCAA CGCGCAGGC AAACAGCTGC GCAAGGAGTC CCAGAAAGAC 300
 CGCAAGAACC CGCTGCCCCC CAGCGTTGGC GTGGTTGACA AGAAAGAGGA GACGAGCCG 360
 40 CCCGTGGCGC TTAAAGAAAG AAGGAATAAG ACGAGTTGA AGAAGACCTG ATCAACAAC 420
 TCAGGGTGAA GGGAAAATAA TTGATAGAAG ACCAGAAAGG CGACCACCTC GTGAACGAAG 480
 45 ATTCGAAAAG CCACTTGAAG AAAAGGTGA AGGAGGCCAA TTTTCAGTTG ATAGACCGAT 540
 TATTGACCGA CCTATTCGAG GTCGTGGTGG TCTTGAAGA GGTGAGGGG GCCGTGGACG 600
 TGGAATGGGC CGAGGAGATG GATTTGATTC TCGTGGCAA CGTGAATTG ATAGGCATAG 660
 50 TGGAAGTGAT AGATCTTCTT TTTCACATTA CAGTGGCCTG AAGCACGAGG ACAAACGTGG 720
 AGGTAGCGGA TCTCACAAC TGGGAACGT CAAAGACGAA TTAACGACT TGGATCAATC 780
 55 AAATGTGACT GAGGAAACAC CTGAAGGTGA AGAACATCAT CAGTGGCAG ACACIGAAAA 840
 TAAGGAGAAT GAAGTGAAG AGGTAAAGA GGAGGTCCA AAAGAGATGA CTTTGGATGA 900
 GTGAAGGCT ATTCAAAATA AGGACCGGGC AAAAGTAGAA TTAAATATCC GAAAACCAA 960
 60

	TGAAGGTGCT GATGGGCAGT GGAAGAAGGG ATTTGTTCTT CATAAATCAA AGAGTGAAGA	1020
	GGCTCATGCT GAAGATTCGG TTATGGACCA TCATTTCCGG AAGCCAGCAA ATGATATAAC	1080
5	GTCTCAGCTG GAGATCAATT TTGGAGACCT TGGCCGCCCA GGACGTGGCG GCAGGGGAGG	1140
	ACGAGGTGGA CGTGGGCGTG GTGGGCGCCC AAACCGTGGC AGCAGGACCG ACAAGTCAAG	1200
	TGCTTCTGCT CCTGATGTGG ATGACCCAGA GGCATTCCCA GCTCTGGCTT AACTGGATGC	1260
10	CATAAGACAA CCCTGGTTCC TTGTGAACC CTTCTGTTC AAGCTTTTGC ATGCTTAAGG	1320
	ATTCCAAACG ACTAAGAAAT TAAAAAATAA AAGACTGTCA TTCATACCAT TCACACCTAA	1380
15	AGACTGAATT TTATCTGTTT TAAAAATGAA CTTCTCCCGC TACACAGAAG TAACAAATAT	1440
	GGTAGTCAGT TTGTATTTA GAAATGTATT GGTAGCAGGG ATGTTTTCAT AATTTTCAGA	1500
	GATTATGCAT TCTTCATGAA TACTTTTGTA TTGCTGCTTG CAAATATGCA TTTCCAAACT	1560
20	TGAAATATAG GTGTGAACAG TGTGTACCAG TTTAAAGCTT TCACITCATT TGTGTTTTTT	1620
	AATTAAGGAT TTAGAAGTTC CCCCAATTAC AAACCTGGTT TAAATATTGG ACATACTGGT	1680
25	TTTAATACCT GCTTTCATA TTCACACATG GTCAACTGGG ACATGTTAAA CTTTGATTTG	1740
	TCAAATTTTA TGCTGTGTGG AATACTAACT ATATGTATTT TAACTTAGTT TTAATATTTT	1800
	CATTTTGGG GAAAAATCTT TTTTCACTTC TCATGATAGC TGTATATAT ATATGCTAAA	1860
30	TCTTTATATA CAGAAATATC AGTACTTGAA CAAATTCAA GCACATTTGG TTTATTAACC	1920
	CTTGCTCCTT GCATGGCTCA TTAGGTTCAA ATTATAACTG ATTTACATTT TCAGCTATAT	1980
35	TTACTTTTTA AATGCTGAG TTTCCCATTT TAAAACTAA ACTAGACATC TTAATTGGTG	2040
	AAAGTGTGTT AACTACTTA TTGTTGGTAG GCACATCGTG TCAAGTGAAG TAGTTTTATA	2100
	GGTATGGGTT TTTTCTCCCC CTTCAACAGG GTGGGTGGAA TAAGTTGATT TGGCCAATGT	2160
40	GTAATATTTA AACTGTTCTG TAAAAAAGT GTCTGGCCAT TTGGTATGAT TTCTGTGTGT	2220
	GAAAGGTCCC AAAATCAAAA TGGTACATCC ATAATCAGCC ACCATTTAAC CCTTCCTTGT	2280
45	TCTAAACAA AAACCAAGG CCGCTGGTIG GTAGGGTGG GTGGGGAGT ATTTTAATTT	2340
	TTGGAATTTG GGAAGCAGAC AGCTTTACTT TGTAAGGTTG GAACAGCAGC ACTATACATG	2400
	AAATATAAAC CAAAAACCTT TACTGTTTCT AAATTTCCCTA GATTGCTATT ATTTGGTTGT	2460
50	AAGTTGAGTA TTCCACAGAA AGTGGTAATT ATCTCTTCTC TCTTCCTCCA TTAGAAAAAT	2520
	AGGTAAATAA TGGATTCCCTA TAATGGGAGC ATCACCACCT ATTAACACAC ACATAGAATG	2580
55	ATGAATTAAA AAAGTTTCT AGGATGTCT TTTATTCTGC CACATTTATT GATAAACAGT	2640
	GAAGGAATTT TTAATAAAT TTAAGAATT GTTGTACAG TCATTTTATG AAATGTTCTA	2700
60	CCTGTATATG GTAATGTCCA GTTTTAAAAA TATTGGACAT CTTCAATCTT AAACATTTCT	2760

ATTTAGCTGA TTGGTTCTCA CATATACTTC TAAAAGAAAC TTTTATGTTA TAAGAGTTAC 2820
TTTTTGATA AGATTATTA ATCTCAGTTA CCTACTATTC TGACATTTTA GGAAGGAGGT 2880
5 AATTGTTTTT AATGATGGAT AAACCTGTGC TGGTGTMTTG GATCTTATGA TGCTGAGCAT 2940
GTTCTGCACT GGTGCTAATG TCTAATATAA TTTTATATTT ACACACATAC GTGCTACCCA 3000
GAGATTAATT TAGTCCATAT GAACTATTGA CCCATTGTTC ATTGAGACAG CAACATACGC 3060
10 ACTCCTAAAT CAGTGTGTTT AGACTTTTCA AGTATCTAAC TCATTTCCAA ACATGTACCA 3120
TGTTTTATAA ACCTCTTGAT TTCCAGCAAC ATACTATAGA AAACACCTGC TACTCAAAAC 3180
15 ACAACTTCTC AGTGTATCC ATTGCTGTGC TGAGAGACAA CATAGCAATA TCTGGTATGT 3240
TGCAAGCTTT CAAGATAGCC TGAACCTAAA AAGTTGGTGC ATTAGTTGTA TCTGATGGAT 3300
ATAAATTTGC CTCCTAGTTC ACTTTGTGTC AAGAGCTAAA ACTGTGAACC TAACTTTCTC 3360
20 TTATTGGTGG GTAATAACTG AAAATAAAGA TTTATTTTCA TGCTCACTTC TTAAAAGTCA 3420
TAAAAACAAT CAAATAGGRT CATGTTTATT GTCATGTGTT TCCTGGKTTT TGACCTGTGT 3480
25 GCACACCCCT GTGTGTTTAT AATTTTTTAA TTGAATTTTA TATGGGGTTT TTATTTGCTA 3540
AAAACCAGGC TGTGAATCA CATTTGGGAA GGTACTTAT CTTAATGACT AATGACTTAA 3600
TTGGGAAAGT TGAATTCTTG TAAAATACAA AATCCAAGGA CTCTTGGA TTTAATCTAA 3660
30 TTGTCACTTC NITAGGCAGA TNCACTTTTT TGGATAATGG AAAGTTAAGC ATACCGAATG 3720
CTACTTTTGG TTGACAAACG GGCCTAATAG TCCGGGGGGA AATCCCTAAC NGGTAAGGNT 3780
35 CCCAAGTATG G 3791

40 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

50 CAGTGCTCGC TCCTGCTCGG GCGCTGCGG CCGGGGCGT CGCCATGACC AGTGAGCTGG 60
ACATCTTCGT GGGGAACAGA CCCTTATCGA CGAGGACGTG TATCGCCTCT GGCTCGATGG 120
TTACTCGGTG ACCGACGCGG TGGCCCTGCG GGTGCGCTCG GGAATCCTGG AGCAGACTGG 180
55 CGCCACGGCA GCGGTGCTNC AGAGCGACAC CATGGACCAT TACCGCACCT TCCACATGCT 240
CGAGCGGCTG CTGCATGCGC CGCCAAGCT ACTGCACCAG YTCATCTTCC AGATTCCGCC 300
60 CTCCCGGCAG GCACTACTCA TCGAGAGGTA CTATGCCTTT RATGAGGCCT TTGTTGCGGA 360

	GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC CAAGAAAGAC CTGGATGACA TCAGCACCAA	420
	AACAGGCATC ACCCTCAAGA GCTGCCGGAG ACAGTTTGAC AACTTTAAAC GGGTCTTCAA	480
5	GGTGGTAGAG GAAATGCGGG GCTCCCTGGT GGACAATATT CAGCAACACT TCCTCCTCTC	540
	TGACCGGTTG GCCAGGGACT ATGCAGCCAT CGTCTTCTTT GCTAACAACC GCTTTGAGAC	600
10	AGGGAAGAAA AAAGTGCAGT ATCTGAGCTT CGGTGACTTT GCCTTCTGCG CTGAGCTCAT	660
	GATCCAAAAC TGGACCTTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT	720
	AGACAAGGAA TTTCTCCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT	780
15	TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC	840
	TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGGCTG GTGAACGTGG CCGCCAAGCT	900
20	GACCCACAAT AAAGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC	960
	CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTC TTCCTGAATC AGTATTCAGC	1020
	GTCTGTCCAC TCCCTCGATG GCTTCCGACA CCAGGCCCTCT GGGACCGCTA CATGGGCACC	1080
25	CTCCGCGGCT GCCTCCTGCG CCTGTATCAT GACTGAGGTG CCTCCCAACG CTCCGCCCAC	1140
	GCTGACAATA AAGTTGCTCT GAGTTTGAG ACTGGTCTC GCTCCGGGGA GCAAGTGGG	1200
30	GGCGTCAGA TGTGCTGTG TCTGTCTCTG AGCACCTGGT GTCCGTGTAC AAGGATGGAT	1260
	GTGTNCNGTG GCTCCTTGGG AACTGAGACA TATCTCAGGG AATGGTGTCT GTGCTCAGCC	1320
35	CATCCACCAG AAGA	1334

40 (2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

	GTGGCGGGGA TGCTGCGAGG GGGTCTCCTG CCCAGGCGG GCGGGCTGCC TACCCTCCAG	60
50	ACTGTCCGCT ATGGCTCCAA GGCTGTTACC CGCCACCGTC GTGTGATGCA CTTTCAGCGG	120
	CAGAAGCTGA TGGCTGTGAC TGAATATATC CCCCCGAAAC CAGCCATCCA CCCATCATGC	180
55	CTGCCATCTC CTCCAGCCC CCCACAGGAG GAGATAGGCC TCATCAGGCT TCTCCGCCGG	240
	GAGATAGCAG CAGTTTTCCA GGACAACCGA ATGATAGCCG TCTGCCAGAA TGTGGCTCTG	300
60	AGTGCAGAGG ACAAGCTTCT TATGCGACAC CAGCTGCGGA AACACAAGAT CCTGATGAAG	360

RTCTTCCCCA ACCAGGTCCT GAAGCCCTTC CTGGAGGATT CCAAGTACCA AAATCTGCTG 420
CCCCTTTTTG TGGGGCACAA CATGCTGCTG GTCAGTGAAG AGCCCAAGGT CAAGGAGATG 480
5 GTACGGATCT TAAGGACTGT GCCATTCTG CCGCTGCTAG GTGGCTGCAT TGATGACACC 540
ATCCTCAGCA GGCAGGGCTT TATCAACTAC TCCAAGCTCC CCAGCCTGCC CCTGGTGACG 600
GGGAGCTTG TAGGAGGCCT CACCTGCCTC ACAGCCGAGA CCCACTCCCT GCTCCAGCAC 660
10 CAGCCCCCTC AGCTGACCAC CTTGTTGGAC CAGTACATCA GAGAGCAACG CGAGAAGGAT 720
TCTGTATGT CGGCCAATGG GAAGCCAGAT CCTGACACTG TTCCGGACTC GTAGCCAGCC 780
15 TGTTTAGCCA GCCCTGCGCA TAAATACACT CTGCGTTATT GGCTGTGCTC TCCTCAATGG 840
GACATGTGGA AGAACTGGG GTCGGGGAGT GTGTTTGCA CTTGGTTTTC ACTAGTAATG 900
ATATTGTCAG GTATAGGGCC ACTTGGAGAT GCAGAGGATT CCATTTCAGA TGTCAGTCAC 960
20 CGGCTTCGTC CTTAGTTTTC CCAACTTGGG ACGTGATAGG AGCAAAGTCT CTCCATTCTC 1020
CAGGTCCAAG GCAGAGATCC TGAAGAGATA GGGCTATTGT CCCCTGCCTC CTGGTCACT 1080
25 GCCTCTTGCT GCACGGGCTC CTGAGCCACC CCCTTGGGGC ACAACCTGCC ACTGCCACAG 1140
TAGCTCAACC AAGCAGTTGT GCTGAGAATG GCACCTGGTG AGAGCCTGCT GTGTGCCAGG 1200
CTTTGTGCTG AGTGCTGTAC ATGTATTAGT TCCTTTACTG CTGACCACAT TGTACCCATT 1260
30 TCACAGAGAA GGAGCAGAGA AATTAAGTGG CTTGCTCAAG GTCATGCAGT TAGTAAGTGG 1320
CAGAACAGGG ACTTGAACCA AGCCCTCTGC TCTGAAGACC GCGTCTGAA TTTCTTCACT 1380
35 AGAGCTTCCT CATCAGGTTA CCCAGAAGTG GGTCCCATCC ACCATCCAGG TGTGCTTGGA 1440
TGTTAGTTCT CCACCCTCGA GGTGTACGCT GTGAAAAGTT TGGGAGCACT GCTTTATAAT 1500
AAAATGAAAT A 1511
40

(2) INFORMATION FOR SEQ ID NO: 217:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGGCCTTACT TTTCTCCCA CAAAGGAGTC GCAGCCACGC TAGCTCTGAC TTGCCACTGT 60
55 GACAAAGTTC ACGTAGCAGG TCTAGGCAAA GACTGGGCAA TTGAGCAGAG GAGACGGACC 120
TGTGAGTCTG ACCRYGAGSC GGRCCCTTC ACCTTGGCTG GGCTGGTCCT GGTCCTTAGG 180
60 TTTTGTGAGG TTGTCTTGT TTGGATCCCT CAACTAGGTG ATAAGCACTG GAGGGGGATG 240

ACCCGCCTTG GACGTGTTTC TTAACTCA TCCATATAAT AGGGCCGTGG GATGGTTGTA 300
5 GAGGTAAAGC AGGATGATGG TGTMTTAAGA CCAGAGCTTG GGACCAGGGC TCCTACACCT 360
AATTTTCTCT CCTGGTAGCT GAACAAAGGT CTAAATTAGC TTAACAAAAG AACAGGCTGC 420
CGTCAGCCAG AGTTCTGAAG GCCATGCTTT CAGTTTCCTT TGTGACAAT TGCTCTCCAG 480
10 TTCCTATGAA AGCACAGAGC CTTAGGGGGC CTGGCCACAG AACACAACCA TCTTAGGCCT 540
GAGCTGTGAA CAGCAGGGGG TTGTGTGCT GTTCTGTTTC TCTGCTTGCC GAACTTTCTC 600
AATAAACCTT ATTTCTTATT TTATATTAC GTNGGTGCTG GG 642
15

(2) INFORMATION FOR SEQ ID NO: 218:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGTCCCACTG TTCCATTMTA TGCTAATAGA TTCCATTCTA GGGCCAGCC GTCTCTTGAC 60
30 TGATGGTGTT CCCTTTAACC CTTGGCATGT ATAATAGAAT TTGGTGAAAT GAAAGAACCC 120
AAATAGGCCA GATAGTCCCC CCAGGCCCTG ATATCCATAA AAGGCTTGGG AATGCATTAT 180
35 GTAATGTGCC TTAGTCTTTT TGTGTTTTA GAAAAAAAA ACAAGATGGG CTCAGATGGA 240
TGCTACGTA AAAATGGTTC CTAGCTGTGT ACTCATAACT TTTCTTTGAA TTGAGTAGTG 300
AAAGGAAGGA GGAGGAAAGG AAATTAAATG TCCTTCTAGT ATTCTCTGGA CTCAAGTCTG 360
40 ACATATGRGA TAATAACCTA TATTGAAATG CCAAGAATTG TATCTGAAAC AAGRGAACAG 420
TTTGACACAT TTATCATGCC TTCATATTAC ATATTAACCTG AAACCAATTA ATAAACATAT 480
45 GAAATATCCA TGCACAAGG CAAAGGCACC TAAACCTTTT GTTCTTTT CTACATAGCA 540
GAAATTGATT TTTTPTTTAT TTTTPTAGGG GAACCTATAT AATTATGACC CAGTGATGTC 600
TTTGGTGAC TTAAGCTTAT GAATTCAGGT TACAATTGAG TTGATTCTAG ATGGTTACTA 660
50 CCTGAAAAG GATGTGGTG CTTATGTGA CACGAGCCAG AGCCTGCTGG GAATAAACAA 720
AGCAGATTCA TGCCAACACC AACTCGTAGC TTTAGTGGA GATGGGAGTG GTCACAGACT 780
55 CCCAAAATGT GGGGCTTTGG ATTTCCACAC CATCCACGT GTGTGTCATC TTCCTCTTTC 840
ACACTCTTGA TGATAATTG AAAATGRTGA AATCACCTCT GAATTGCCT ATAGCATGAG 900
CACATTCTTA TGACAACATA ACAAATAGTT CATAATGTGA ATATTAGAAA CTGTTACAGC 960
60

CTGCAGTTAC CATAATTTTC CATGTTTGTG GAATTGATAT TGAAATAGCA GGGCTAAGGA 1020
ATTACTGGCA AGTTTTCAGCC TGTGGGTAAT ACCTTAGGGT TATTTAAATA TTTGTAATTT 1080
5 TATTTAAATG TTCATGAATG TTTGAAAGGA ACAAATTAT CAGGGATGGC TCTTTGCCAT 1140
GGGTCTTATT TTCACCTCT TTTCTGTAAG AAAAAAGAAC AATGTCTTAA TGTATTTTAA 1200
AAGTTTTTGG TATAGTTTCT AATTCCAATT TTAATAAAG T 1241
10

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

TGTTTATGTG ACCTAAAACA TACACACATG CACACACACA TACATATCCA TTCATTCAAT 60
25 CATTCAGTGT GTGTTTCCAG TGTCTGTGTG TCACTGTTTA TGCAGTTTCC ATTTCCCACT 120
GAATTATGAG TGGAGGGCAA CTTTCTAAC CAGATTGTCT TTTCAGAACA AAGACCKGGG 180
30 RATTGAGGAA GAGTTTGGAA AGAGGGAGAG GCAAGGAAAG AGAGCTTTAA ATTGAAAGGT 240
TAATTTCTTA AGAGGAACCT GGGCTGAATG ACTACAGTGT TATACCTTCC AATCTTTGCA 300
GGTGGGCATG GAACACTGCT TGTATCACTC TGTGCACGGT ATAAATCCAT ATATCCACAA 360
35 AAACACACAT CCATCCATCA ACATATACAT GGTTTGGGAT GAGCAGGTCA ATAGTTTGA 420
GAGGGAGTTT GTTCCTTTT TTTTCTCATT ATACTCTTAA ATTGTTGTCA GTTATCAAAC 480
40 AAACAAACAG AAAAATGTGT TGGGAAAAAC CTTGCATACG CCTTTTCTAT CMAGTGCTTT 540
AAAATATAGA CTAAATACAC ACATCCTGCC AGTTTTTCT TACAGTGACA GTATCCTTAC 600
CTGCCATTTA ATATTAGCCT CGTATTTTTC TCACGTATAT TTACCTGTGA CTTGTATTTG 660
45 TTATTTAAAC AGGAAAAAAA ACATTCAAAA AAAGAAAAAT TAACTGTAGC GCTTCATTAT 720
ACTATTATAT TATTATTATT ATTGTGACAT TTTGGAATAC TGTGAAGTTT TATCTCTTGC 780
50 ATATACTTTA TACGGAAGTA TTACGCCTTA AAAATACGAA AATAAATTTT ACAAGGTTTC 840
TGTTTTGTGT GGAAGAGTAA TTGATGTTGC TAAGAATGAT GTTTGTTTTT TTGGGGTTTT 900
TGTGTTTTTT TTTTAAATG TTACCAGCAC TTTTMTGTGA AGTTTCACTT TCCGAGGTAT 960
55 TGTACAAGTT CACACTGTTT GTGAAGTTT AATATGAAGG AATAATTAAA AAAAAAAAAA 1020
AAACCNCGGG GGGGGCCCGG TCCCATTTGN CCCAAGGGGG CGGTTACGGG GTCACGGCCG 1080
60

(2) INFORMATION FOR SEQ ID NO: 220:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TGAATTGAGG GCTTAAAGAT AAACATATGG GRTTGGAGTT GTGTGTCCAT AGGGTTTCAC	60
15 TGCCTATTITG ATTTGAGTTT ATCCCTATTTA ATTTTITACA GTGAAATTTT ATTAAAGTAT	120
AATGTACATA TATTTTCAGT GGATTTTGCT CTGAAGGTTT TCCAGTGGTC TGACTACGAG	180
20 ATAGTCCGGC TTCAGCTGTG GGATATTGCA GGGCAGGAGC GCTTCACCTC TATGACACGA	240
TTGTATTATC GGGATGCCTC TGCCTGTGTT ATTATGTTTG ACGTTACCAA TGCCACTACC	300
TTCAGCAACA GCCAGAGGTG GAAACAGGAC CTAGACAGCA AGCTCACACT ACCCAATGGA	360
25 GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC AAGTGTGATC TGTCCCCTTG GGCAGTGAGC	420
CGGGASCAGA TTGACCGGTT CAGTAAAGAG AACGGTTTCA CAGGTTGGAC AGAAACATCA	480
30 GTCAAGGAGA AAAAAATAT TAATGAGGCT ATGAGAGTCC TCATTGAAAA GATGATGAGA	540
AATTCCACAG AAGATATCAT GTCTTTGTCC ACCCAAGGGG ACTACATCAA TCTACAAACC	600
AAGTCCTCCA GCTGGTCTG CTGCTAGTAG TGTITGGYTT ATTTTCCATC CCAGTTCTGG	660
35 GAGGTCTTTT AAGTCTCTTC CCTTTGGTTG CCCACCTGAC MATTTTATTA AGTACATTG	720
AATGTCTCC TGACTIONT CCAGTAAGGA GGCCCATTTG CACTTAGAAA AGACACCTGG	780
40 AACCCAKGTG CATTTCTGCA TCTCTGGAT TAGCCTTISA CATGTTGCTG RCTCACATTA	840
GTGCCAGTTA GTCCCTTCGG TGTAAGATCT TCTCATCAGC CCTCAATTG TGATCCGGAA	900
TTTTGTGAGA AGGATKAGAA ATCAGCACCT GCGTTTTAGA GATCATAATT CTCACCTACT	960
45 TCTGAGCTTA TTTTCCATT TGATATTCAT TGATATCATG ACTTCCAATT GAGAGGAAAA	1020
TGAGATCAAA TGTCAATTCC CAAATTTCTT GTAGGCCGTT GTTTCAGATT CTTTCTGTCT	1080
50 TGGAAATGTA ACATCTGATT CTGGAATGCA GAAGGAGGGG TCTGGGCATC TGTGGATTTT	1140
TGGCTACTAG AAGTGCCCA GAAGTCACTG TATTTTGAAC ACTTCTAACG TCATAATTAA	1200
GTCTCTCTG TCTTGGGCAT CAAGANTAGT TCCAATTTT TGGGCCGGGG CAGGGTGG	1258

55

(2) INFORMATION FOR SEQ ID NO: 221:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	CACAATATAT GAAATAGTAC CCTCTAAAAA AGAGAAAAAA AAAATCAGGC GGTCAAACCTT	60
10	AGAGCAACAT TGTCTTATTA AAGCATAGTT TATTTCACTA GAAAAAATTT AATATCAAGG	120
	ACTATTACAT ACTTCATTAC TAGGAAGTTC TTTTAAAAAT GACACTTAAA ACAATCACTG	180
15	AAAACCTGAT CCACATCACA CCCTGTTTAT TTTCTTAAA CATCTTGGAA GCCTAAGCTT	240
	CTGAGAATCA TGTGGCAAGT GTGATGGGCA GTAAAATACC AGAGAAGATG TTTAGTAGCA	300
	ATTAAAGGCT GTTTGCACCT TTAAGGACCA GCTGGGCTGT AGTGATTCTT GGGGCCAGAG	360
20	TGGCATTATG TTTTACAAA ATAATGACAT ATGTCACATG TTTGCATGTT TGTTCCTTG	420
	TTGAATTTTT GAACAGCCAG TTGACCAATC ATAGAAAGTA TTAATTTCTT TCATATGGTT	480
25	TTTGGTTTAC TGGCTTAAGA GGTTCCTCAG AATATCTATG GCCACAGCAG CATACCAGTT	540
	TCCATCCTAA TAGGAATGAA ATTAATTTTG TATCTACTGA TAACAGAATC TGGGTCACAT	600
	GAAAAAAAT CATTTTATCC GTCTTTTAAG TATATGTTTA AAATAATAAT TTATGTGTCT	660
30	GCATATTGCA GAACAGCTCT GAGAGCAACA GTTCCCATTT AACTCTTTCT GACCAATAGT	720
	GCTGGCACCG TTGCTTCCTC TTTGGGAAGA GGAAAGGGTG TGTGAACATG GCTAACAAATC	780
35	TTCAAATACC CAAATGTGA TAGCATAAAT AAAGTAITTA TTTTATGCCT CAGTATATTA	840
	TTATTTAATT TTTTAGGTAA TGCCTATCTC TTGGTCTATT AAGGAAAGAA GCAATCAGTA	900
	GAGAATTCAG GATAGTTTTG TTTAAATCTT TGCAGATTAC ATGTTTTTAC AGTGGCCTGC	960
40	TATTGAGGAA AGGTATTCCT CYATACAACT TGTTTTAACC TTTGAGAACA TTGACAGAAA	1020
	TTATGCAATG GTTTGTGTAG ATACGGACTT GATGGTGCTG TTTAATCAGT TTGCTTCCAA	1080
45	AGTGGCCTAC TCAAGAGGCC CTAAGACTGG TAGAAATTAA AAGGATTTCA AAAACTTTCT	1140
	ATTCTTTCT TAAACCTACC AGCAAACCTAG GATTGTGATA GCAATGAATG GTATGATGAA	1200
	GAAAGTTTGA CCAAATTGT TTTTGTGTG TTGTGTGTG TTTGAATTTG AAATCATTCT	1260
50	TATTCCTTTT AAGAATGTTT ATGTATGAGT GTGAAGATGC TAGCGAACCT ATGCTCAGAT	1320
	ATTCATCGTA AGTCTCCCTT CACCTGTTAC AGAGTTTCAG ATCGGTCACCT GATAGTATGT	1380
55	ATTTCMTAG TAAGAATGTG TTAATAATTAC AATGATCTTT TAAAAAGATG ATGCAGTTCT	1440
	GTATTTATTG TGCTGTGTCT GGTCTAAGT GGAGCCAATT AAACAAGTTT CATATGTATT	1500
	TTTCCAGTGT TGAATCTCAC AACTGTACT TTGAAAATTT CCTTCCATCC TGAATAACGA	1560
60	ATAGAAGAGG CCATATATAT TGCCTCCTTA TCCTTGAGAT TTCCTACCT TTATGTTAAA	1620

	AGTTGTGTAT AATTGTTAAA ATCTGTGAAA GAATAAAAAG TGGATTTAA. TTAAAAAAA	1680
	AAAAAAAA AAA	1693
5		
	(2) INFORMATION FOR SEQ ID NO: 222:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1196 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:	
	ACGCGTGGGT CGACCCACGC GTCCGCGACN TGGCGTGGTG GGAAGGGAG AAGGATTGT	60
20	AAACCCCGGA GCGAGGTTCT GCTTACCCGA GGCCGCTGCT GTGCGGAGAC CCCC GGGTGA	120
	AGCCACCGTC ATCATGTCTG ACCAGGAGGC AAAACCTTCA ACTGAGGACT TGGGGGATAA	180
25	GAAGGAAGGT GAATATATTA AACTCAAAGT CATTGGACAG GATAGCAGTG AGATTCACCT	240
	CAAAGTGAAA ATGACAACAC ATCTCAAGAA ACTCAAAGAA TCATACTGTC AAAGACAGGG	300
	TGTTCCAATG AATTCACCTCA GGTTCCTCTT TGAGGGTCAG AGAATTGCTG ATAATCATA	360
30	TCCAAAAGAA CTGGGAATGG AGGAAGAAGA TGTGATTGAA GTTTATCAGG AACAAACGGG	420
	GGGTCATTCA ACAGTTTAGA TATTCTTTTT ATTTTTTTTC TTTTCCCTCA ATCCTTTTTT	480
35	ATTTTTAAAA ATAGTTCCTT TGTAATGTGG TGTTCAAAAC GGAATTGAAA ACTGGCACCC	540
	CATCTCTTTG AAACATCTGG TAATTGAAT TCTAGTGCTC ATTATTCATT ATTGTTTGT	600
	TTCATITGTC TGATTTTTGG TGATCAAGCC TCAGTCCCCT TCATATTACC CTCCTCTTT	660
40	TAAAAATTAC GTGTGCACAG AGAGGTCACC TTTTTCAGGA CATTGCATTT TCAGGCTTGT	720
	GGTGATAAAT AAGATCGACC AATGCAAGTG TTCATAATGA CTTTCCAATT GGCCCTGATG	780
45	TTCTAGCATG TGATTACTTC ACTCCTGGAC TGTGACTTTC AGTGGGAGAT GGAAGTTTTT	840
	CAGAGAACTG AACTGTGGAA AAATGACCTT TCCTTAACTT GAAGCTACTT TTAATTTTG	900
	AGGGTCTGGA CAAAAGAAG AGGAATATCA GGTGGAAGTC AAGATGACAG ATAAGGTGAG	960
50	AGTAATGACT AACTCAAAG ATGGCTTCAC TGAAGAAAAG GCATTTTAAG ATTTTTTAAA	1020
	AATCTTGTC GAAGATCCCA GAAAAGTTCT AATTTTCATT AGCAATTAAT AAAGCTATAC	1080
55	ATGCAGAAAT GAATACAACA GAACACTGCT CTTTTTGATT TTATTTGTAC TTTTGGCCT	1140
	GGGATATGGG TTTTAAATGG ACATTGTCTG TACCAGCTTC ATTAAAATAA ACAATA	1196
60		

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

10 TCAGGGAGGT GGCAGGAAAG GCTTGGAACA GCTGCCGGAG TGACGGAGCG GCGGCCCCGC 60
CCGTTTGC GC TGGAGGTCTGA AGCTTCCAGG TAGCGGCCCG CAGAGCCTGA CCCAGGCTCT 120
15 GGACATCCTG AGCCCAAGTC CCCCACTC AGTGCACTGA TGAGTGCCTG AGTGAAGGTG 180
ACAGGGCAGA ACCAGGAGCA ATTCTGCTC CTAGCCAAGT CGGCCAAGG GGCAGCGCTG 240
20 GCCACACTCA TCCATCAGGT GCTGGAGGCC CCTGGTGTCT ACGTGTCTTG AGAAGTGTG 300
GACATGCCCA ATGTTAGAGA GCTGGCTGAG AGTGACTTTG CCTCTACCTT CCGGCTGCTC 360
ACAGTGTCTG CTTATGGGAC ATACGCTGAC TACTTAGCTG AAGCCCGGAA TCTTCCTCCA 420
25 CTAACAGAGG CTCAGAAGAA TAAGCTTCGA CACCTCTCAG TTGTCACCCT GGCTGCTAAA 480
GTAAAGTGTA TCCCATATGC AGTGTGCTG GAGGTCTTGC CCTGCGTAAT GTGCGGCAGC 540
30 TGAAGACCT TGTGATGAG GCTGTGTATG CTGACGTGCT TCGTGGCTCC CTGGACCAGC 600
GCAACCAGCG GCTCGAGGTT GACTACAGCA TCGGGCGGGA CATCCAGCGC CAGGACCTCA 660
GTGCCATTGC CCGAACCTG CAGGAATGGT GTGTGGGCTG TRAGGTCTG CTGTGAGCA 720
35 TTGAGGAGCA GGTGAGCCGT GCCAACCAAC ACAAGGAGCA GCAGCTGGGC CTGAAGCAGC 780
AGATTGAGAG TGAGGTGCC AACCTTAAAA AAACCATTA AGTTACGACG GCAGCAGCAG 840
40 CCGCAGCCAC ATCTCAGGAC CCTGAGCAAC ACCTGACTGA GCTGAGGGAA CCAGCTCCTG 900
GCACCAACCA GCGCCASCCA GCAAGAAAGC CTCAAAGGGC AAGGGGCTCC GAGGGAGCGC 960
CAAGATTGCG TCCAAGTCGA ATTGAAAGRA CTGTCTTTTC CTCCCTGGGG ATGTGGGGTC 1020
45 CCAGCTGCCT GCCTGCCTCT TAGGAGTCTT CAGAGAGCCT TCTGTGCCCC TGGCCAGCTG 1080
ATAATCCTAG GTTCATGACC CTTACCTCC CTTAACCCCA AACATAGATC ACACCTTCTC 1140
50 TAGGGAGGAG KCAAATGTAG GTCATGTTTT TGTGTTACT TTCTGTTTTT TGTGACTTCA 1200
TGTGTTCCAT TGCTCCCCGC TGCCATGCTC TCTCCCTTGT TTCTTAAGA GCTCAGCATC 1260
TGTCCCTGTT CATTACATGT CATTGAGTAG GTGGGTAGCC CTGATGGGGG TCGCTCTGTC 1320
55 TGGAGCATAA CCCACAGGCG TTTTCTGTC CACCCCATCC CTGCATGCCT GATCCCCAGT 1380
TCCTATACCC TACCCCTGAC CTATTGAGCA GCCTCTGAAG AGCCATAGGG CCCCCACCTT 1440
60 TACTCACACC CTGAGAATTC TGGAGCCAG TCTGCCATGC CAGGAGTCAC TGGACATGTT 1500

CATCCTAGAA TCCTGTCACA CTACAGTCAT TTCTTTTCCT CTCTCTGGCC CTTGGGTCCT 1560
GGGAATGCTG CTGCTTCAAC CCCAGAGCCT AAGAATGGCA GCCGTTTCTT AACATGTTGA 1620
5 GAGATGATTC TTCTTG GCC CTGCCATCT CGGAAGCTT GATGGCAATC CTGGAAGGGT 1680
TTAATCTCCT TTTGTGAGTT TGGTGGGGAA GGAAGGGTA TATAGATTGT ATTAAAAAA 1740
10 AAAAGGTATA TATGCATATA TCTATATATA ATATGACGCA GAAATAAATC T 1791

15 (2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

25 AACTAGTAGG ATCCAAAGAA TTCGGCACAG CGGCACAGCA TTGTTGAGCT TTCTGTGTG 60
TGTGGGGCCC TCAAGCGAGC TCGACTGGTC CATCTGGGG TAGCGASGTG GTGTTTGTGA 120
AAAAGGACGA TGCCATCACC GCATAYAAGA AGTACAACAA CCGGTGTCTG GACGGGCAGC 180
30 CGATGAAGTG CAACCTTCAC ATGAATGGGA ATGTTATCAC CTCAGACCAG CCCATCCTGC 240
TGCGGCTGAG TGACAGCCCA TCAATGAAAA AGGAGAGCGA GCTGCCTCGC AGGGTGAACT 300
35 CTGCCTCCTC CTCCAACCCC CTTCCCGAAG TGGACCCTGA CACCATCCTG AAGGCACTCT 360
TCAAGTCCTC AGGGGCTCT KTGACCACGC AGCCACAGA WTTCAAAATC AAGCTTTGAG 420
CAGGGGAGTR AGGCAGCCAG AAGTGGGGGC AGAGGAGGGT GGCTCTGTTT CCCCAAGGCA 480
40 AAGCTTATGA CCAATGGGCC ATCGGACTGG AGACCCTGA TTGTGGGAAG GGTGCCAGG 540
GATAAAGAGC TTCCTCACTG GATGGGACCC GCCTTTCTGT GTGTGTCTCT GCCCTGTGCT 600
45 CTCTCTCTA CGTTAACGTT TCCTGTAGTA TGTTCTTCA TCTCATCGCC AAGGTAGGCT 660
TGTTTMTM AGTGTGTGCC TCCCCGAGCC TCAGCCCCAA GCTGATTCT TATCTGGAAA 720
TGGTACACTG AATCTCTGG GTGGCTTCT TGTTGCCCCA TGGGATGCAG CGTGGGGCT 780
50 GTCTGAAGGA CCCTGCTTTT TCCAGGGGCC GAGGGGCTGC CTTCCTTTG TGTGTATTAA 840
GCTTTTCAA CAATGGAGGG GATGGAGAGC CTTGGTGTCC TGACGGGAGC CAGGTCCGCC 900
55 TGAGAGCTGT GCCCTCCTC TGTCTGTCA GTGGAGGTGC CTGGGTGGG AGCAGGTCTC 960
AGGCCTCTTG TCCTCTCCCC AGTGGCTCCA GGCCTCACTA GTGCCAAGG CAGGATGAGG 1020
CTGACCCGCT GGAAGAGTC TATCTAAGCT CTGGCTTGG AGTCCCGTGT CGTCTCCRCC 1080
60

CAGAGGAAGT TCTCCAGAGT TCACCTTTCC CTMTTCCTTG AGTTGTGCTG AATGCCCCAC 1140
 CCCAGCTCTC TTTCCTTCTT GGGTGTCTTT GCTGGGAGGG GGCTGTGTTG TGAGCCCTCC 1200
 5 CGGTTCACAC CTCGCCTGGC ACTTAACCAC ACCCTGGTTT TGTGTAGCCG CCAGCTCTCT 1260
 TCTGGTTGGG CCTTTGAAAG GCTCAGCCTC CCATTGTGCA GTGCTTGGGT TTGGAGCTTA 1320
 10 TTGAATGGA AGAGGTCAGT TTGTTCTGG CTCTCCATT TGGCCTCAG TTGTCTACAG 1380
 GACAGTGGTC AGGGATGCCT GGAGGCATAT ATCCAGCTGC CACCAAGGGG CACTGTTTGT 1440
 TCCCACTTAT GTGAGTGACC CCATCCATCC ATGACCAGAG GATTATTTTC CTGCCTTGGC 1500
 15 AGAGGAGGAG GAGTCAAGGG AGCAGGGCAG CTCTACCAGG CAAGGTGTTT CCCCAGCATA 1560
 GGCGCAGACA GTTGGGACGA AACTTCAGAG CCCAGGCAGT CCCTGAATGA CCAGGCCAGT 1620
 GTTGTCACTG AGTGGTCCCC TGCTGGTTGG GAGTGAAGAG AATCCAGGCT GGCAGAGCTG 1680
 20 GAGCCAGTTG GGGAGCACGG TTCTGGGAGC TCTGCAAAAT CAGTAGCAAG TGCTGGAAAA 1740
 GGCACATGCC GAAGATACTC AAGAGCTCCC AAGATTGCT TGAGGCTAGC CCAGTGAAAA 1800
 25 AAACCAGAGA CTCATGTTTC CAGGGGTCAG TCTGTCAGGC AGGAAGGACC CAGGATTTGA 1860
 ACCCAGCTTC AGTGTGCAGG CTCTGAGGCT GCCCAGGACG GGAAAGTCCA AGGAAGGGGC 1920
 CTGGTGGTGC TCCACTTGCA GTTCTTTAAA GAATGCTGCT TTTTATCTC CTAACCTTTT 1980
 30 CAAGTGGGTG CAGACTTCTC GTTAGCAGCT GGAAGACATT CCTCCACAC TTTTCCCTTC 2040
 CTGGCCCAAG AGAGCATCCA GAAGGCAGTA GGACCTGGTT TTTCAGGTAC TGGGAGCCGG 2100
 35 GGGTCACTG CTGCACTGT GCTTAGGGTA GGGATGGTAA ATATCCTCCC TGCATGGCTT 2160
 TATCCTCCCT CTCATCCCAA AGCAGGTATC TTCTGGTTGT CACAGAGTTT CATGAGTCC 2220
 AGCTGCAGCC ACGTGGCCAT CTGGAGCTGG TGCTATAGGT GACCATCTGG TACATTGAGG 2280
 40 GGACCTGTTT GCCTCCTCCA CTCTATAAGC AGTCATCTTG GGAGACCGGG AGGAGAAGGT 2340
 GGTGGGCTAG TCCTGTGTCC TCCTCCACTT CCCATGCCTC TATGTTACCC ATCTGTGTCT 2400
 45 CCTGTGCAGA AGGAGAGGAA GGGCATTAAG GAGATGAAGG GTGATTATGT ATTACTTATC 2460
 CATTTCTGAA TAAACATTG TTATTCTAA AAAAAAAAAA AAAAACTCG AGGGGGG 2517

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(2) INFORMATION FOR SEQ ID NO: 225:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

	TTGTANCTAA TCGAGGATTG ATTCTAATGA CAGAGTCTTT CAACACTTTG CACATGATGT	60
	ATCAGGAAGC TACAGCTTGC CATGTGACTG GAGATTTAGT AGAACTTCTG TCAATATTTT	120
5	TTTCGGTTTT GAAGTCTACA CGCCCTTATC TTCAGAGAAA AGATGTGAAA CAAGCATTAA	180
	TCCAGTGGCA GGAGCGAATT GAATTTGCCC ATAACTGTT AACTCTTCTT AATTCCTATA	240
10	GTCCCTCAGA ACTTAGAAAT GCCTGTATAG ATGTCCTCAA GGAACCTGTA CTTTGTAGTC	300
	CCCATGATTT TTTTCATACT CTGGTTCCCT TTCTACAACA CAACCATTGT ACTTACCATC	360
	ACAGTAATAT ACCAATGTCT CTTGGACCTT ATTTCCCTTG TCRAGAAAAT ATCAAGCTAA	420
15	TAGGAGGGAA AAGCAATATT CGGCCTCCGC GCCCTGAACT CAATATGTGC CTCTTGCCCA	480
	CAATGGTGA AACCAGTAAG GGCAAAGATG ACGTTTATGA TCGTATGCTG CTAGACTACT	540
20	TCTTTCTTA TCATCAGTTC ATCCATCTAT TATGCCGAGT TGCAATCAAC TGTGAAAAAT	600
	TTACTGAAAC ATTAGTTAAG CTGAGTGTC TAGTTGCCTA TGAAGGTTTG CCACCTTCATC	660
	TTGCACTGTT CCCCAACTT TGGACTGAGC TATGCCAGAC TCAGTCTGCT ATGTCAAAAA	720
25	ACTGCATCAA GCTTTTGTGT GAAGATCCTG TTTTCGCAGA ATATATTTAA TGTATCCTAA	780
	TGGATGAAAG AACTTTTTTA AACACAACA TTGTCTACAC GTTCATGACA CATTTCCCTC	840
30	TAAAGTTCA AAGTCAAGTG TTTTCTGAAG CAACTGTGC CAATTTGATC AGCACTCTTA	900
	TTACAACTT GATAAGCCAG TATCAGAACC TACAGTCTGA TTTCTCCAAC CGAGTTGAAA	960
	TTTCCAAAGC AAGTGCTTCT TTAATGGGG ACCTGAGGGC ACTCGCTTTG CTCCTGTCAG	1020
35	TACACACTCC CAAACAGTTA AACCAGCTC TAATTCCAAC TCTGCAAGAG CTTTTAAGCA	1080
	AATGCAGGAC TTGTCTGCAA CAGAGAACT CACTCCAAGA GCAAGAAGCC AAAGAAAGAA	1140
40	AAACTAAAGA TGATGAAGGA GCAACTCCCA TTAAGGGCG GCGTGTAGC AGTGATGAGG	1200
	AGCACACTGT AGACAGCTGC ATCAGTGACA TGAAAACAGA AACCAGGGAG GTCCTGACCC	1260
	CAACGAGCAC TTCTGACAAT GAGACCAGAG ACTCCTCAAT TATTGATCCA GGAACGAGC	1320
45	AAGATCTTCC TTCCCCTGAA AATAGTTCTG TTAAAGAATA CCGAATGGAA GTTCCATCTT	1380
	CGTTTTTCAA AGACATGTCA AATATCAGGT CACAGCATGC AGAAGAACAG TCCAACAATG	1440
50	GTAGATATGA CGATGTAAA GAATTTAAAG ACCTCCACTG TTCCAAGGAT TCTACCCCTAG	1500
	CCGAGGAAGA ATCTGAGTTC CCTTCTACTT CTATCTCTGC AGTTCTGTCT GACTTAGCTG	1560
	ACTTGAGAAG CTGTGATGGC CAAGCTTTGC CCTCCAGGA CCCTGAGGTT GCTTTATCTC	1620
55	TCAGTTGTGG CCATTCCAGA GGACTCTTTA GTCATATGCA GCAACATGAC ATTTTAGATA	1680
	CCCTGTGTAG GACCATTGAA TCTACAATCC ATGTCGTAC AAGGGATATC TGGCAAAGGA	1740
60	AACCAAGCTG CTTCTTGACA TTAGGTGTAG CATGTCTACT TTTAAGTCCC TCACCCCAA	1800

CCCCCATGCT GTTGTATATA GTTTTGCTTA TTTGTTTTTG TGCTTCAGTT TGTCCAGTGC 1860
 TCTCTGCTTG AATGGCAAGA TAGATTTATA GGCTTAATTC TTGGTCAGGC AGAACTCCAG 1920
 5 ATGAAAAAAA CTTGCATCTT CAGTATACTT CCTAAAGGGC AATCAGATAA TGGATATGTT 1980
 TTATGTAATT AAGAGTTCAC TTTAGTGGCT TTCATTTAAT ATGGCTGTCT GGAAGAACA 2040
 10 GGGTTGCCTA GCCTGTACA ATGTAATTTA AACTTACAGC ATTTTACTG TGTATGATAT 2100
 GGTGTCCTCT GTGCCAGTTT TGTACCTTAT AGAGGCAGAT TGCTCCGAT CGCTGTGGTT 2160
 CTTATTATCA AAATTAAGTT TACTTGTATA CGGAACAACC ACAAGAAATT TGATTCTGTA 2220
 15 AAGAATCCTC TTTAGCTGTG GCCTGGCAGT ATATAAATGG TGCTTTATTT AACAGAATAC 2280
 CTGTGGAGGA AATAAAGCAC ACTTGATGTA AAAATAATTG TTTTATTTTT ATTGACATGA 2340
 20 CTGATTGATT GCTATTCTGT GCACTNAATT AAAGTATTG TGATGACTTA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAA 2424

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(2) INFORMATION FOR SEQ ID NO: 226:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ATATAGGACG GATAATCTGT TTACATTCTG TTCTTCTCGA TGCACTCACA AGCGGGTAAC 60
 TAGGTGACAA GAAACAAG ATCTTATTCA AAAGAGTCT TACAGCAACC CAACGTCTCA 120
 40 TCTTCCATA GTAAAGATGA CGCGCCTTG AGGTAAGCTA CAGGCAACAC CACTCCGCG 180
 TTTCTCTTGC GCCCTGGTCC AAGATGCCCG ATGAAGCCAC GCGACGTGTT GTGTCTGAGA 240
 45 TCCCGGTGCT GAAGACTAAC GCCGGACCCC GAGATCGTGA GTTGTGGGTG CAGCGACTGA 300
 AGGAGGAATA TCAGTCCCTT ATCCGGTATG TGGAGAACAA CAAGAATGCT GACAACGATT 360
 GGTTCGGACT GGAGTCCAAC AAGGAAGGAA CTCGGTGGTT TGGAAAATGC TGGTATATCC 420
 50 ATGACCTCCT GAAATATGAG TTTGACATCG AGTTTGACAT TCCTATCACA TATCCTACTA 480
 CTGCCCCAGA AATTGCAGTT CTTGAGCTGG ATGGAAGAC AGCAAAGATG TACAGGGGTG 540
 55 GCAAAATATG CCTGACGGAT CATTTCAAAC CTTGTGGGC CAGGAATGTG CCCAAATTTG 600
 GACTAGCTCA TCTCATGGCT CTGGGCTGG GTCCATGGCT GGCAGTGGAA ATCCCTGATC 660
 TGATTCAGAA GGGCGTCATC CAACACAAAG AGAAATGCAA CCAATGAAGA ATCAAGCCAC 720
 60

TGAGGCAGGG CAGAGGGACC TTTGATAGGC TACGATACTA TTTTCCTGTG CATCACACTT 780
 AACTCATCTA ACTGCTTCCC CGGACACCCT CCACCTCTAG TTGTTACTAA GTAGCTGCAG 840
 5 TAGGCATTGC TGGGAAGAA ACAACACAC ACCAAACAGT ACTGCTACTT AGTTTCTAAG 900
 GCTGCACAGG GAAGGGAAG ACTGGGCTTT GGACAATCTA GAGGTAATTT ATATCCGCCC 960
 CCAGGTGGAG CAACATGCGA TTCTGGAGGC ACGGGGGTAA CTGAAAGTGA GTACATATAG 1020
 10 TCTTTCTGGT TTCTGGAGAT AACCCATCAA TAAAAGCTGC TTCTCTCTGG TAAAAAAG 1080

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

25 TTGCATTAC AATTACTGG AGGCAGGCAG GGCAGTTGC ATGCTGGGGG TGGCTGCATG 60
 GSCTGCCASC TCTCTGGGT TTGAAGGATG CGGTACASCT GCTTCAGCTG AGCAACGATG 120
 30 TTATCCTTGA TGTCTGGGT TGAGATCTGC AGGCGGACAC TGCCACTATC AAAGGATCGT 180
 GTGAAATCAC CAGAAAACAT CTCGTAGATC ATCCGAGCCA CTACTGGAAT GACCTGAACC 240
 AAGATGAGTT TCCTTTCCAA TGGTTTCCCA TCTGGCCATT CTTCCCCAAA GCATAAGTAG 300
 35 ATCTCAAACG GTGGCTGCTT CTCTATCTGT CCTTTCTGGT GGGCAATGAG ATCGCTAAGG 360
 AATGTTTCCA GACAAAATAG CTTGACCTTC TTTTGCTCT CAATCAGGTT GGGAGCAACA 420
 40 AGTGATGGGG CACATGGCCC AGACCAGTAC ACCTTGCACT GGCACAGYCT GATGGCATAA 480
 ATGGCATGAC CGCTGACCTC CAGGATCAGT CCTCTGTCCA TGACGTCCAG CAGCTTGCTA 540
 GTGAACAGCT TCTGCTTCTC ATTGGTAATA TGCTCAGGAC CTGGGAATTT GACCTGCTCC 600
 45 AGNCTGACGG GACCAAAGAG CTCTCCTCTG TCAGGCATGG GACCCAGGTC CCCATAGAAG 660
 AGTCGGCAGC CCTGAGGGTT GCTCACGGTC ATGGTCCTGC CCGTACTCCT TCCCACGGTA 720
 50 CTGAAACTTG ATGTCCAGGT CAGTCATTGG GAGAGAGCTG ATCCACAGTT CTGGAGAGCT 780
 ATAGAAGGRC TGTATAGGTG CCTGGGGWAC TTCCATCTCC AGGGGTTTCTG TTTTGGGCCA 840
 CACTGCCTCC GGSCTGCAGT TGCCACACT GCAATTGCCC AACTGGCTG GCGCCATGGG 900
 55 AGAACCATTG ATGTTTCAAGG AGGGGAAGGT GTCCTGGATG GGAACATGGT GCTGCGACTG 960
 ATCCAGCTCA TCTTCTCAT CTCTTTCATC CACATCATTA TCCTTCTCAT CCCAGGGAGC 1020
 60 AGACCTGTG GATCCTGGGT TAATGATCGA SCCCTGGGGC TGAGGGATGT CACACACTTG 1080

ATATATCTTC ACTGGGTTC TGGGCACCTC CCTTGGTGCC ATCCATACAT CCAGGTTGAA 1140
 TTCTCTGCTC TTATPGAGAG CACAGCGCAG CTGGGCCTTC CATTTAGCTG GGTGAGGGTC 1200
 5 ATCCACCCCT TCCTGGTACT TCCCTGTCTC TACAGCCCAG GCCTTAAAAA TGGTATTTTC 1260
 CTCTTCTGTG TGAGGGCTAT GCCGGGTGGC ATGTTTCCAG GGAATCTGGA AGCGTTTAGA 1320
 10 GTCCCTGTGT AGCCAG 1336

15 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

25 TCAGCTGGTC CCTTCCTTGT GTCCTGGGGG ACCTGCTGGC GGCCTCTTCC TGGGAGCCAT 60
 GACCTCAGAC CCCACCCACA CTCCAGATCG AGACCCCTGC CTCCCCCGG CAAATGTCTT 120
 CCCGCTGCCT TGCAGCCTGC ACTTTGCACA TGCTCAGCCC CAGCACAGTC CCACTGGCCC 180
 30 CTCAMCTCCC CTTCCCTGAG CTCCTTCCCA AGGACTCCTG GTCAGTGCCT GCTGTGCAKT 240
 CAGAGGCCCA GGGTCCAGCA GCCCGGGGGG AACGGGTGCT GCCTSTTCTT CCAGTTAGCT 300
 35 CCAGYTCAGG TCTGAGACCC GTGYTGAGTA AAGGTCTGAG CAMCGACCGT GCCCTCTGCC 360
 CAGGGCTGGG TCCTGAGCAG CTGGTTTTC TGCAGGAAGG TTGGAGCAAG CAAAGTCCTT 420
 CTCAGCCCTC AGGGTCAGCT GCCCAGACTG GGGCGGATGC AGAGAGGCAG GTGGGCTGTG 480
 40 GCTGGACTGG TCCGGAGCTG GCTTCCTTAC CAGAAAAGCC TCAGCCTTCC TCTGGAAGCA 540
 TCCCCCGTTC TGGGCAAGGG GGAAGGGCTC CTTTAAGGGG TGTGCTTTCC CAGTGGGGAG 600
 45 CAGTCTGGCC CTGCCCCCTA CTAAAGCCTC TGCTCTCAGC ACTTTCCCCC AAGTCCTTGT 660
 AACTTGCTTG AAGGTGGGTT CTGGCTGCCA GCCAGTCCCT GGACAAACTC TCCTGCCCTT 720
 TTTAAATTTC ACTCATTTTG TATAAACCCA GCAGGCTGGT GTTTACTTAG CCCTGTAGCT 780
 50 TTTTTCATTT TTTCTTCCG TCTTCTTCT TGAGTTCAGG GTTCAATATT GCCTCCTCGC 840
 CCTGGTGAGG GGAGGTGCTG CTTTCTTGCC CCACCTGCCG GCTGGTTCCA GCAGCGCTGG 900
 55 NGCCAGCTG GGGGGCCGG ATGGGGCTT CTCTCTCTG GAGGGGTGCA GGTGCCCTCC 960
 CCAGGCTGGG AGGGTTCCTT CCCTAGCTCC CCATCTGCCC CCGCTGGTGA GAGTTGGGCT 1020
 TCTTGGTCTT GGAACCTCCCT GGCATTGGGA ACAGAGCATT TCCAGCATTT GTTGTGTGTG 1080
 60

	TTTTACTCAC CTAACCCTTA GAAAATGAAT GTTAGAAGGT GCCTGCCGAG GCGGGACAGA	1140
	GTGTTTGCTC GCGCTGGAGA AGGCTCTGCT CAGCCCTGAG AGTCCCTTCC TGCCCCACCG	1200
5	ATACTGGCAC TTAAAAAGG AAGCTGACCG CACAGTGTC AGACGAATTG GCCCCAGAA	1260
	GATGGGGAGT TCTGTCCTGC CCTTCTGTGT CTGCGTGACC TCACCCAGCC TAGGAGGGAG	1320
10	GTGCATTGAG GGTAGATTTG CCTCTCATTC AAAGTTCTGG GGCTTTGGGY GGAAAACAGC	1380
	CAGCTTTGGC GCTGTTGGG AGACTCCTCC AGACCAGGAA CCCAGAAGG AGACAGAGCC	1440
	TGCCACATCC TCCCACGCC GGCCTGGGC CAGGGTGATT GGAAGTGAAG TTTGGCCACA	1500
15	ACCAAATTGA TGCTGGCTGG AACCAGAGGC CAGAAAGCCT GGCCTTGTC CCATGTGGGA	1560
	GCCCTGTCT CAGCCCTCTT GTCCCTTGA GTCAGTGAA TTCCCACCG GTGCCACAG	1620
20	CTCTGGACT TCAAATCTA TATATTGAGA GAGTTGGAGA GTATATCAGA GATATTTTG	1680
	GAAAGGAGTT GGTCTATGCA ATGTCAGTTT GGAATCTTCT TGAAAGTTA ATGTTTTTAT	1740
	TAGGAGATTT AAAGAAAATA AAGGTCTACA ATATCTTTAG GTTTTTTTTT TTTCTGTTT	1800
25	ACCGCACAAA CTGACCACAT GGCATGTCTA TCAGGATGGA GGTGTCCAT GTTCTCTCT	1860
	GTCTTTAGG AGGTGATAAG GAGATGGSCG RAGGGGTGTT TTTTCTTTG ACTCCCCTCC	1920
30	TTTCTAACAG AATGTTGCCA CCACTGCTTG AGTGGGCTGT GTTGTTCCT CTGTCCCAGC	1980
	TTCTGTGTGA GAAATAACA TTGTTAGGGG AACTCAGGCT AGTGTACCG TCTTGTTTG	2040
	GGG	2043
35		

(2) INFORMATION FOR SEQ ID NO: 229:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

	TAAAAAGAAG CGGGAGAATC TGGCGTCGC TCTAGAGATC GATGGGCTAG AGGAGAAGCT	60
50	GTCCAGTGT CGGAGAGACC TGGAGGCCGT GAACTCCAGA CTCCACAGCC GGGAGCTGAG	120
	CCCAGAGGCC AGGAGGTCCC TGGAGAAGGA GAAAAACAGC CTAATGAACA AAGCCTCCAA	180
55	CTACGAGAAG GAACTGAAGT TTCTTCGGCA AGAGAACCGG AAGAACATGC TGCTCTCTGT	240
	GGCCATCTTT ATCCTCCTGA CGCTCGTCTA TGCCTACTGG ACCATGTGAG CCTGGCACTT	300
	CCCCACAACC AGCACAGGCT TCCACTTGGC CCCTTGGTCA GGATCAAGCA GGCACATCAA	360
60	GCCTCAATAG GACCAAGGTG CTGGGGTGTT CCCCTCCCAA CCTAGTGTTC AAGCATGGCT	420

TCCTGGCGGC CCAGGCCTTG CCTCCCTGGC CTGCTGGGGG GTTCCGGGTC TCCAGAAGGA 480
CATGGTGCTG GTCCCTCCCT TAGCCCAAGG GAGAGGCAWT AAAGACACAA AGCTGGAAAT 540
5

(2) INFORMATION FOR SEQ ID NO: 230:
10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:
AATTGTGAAA TATTAGAATA TTGTTACTAT TTGACCCAAC TCAAAATCTC CATGGGAAAA 60
20 TACCTGTGCGA TACCCACAGT ATTGTTGAAA ATAATCAGAT GCAGTATCAC AGCTGTGTCA 120
GACTCTAGTA CCAGTTGGGC AATCAAGGCA CAGCTAAAAA TTGAAAACAA AGATCTGGAC 180
25 AACAAAACAG CCAAAGGTGG GGGTCAAGAA GCTCTGACGT GTACCTAGCT GTAGAATGCT 240
ATGCACACGT GCCAGGTGTA GTGTGCATAT CCAGGAAAAA CTGCAGAGAG CCCCAGTCTT 300
CAMCTCTGGT TGACCATGAG CTCTGTGTAA GCAGGAAGTG AAGGCTAAGG CAGATTTAAG 360
30 CTCTGAAAGC ATTCCACAAC ATACACACAA ATCGTGCAAA GCATTAAGGA AATCTTGTTA 420
CTGCTAAGTG TTGCTGACCC AGGAACAA 448
35

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:
GTATGCTGCC CCAAACCAAT ATGTGTGGCT GCCTTTWACC TGACTTCTCC AACATGTAGC 60
50 CCCAAGAGGA GGCTCTAGA CTRAGGGAGG GGCTGGTGAC CCAGGTGTGG TGGGGCTGCA 120
TGARACTACC AGAGAGACAG ACATTCTGGA ACTCACCCCTG GGGGATCCAG TGGATCTGCC 180
TATGGTCTGG TCCACCCCAG ACCTGTGAGA TGTTCCTCAT GAGGATGCAC TTGTGCTTCT 240
55 GCAAGTATTG CTGCAGCTTC ATAGTGACTC CCACCAGCAC CAGCAATACA GYTAGCTACC 300
TGTGGCCTTG GATCTCAGCC AGCATGGCTG GGAGAGGGAG CARCTGGGCA TGTACCCTAA 360
60 ATGCTGTTAC CAGGAAGGA CTCCCAGAGT GAAGACAAGT AGGGACT 407

5 (2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

15 GTATTTGATT TCAGGCTGCT AAATGGGCTC ATTTAGCATT CATTCTTGA TG TAGACATT 60
AAAAAAAAA CTGAATAGCA TTCTTTCCAG GNTAACTAAT AAAGCAGACA TGCTAAGCCT 120
ATAAATACAT CAGCACTGCA GCACACGTTT AAGGTTGCCA CGGACAAGGA TCACACAATA 180
20 GAGAACTCG TAGTTCGGTC TGCTCACAAG ACCCAGAACA TTGATCAGTT TTTGTTGTTG 240
GTTTATTATT TTCTGTAA AAAATTGTGA AAAGTTTGT TTAGCTAGAT GATATTTTAA 300
25 TAGCTGCGAG TGCTTTGGAA CTATAAGAT GTCACTACTT AACACACATA CCTTATGTTT 360
TGTTTGTGTT TGTTTACAC TCAGTATAAA TCAGGAGAAG TTAGCCAACC ATCTAGCATT 420
TAGAATCCTC TTTTTATTG TCTTCTAAGG ATATGGATGT TCCCATAACA GCAACAAAAC 480
30 AGCAACAAAA ACATTCATA AATATCACTT GATAGACTGT AAGCACCTGC TTAACTTTGT 540
GTNCCAAATA TTTAGTGTGT ATATATATAT ATATATACAC ACACACACAC ATATATATTC 600
35 AACAAATAAA GCAAAATATA ACATGCATTT CACATTTTGT CTTTCCCTGT TACGATTTTA 660
ATAGCAGAAC TGATGACAA GTTAGGTGA TCCTAGCATA TGTTAAATTC AAATTAATGT 720
AAAACAGATT AACAACAACA AAGAACTGT CTATTGAGT GAAGTCATGC TTTCTATTAT 780
40 AATAACTTGG CTTGGTTAT CCATCAAATG CACACTTATA CTGTTATCTG 830

45

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55 CCAGAAGAAA GACCAATCTA GAATATGGAA CTCTAATCAC TTCTAGTATT TCAACTTCCT 60
AGCAGAAATG AACTTGGCCC TAGACCTAGG GGATAAGCAA TGTTCTTTAT GTAGCCAATG 120
60 CTACGGAAAC AAAAGAGGTG AAAGAGACCC TTTTTTTATA CTTAATGTAC ATATATTGAC 180

5 TTTTIGAGCA AGAATGCCAG AAATAGCCTT CATTTCTACC CTGCAAAATA ATCCAGATCT 240
 GCTTCTCTAAA ATGRANTCAG TTTCTAAAGT GAAACATGCA ATATTTATGC TCTGACTGAC 300
 TCCTGAATTG GARGAGGAAG RACTTCTGTT TACAGAAAAC YGTATTGTTA TATATGTCAG 360
 GCTGTGTATT GTGACTATCA GCATTCTGGT GCAAATGAAC TTTTCTCCAT CATCGACTGT 420
 10 GGAAAATGA TACTTTTAAA GCATATTCTT CTATGAGCAC AGGTCCTCCT AGTGAAACTT 480
 AATTGACAA AGGGTGTCTAT ATGCTTTCTT AACCTGAWTT GTATTAACAT TCACAGAGCC 540
 TACATTTTCT CATTAGGGTT RTGATGCTCA GTATCTTTCC AAGTGCCAGG CAGRGCCTTC 600
 15 CTMTCTGAT CAAACATACC ATTTTTTGTA TTTCACAACT ATAGACAGTC ACTTCTGCAG 660
 TCCCAATTGA AAAATGCAGA ACTGCTTTAT CCAAGAATGC TGAAAAATAC TGTCTATCC 720
 20 AGGTTTCTTA AACTATAAAA GCAGATTTTG CTTTGTGTTG TTAATCATAG GCATGGCCGA 780
 GCATTGTGGA TTAGCTGAG GCTTAAAATC AGATGCATGT CTGGTAAGAT GACCACTGTC 840
 TCACTATCAA GAGCCTGCAG AGCCATTTTC CAGACCTGTG ATTGCCCAGA ACACATAGTC 900
 25 CCCACGTTTC TAATTGGAG CAAATCTAAA AG 932

30

(2) INFORMATION FOR SEQ ID NO: 234:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

TTAGCAGGGT GAGCTGTTAA AACAGCACAC ATCTCTCATC CCCTCTTCCT TTATTCCCCC 60
 CTGGGTTTCA GAAAGGAAGG ATATATGGGG ACCACCTCCC CCTTCTTTGA TCCCAGCATC 120
 45 TCAGTCCCCC TCCCAACCCT CCATATGGCT CTCAATGGTG CTCACTTGCT TGGAAGCAGG 180
 CTCCAATAG GGAGGGGSCT GCCCTCTACA GTCTCTTTGA CTGTAAGACA GGGCTCTGTA 240
 TCAGTGAGAC GATGAGAAAA GTCCCAGGCT AATGGCAGAA ATTTGCACTT TGAACATGTG 300
 50 TGTTTTGTG TTGTGGAACC TGAGATTCCT TATTTATTAA CAGGAAGTCT GATTTTTTTT 360
 TTTTGAGTC TTTGTTGCTA TATTTGTGG GGCTGGGAGA GAGAGATTAG ATTATTTTGA 420
 55 CATGGGATCC CTTCATAAC AGGTACTTTG AAGGCAAGAC ATAGGGTTGA AGAAGCACAA 480
 CCAGCCTCTG AATCATAGC TCTCCAGTGG CTTTAAAGA AAGCTGGTCC TCAGCACTAA 540
 CAAAATCACT ACAATAGCCT AGTGCTTTT TGGAAGCCTT TTAGGGAAG AATGTTAGGT 600
 60

	TCATGGTAAC TAGTATGCTC TTTGAGATTT TTACAGTGTT GAAACTTAAG AATTTTGAGA	660
	GGGTGAGGAG GGTGTTCAG AATCTAAATT ACAGATAGAT GATTGTTTCT TGTGAATTTG	720
5	TTTCTTTTCC TTTTMTTTG TCCCTACCAT TTCCTTACAT TTCCCTTGGG GCCCATCTCT	780
	GGCTCCCTGC TTTTGTTC TTTGCTTTGCT TTATCAGTTC ATTCCAGCTC CCTGTTAGTG	840
10	AAGGACACTG CTGTTAGTGA AGGAACAAAG TCTATGAGTC CTAATAATTTT AAGTCAAAGA	900
	AAACTGCTCT GTTCCCTTT TAGTAACACT TCTGAAGAGG AAAAATTCA ATAGCCAAAG	960
	TTAATAATCC TATATAATAA TTGCTTTGGC TTTCACCTAA AATTCTGGGC ATCACAATTT	1020
15	CCTTGGGATA GAGGTGTGT TGGGGAATAG ATTGCTTATT GCTGTTCACT GGAGAGAAAA	1080
	GGTAGTGT TTGTACAAG TCATACCGCC AGAAGCCCCA AATCCTATTT TGGCTCATCT	1140
20	TCAGGTAAAG AGTAATTCCT ATCCTGTGTG CCTCAGAAGC TAGAATCGAA GGCTTACCCT	1200
	ATTCAATGTT TATTGTGAGA AATGCATGAT GGCTCTTGA AAGAATGACG TTTTGCTGGA	1260
	AAAAAAAAA AGAACAGTTT GTGTTTCACA AACATGGCTT ATCAATTTTT TCAAAGAATT	1320
25	CTTTTTTCCC AAAAAGAGGA GTAACAAAT GTCATTTCTG AAAGAGGCTT ACTTTATACC	1380
	AACCTAGTGC AGCATTGGG ATGCCAGGA ACAGAGAGTG AGACACCTAC AATCACCAGT	1440
30	CICAAATGCG CTATTGTTTC TTTTCAGAGT GTTGCAGATT TGCCATTTCT CCATAATATG	1500
	GGGATAGAAA ATGGAATAAA GATAGAAGG ATGTAGAATA TGCTTTCTTG CCAACATGGT	1560
	TTGGAGTCGA CTTTGGTATA TTGACTAGAT TTGAAAATAC AAGATTGATT AGATGAATCT	1620
35	ACAAAAAGT TGTCTCCTC TCAGGTCCCT TTTACACTTT TTGACTAACT AGCATCTATA	1680
	TTCCACACTT AGCTTTTMTG TCACACTTAT CCTTTGTCTC CGTAAATTTT ATTTGCAGTG	1740
40	GTTAGTCATC AGATATTTTA GCCACCTACA CAAAAGCAAA CTGCATTTTT AAAAATCTTT	1800
	CTGAGATGGG AGAAAAATGA TTCTCCTTTC CTATACCGCT CTCCCAACAA AAAACAACCT	1860
	AGTAGTTCT ACTAATTAGA AACTTGCTGT ACTTTTCTTT TTCTTTTAGG GGTCAAGGAC	1920
45	CCTCTTTATA GCTACCATTT GCCTACAATA AATTATTGCA GCAGTTTGCA ATACTAAAAT	1980
	ATTTTTTATA GACTTTATAT TTTTCCTTTT GATAAAGGGA TGCTGCATAG TAGAGTTGGT	2040
50	GTAATTAAAC TATCTCAGCC GTTCCCTGC TTTCCCTTCT GCTCCATATG CCTCATTTGC	2100
	CTTCCAGGA GCTCTTTTAA TCTTAAAGTT CTACATTTCA TGCTCTTAGT CAAATTCTGT	2160
	TACCTTTTTA ATAACCTCTC CCACTGCATA TTTCATCTT GAATGGTGG TTCTAAATTC	2220
55	TGAAACTGTA GTTGAGATAC AGCTATTTAA TATTTCTGGG AGATGTGCAT CCTCTTCTT	2280
	KGTGGTTGCC CAAGGTTGTT TTGCGTAACT GAGACTCCTT GATATGCTTC AGAGAATTTA	2340
60	GGCAAACACT GGCCATGGCC GTGGGAGTAC TGGGAGTAAA ATAAAAATAT CGAGGTATAG	2400

ACTAGCATCC ACATAGAGCA CTTGAACCTC CTTTGTACCT GTTTGGGGAA AAAGTATAAT 2460
 GAGTGTACTA CCAATCTAAC TAAGATTATT ATAGTCTGGT TGTTTGAAAT ACCATTTTTT 2520
 5 TCTCCTTTTG TGTTTTTCCC ACTTTCCAAT GTACTCAAGA AAATGAACA AATGTAATGG 2580
 ATCAATTTAA AATATTTTAT TTCTTAAAAG CCTTTTTTGC CTGTTGTAAT GTGCAGGACC 2640
 CTTCTCCTTT CATGGGAGAG ACAGGTAGTT ACCTGAATAT AGGTGAAAA GGTATGTAA 2700
 10 AAAGAAATTA TAATAAAAGG GATACTTTCG TTTTCAAATC TTTGTTTTCT CTTATCTAG 2760
 GTAAGGCATA TAAAAATAA ATATGT 2786

15

(2) INFORMATION FOR SEQ ID NO: 235:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

GGGTGCAGGA ATTCGGCAGC AGAGAATGTT TGATTTTCTT TCCTATTTTA AGGATCTTCT 60
 30 CTCTTGTTGA TGTGAAAAC TTACCTTAGT GAAGATGTTT TTCAACATGC TGTGTCCTT 120
 TACCTGCATA ATCAGAGCTA TGCATCTATT CAAAGTGATG ATCTGTGGGA TAGTTTTAAT 180
 GAGGTCACAA ACCAAACACT AGATGTAAAG AGAATGATGA AAACCTGGAC CCTGCAGAAA 240
 35 GGATTTCTTT TAGTGACTGT TCAAAAGAAA GGAAAGGAAC TTTTATACA ACAAGAGAGA 300
 TTCTTTTAA ATATGAAGCC TGAAATTCAG CCTTCAGATA CAAGGTACAT GCCCTCTTTC 360
 40 TTTTCATGCC ATCTCTTTTG CACTCTCAGG TGGAAATATT TTTAAGTGT TTATAATCAT 420
 AAGTTCTTGT GAAACCTAAC AAGATTATCC CTTCTTAA 458

45

(2) INFORMATION FOR SEQ ID NO: 236:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AGGATGAAGA GGAAATTATC TCTTGATTG CTCTCCAGGA AATCCTTCTC TATACTTTAA 60
 AAGCTCTTGT TCTTTTCTAG GATCCAAATG TGCTGATTGC TGCTAACAGT CAGGGTACAA 120
 60

TTAAGGTGCT AGAATTGGTA TGAAGGGTTA ACTCAAGTCA AATTGTACTT GATCCTGCTG 180
 AAATACATCT GCAGCTGACA ATGAGAGARG AAACAGAAAA TGTCATGTGA TGTCTCTCCC 240
 5 CAAAGTCATC ATGGGTTTTG GATTGTGTTT GAATATTTTT TCTTTTTTTC TTKTCCCTCC 300
 TTTATGAGCC TTTGGGACAT TGGGAATACC CAGCCAACCTC TCCACCATCA ATGTAACCTC 360
 ATGGACATG CTGCTCTTGG TGGTGTATC TAATTMTTGT GATAGGGAAA CAAATTCTTT 420
 10 TGAATAAAAA TAAATAACWA AACAATAAAA GTTTATTGAG CCACAGTTGA GCTTGGAAAG 480
 TTTTGTCAA ATGCNGCAAG AGATAACTCT TTTTANGAAG TAGCATATGT GAACTATAAT 540
 15 GTAACAGTGA ATAATTGTA AAGTTCGTAT TTCCCAACCT CTTTGGGAAT T 591

20 (2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1286 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

30 TCTTTTAAAG GTACAGCAGG GAAGAACTGG AAATCAGAG AAAGAACTG CCCTTCCATC 60
 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 120
 GAGATTACCT GGGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGC 180
 35 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 240
 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTTCCTT CCAGGAGCTC CTCCTACTCA 300
 40 CCTTCCACCT CTTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 360
 TCCACCACCG GGTTTTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 420
 AGAAAGTGGA CATTCCTCTG GTTATGATAG TSGTCTGCA CGTGCAATTC CATATGGCAA 480
 45 TGCGATGAAG AACGATACAG ATACAGGGAA TATGCAGAAA GAGGTTATGA GCGTCACAGA 540
 GCAAGTCGAG AAAANGAAGA ACGACATAGA GAAAGACGAC ACAGGGAGAA AGAGGAAACC 600
 50 AGACATAAGT CTTCTCGAAG TAATAGTAGA CGTCGCCATG AAAGTGAAGA AGGAGATAGT 660
 CACAGGAGAC ACAAACACAA AAAATCTAAA AGAAGCAAAG AAGGAAAAGA AGCGGGCAGT 720
 GAGCCTGCCC CTGAACAGGA GAGCACCGAA GCTACACCTG CAGAATAGGC ATGGTTTTGG 780
 55 CCTTTGTGT ATATTAGTAC CAGAAGTAGA TACTATAAAT CTTGTTATTT TTCTGGATAA 840
 TGTTTAAGAA ATTTACCTTA AATCTTGTTC TGTTTGTTAG TATGAAAAGT TAACTTTTTT 900
 60 TCCAAAATAA AAGAGTGAAT TTTTCATGTT AAGTTAAAAA TCTTTGTCTT GTACTATTTT 960

AAAAATAAAA AGACAGCAAT GACTTTATAT CCAAGAAAGG AATGTGAATG AGTCACTTAA 1020
CAGGGAATCT AAAGAGCTGT GTTAGCTGTG TACATACACA GATTATCTGA GAAAAGGTCA 1080
5 AGGGTTCCAC TTGGGCCACA GTTTTMTTGT TAATCAAACA CCACTCTCTT AAGRGGCTGC 1140
ATCACAAARG GCAACCAARG GGCCCTCTT ARGGCTTTGA GGATTAAAC TAGTCITTTAT 1200
10 CCATTACTGC TGTGGACACT CTGGCTTTRG TATWTTTAGG GGGGNTCCTT ACCTTTTTTTT 1260
GGTTTTCCNC ACCTTTTTTG TTGGGC 1286

15

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ATGGCAGCGC AGAAGGACCA GCAGAAAGAT GCCGAGGCGG AAGGGCTGAG CGGCACGACC 60
CTGCTGCCGA AGCTGATTCC CTCCGGTGCA GGCCGGGAGT GGCTGGAGCG GCGCCGCGCG 120
30 ACCATCCGGC CCTGGAGCAC CTTCTGGGAC CAGCAGCGCT TCTCACGGCC CCGCAACCTG 180
GGAGAGCTGT GCCAGCGCCT CGTACGCAAC GTGGAGTACT ACCAGAGCAA CTATGTGTTT 240
35 GTGTTCTTGG GCCTCATCCT GTACTGTGTG GTGACGTCCC CTATGTTGCT GGTGGCTCTG 300
GCTGTCTTTT TCGGCGCCTG TTAACATTCT CTATCTGCCG ACCTTGGAGT CCAAGCTTGT 360
CCTCTTTGGC CGAAAGGTGA GCCCAGCGCA TCATATGCTC TGGCTGGAGG CATCTCCTTC 420
40 CCCTTCTTCT GGCTGGCTGG TGCGGGCTCG GCCGTCTTCT GGGTGTCTGG AGCCACCCTG 480
GTGGTCATCG GCTCCACGCG TGCTTTCCAC CAGATTGAGG CTGTGGACGG GGAGGAGCTG 540
45 CAGATGGAAC CCGTGTGAGG TGTCTTCTGG GACCTGCCGG CCTCCCGGGC CAGCTGCCCC 600
ACCCCTGCCC ATGCCTGTCC TGCACGGTCT GCTGCTCGGG CCCACAGCGC CGTCCCATCA 660
CAAGCCCGGG GAGGGATCCC GCCTTTGAAA ATAAAGCTGT TATGGGTGTC ATTCAAAAAA 720
50 AAAAAAAAAA AAAA 734

55

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5 CGGGGTCTTC AGGGTACCGG GCTGGTTACA GCAGCTCTAC CCCTCACGAC GCARACATGG 60
CAGCGCAGAA GGACCAGCAG AAAGATGCCG AGGCGGAAGG GCTGAGCGGC ACGACCCTGC 120
10 TGCCGAAGCT GATTCCCTCC GGTGCAGGCC GGGAGTGGCT GGAGCGGCGC CGCGCGACCA 180
TCCGGCCCTG GAGCACCTTC GTGGACCAGC AGCGCTTCTC ACGGCCCCGC AACCTGGGAG 240
AGCTGTGCCA GCGCCTCGTA CGCAACGTGG AGTACTACCA GAGCAACTAT GTGTTGCTGT 300
15 TCCTGGGCCT CATCTGTAC TGTGTGGTGA CGTCCCCTAT GTTGCTGGTG GCTCTGGCTG 360
TCTTTTTCGG CGCCTGTTAC ATTCTCTATC TGCGCACCTT GGAGTCCAAG CTTGTGCTCT 420
20 TTGGCCGAGA GGTGAGCCCA GCGCATCAGT ATGCTCTGGC TGGAGGCATC TCCTTCCCCT 480
TCTTCTGGCT GGCTGGTGCG GGCTCGGCCG TCTTCTGGGT GCTGGGAGCC ACCCTGGTGG 540
TCATCGGCTC CCACGCTGCC TTCCACCAGA TTGAGGCTGT GGACGGGGAG GAGCTGCAGA 600
25 TGGAACCCGT GTGAGGTGTC TTCTGGGACC TGCCGGCCTC CCGGGCCAGC TGCCCCACCC 660
CTGCCCATGC CTGTCTGCA CGGCTCTGCT GCTCGGGCCC ACAGCGCCGT CCCATCACAA 720
30 GCCCCGGGAG GGATCCCCGC TTTGAAAATA AAGCTGTAT GGTGTGCTT CAGGAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 809

35

(2) INFORMATION FOR SEQ ID NO: 240:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCGACCCACG CGTCCGGCAA CATGGCGGCT GCCGTGGTGC AGCGCCCGGG CTGAGCGACA 60
GCAAGTGCGAG CGGGCTCCTA CCCCGGGTGA GGGGTGGCCT CCGCGTGGGA TCGTGCCCTC 120
50 TTCAGCCCGC TCCTGTCCCC GACATCACGT GTATTCCGCA CGTCCCCTCC GCGCTGTGTG 180
TCTACTGAGA CGGGGAGGCG TGACAGGGCC CGGGTCCCTT CTCAGTGGTG CTCTGTGCTT 240
55 CAGGGCAAGC TCCCCGTCTC CGGGCGCACT TCCCTCGCCT GTGTTCGGTC CATCCTCCTT 300
TCTCCAGCCT CCTCCCCTCG CAGGCGGATG AMCCGGACGA CGGGCCAGTG CCTGGCACCC 360
CGGGGTGCCC ARGGTCCAMG GGAACCCGA AGTCCGAGGA GCCCGARGTC CCGAACCAGG 420
60

	ARGGGCTGCA GCGCATCAMC GGCCCTGTCTC CCGGCCGTTT GGCTCTCATA GTGGCGGTGC	480
	TGTGCTACAT CAATCTCCTG AACTACATGG ACCGCTTCAC CGTGGCTGGC GTCCTTCCCG	540
5	ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG ACCGTGTTC	600
	TCTCCAGTTA CATGGTGTGT GCACCTGTGT TTGGCTACCT GGGTGACAGG TACAATCGGA	660
10	AGTATCTCAT GTGCGGGGC ATTGCCTTCT GGTCCCTGGT GAACTGGGG TCATCCTTCA	720
	TCCCCGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTGCGGGAGG	780
	CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGGA	840
15	CCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG GCTACATTGC	900
	AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG TGACACCGGG	960
20	TCTAGGAGTG GTGGCCGTTT TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC CAAGGGGAGC	1020
	CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGGG CAGATCTGAG	1080
	GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG CTGTGGCCTT	1140
25	TGTCACGGGC TCCCTGGCTC TGTGGGCTCC GGCATTCTCG CTGGGTTCCT GCGTGGTCTT	1200
	TGGGGAGACC CCACCCCTGC TTCCCGGAGA CTCCTGCTCT TCCTCTGACA GTCTCATCTT	1260
30	TGGACTCATC ACCTGCCTGA CCGGAGTCTT GGGTGTGGGC CTGGGTGTGG AGATCAGCCG	1320
	CCGGCTCCGC CACTCCAACC CCCGGGCTGA TCCCTTGGTC TGTGCCACTG GCCTCCTGGG	1380
	CTCTGCACCC TTCTCTTCC TGTCCCTTGC CTGCGCCCGT GGTAGCATCG TGGCCACTTA	1440
35	TATTTTATC TTCTATTGAG AGACCTCCT GTCCATGAAC TGGGCCATCG TGGCCGACAT	1500
	TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACCGCC GAGGCCTTCC AGATCGTGCT	1560
40	GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT CTGACCGCCT	1620
	GCGCCGAAC TGGCCCCCTT CTTCTTTGTC CGAGTTCCGG GCTCTGCAGT TCTCGCTCAT	1680
	GCTCTGCGG TTTGTTGGG CACTGGGCGG CGCACTTTC TGGGCACCGC CATCTTCATT	1740
45	GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC	1800
	ACAGACGACC GGATTGTGGT GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT	1860
50	GTGCTCATCT GAGARGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT GGCCCTGGGC	1920
	CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA GAGGGACCCT	1980
	GGCCCGTGTG CCAGCTCCCA GAACTACMT GGTAGCTCA GGGGAGGAGG TGGGGGTCCA	2040
55	GGAGGGGAT CCTCTCCAC AGGGGAGCC CCAAGGGCTC GGTGCTATTT GTAACGGAAT	2100
	AAAATTTGTA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG CCTCTGATCT	2160
60	TGCACCCCGT CTTCAACCCA GGGCTCCTGA AGACTGTGGG T	2201

(2) INFORMATION FOR SEQ ID NO: 241:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

15 GTCCCTCCCG ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG 60
ACCGTGTTCA TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG 120
TACAATCGGA AGTATCTCAT GTGCGGGGGC ATTGCCTTCT GGTCCCTGGT GACACTGGGG 180
20 TCATSCITCA TCCCCGGAGA GCATTTCCTG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG 240
GTGCGGGAGG CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTTGGC 300
GACCAGCGGA SCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG 360
25 GCTACATGCG AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG 420
TGACACCGGG TCTAGGAGTG GTGGCCGTTC TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC 480
30 CAAGGGGAGC CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACCC TCGTGGTGGG 540
CAGATYTGAG GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG 600
CTGTGGCCTT TGTACGGGC TCCCTGGCTC TGTGGGCTCC GGCATTCTTG CTGCGTCC 660
35 GCGTGGTCTT TGGGAGACC CCAACCTGCC TTCCCGAGA CTCTGCTCT TCCTCTGACA 720
GTCTCATCTT TGGACTCATC ACCTGCCTGA CCGGAGTCTT GGTGTGGGC CTGGGTGTGG 780
40 AGATCAGCCG CCGGYTCCGC CACTCCAACC CCCGGGCTGA TCCCTGGTC TGTGCCACTG 840
GCCTCCTGGG CTCTGCACCC TTCTCTTTC TGTCCCTTGC CTGCGCCCGT GGTAGCATCG 900
TGGCCACTTA TATTTTCATC TTCATTGGAG AGACCTCTCT GTCCATGAAC TGGGCCATCG 960
45 TGGCCGACAT TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACCGCC GAGGCCTTCC 1020
AGATCGTGCT GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCTTGATCT 1080
50 CTGACCCCTT GCGCCGGAAC TGGCCCCCTT CCTTCTTGTG CGAGTTCGG GCTCTGCAGT 1140
TCTCCCTCAT GCTCTGCGCG TTTGTTGGGG CACTGGGCGG CGCACTTTCC TGGGCACCGN 1200
CATCTTCATT GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA 1260
55 AGCAGGGTCC ACAGACGACC GGATTGTGGT GCGCCAGCGG GCGCGCTCCA CCCGCGTGCC 1320
CGTGCCAGT GTGCTCATCT GAGAGGCTGC CGCTACCTA CCTGCACATC TGCCACAGCT 1380
60 KGCCCTGGGC CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA 1440

5 GAGGGACCCT GGGCCGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG 1500
TGGGGGTCCA GGAGGGGGAT CCTCTCCAC AGGGGNCACC CCAAGGGCTC GTGCTATTT 1560
GTAACGGAAT AAAATTGTGTA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG 1620
CCTCTGATCT TGCACCCCGT CTTCACCCCA GGGCTCCTGA A 1661
10

(2) INFORMATION FOR SEQ ID NO: 242:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

NGACAGAAAA GCAGAAGATG AGACTCTGTT CATTCACTTT TCCTAGGCC ATCCTGTGGT 60
25 CATCTTTCCC CCTCCCATCA TACCTCCTCC TTCTGGAGC CTCTGCCGGC TTGGCTGTAA 120
TGGTGGCACT TACCTGGATA TTTCAGTGGG AGGATGAAAG GCGAGACTCA CCCTACGGG 180
TGGGACAGAT GGGGAGAGGA AAAAGGCAGA GATNGCCAGG AGAGGGGTGC AGGACAAACC 240
30 AGAGAGGTTG GGTACGGGA AAAGTGINGG GAGAAAGTGG GGTGCAGGCC CTGCAGGCCG 300
GTTTAGCCAG CAGCTGCCGC CTCCCCGGGC CCTTGGCATC CAACTTCGCA GACAGGGTAC 360
35 CAGCCTCCTG GTGTGTATCA TAGGATTTGT TCACATAGTG TTATGCATGA TCTTCGTAAG 420
GTTAAGAAGC CGTGGTGGTG CACCATGACA TCCAACCCGT ATATATAAAG ATAAATATAT 480
ATATATATGT ATGTAAATTA TAGCACTGAG GGCCCTGCTG CCCTGCTGGA CCAAGCAAAA 540
40 CTAAGCCTTT TGGTTTGGGT ATTATGTTTC GTTTTGTAT TTGTTTGT TTGTGGCTTG 600
TCTTATGTCG TGATAGCACA AGTGCCAGTC GGATTGCTCT GTATTACAGA ATAGTGTTTT 660
45 TAATTCATCA ATGTCTAGT TAATGTCTAC CTCAGCACCT CCTCTTAGCC TAATTTTAGG 720
AGGTGCCCCA ATTTTGTTC TTCAATTTTA CTGGTACTT TTTTGTACAA ATCAATCTCT 780
TTCTCTCTTT CTCTCCTCCC CACCTCTCAC CCTTGCCCTC TCCATCTCCC TCTCCCGCCC 840
50 TCCCCTCCTC CCTCTGGCTC CCGTCTCAT TTCTGTCCAC TCCATCTCT CTCCCTCTCT 900
CCTGCCTCCT GCTGCCCCCT CCCCAGCCCA CTTSCCCGAG TTGTGCTTGC CGCTCCTTAT 960
55 CTGTCTAGT TCCGAAGCAG TTCACTCGA AGTTGTGCAG TCCTGGTTGC AGCTTTCCGC 1020
ATCTGCCTTC GTTTCGTGTA GATGACGCG TTTCTTTGTA ATTTCACTGT TTCTGACAAG 1080
ATTTAAAAA AAAAAAGGA AAAAAA AAAAAAAC TCGAGGGGG GCCCGGTACC 1140
60

CAATTG

1146

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(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

15

AACCACGGC TGCTGCGGCA GGGCGTGGAG GGCAGAGGGC CGCGGAGGCG CAGTTGCAAA 60

CATGGCTCAG AGCAGAGACG GCGGAAACCC GTTCGCCGAG CCCAGCGAGC TTGACAACCC 120

20

CTTTCAGCCA CCACCAGCCT ATGAGCCTCC AGCCCCTGCC CCATTGCCCTC CACCCTCAGC 180

TCCCTCCTTG CAGCCCTCGA GAAAGCTCAG CCCACAGAA CCTAAGAACT ATGGCTCATA 240

25

CAGCACTCAG GCCTCAGCTG CAGCAGCCAC AGCTGAGCTG CTGAAGAAAC AGGAGGAGCT 300

CAACCGGAAG GCAGAGGAGT TGGACCGAAG GAGNCGAGAG CTGCAGCATG CTGCCCTGGG 360

RGGCAGAGCT ACTCGACAGA ACAATGGGCC CCTCTACCT TCTTTTGTGTC CAGTTCAGCC 420

30

CTGCTTTTTC CAGGACATCT CCATGGAGAT CCCCCAAGAA TTTCAGAAGA CTGTATCCAC 480

CATGTACTAC CTCTGGATGT GCAGCAGST GGCTCTTCTC CTGAACTTCC TCGCCTGCCT 540

35

GGCCAGCTTC TGTGTGGAAC CCAACAATGG CGCAGGCTTT GGGCTTTCTA TCCTCTGGGT 600

CCTCCTTTTC ACTCCCTGCT CCTTTGTCTG CTGGTACCGC CCCATGTATA AGGCTTTCCG 660

GAGTGACAGT TCATTCAATT TCTTCGTTTT CTTCCTCATT TTCTTCGTCC AGGATGTGCT 720

40

CTTTGTCTTC CAGGCCATTG GTATCCAGG TTGGGGATTC AGTGGCTGGA TCTCTGCTCT 780

GGTGGTGGCG AAGGCAACAC AGCAGTATCC GTGCTCATGC TGCTGGTCGC CCGCTCTTTC 840

45

ACTGGCATTC CTGTGCTAGG AATTGTCTAT CTGAAACGGA TCCACTCCTT ATACCGCCGC 900

ACAGGTGCCA GCTTTCAGAA GGCCAGCAA GAATTTGCTG CTGGTGTCTT CTCCAACCTT 960

GCGGTGCGAA CGGCARCTTG CCAATGCAGC CGCTGGGGCT GCTGAAAATG CCTTCCGGGC 1020

50

CCCGTGACCC CTGACTGGGA TGCCCTGGCC CTGCTACTTG AGGGAGCTGA CTTAGCTCCC 1080

GTCCCTAAGG TCTCTGGGAC TTGGAGAGAC ATCACTAACT GATGGCTCCT CCGTAGTGCT 1140

55

CCCAATCCTA TGGCCATGAC TGCTGAACCT GACAGGCGTG TGGGAGTTT ACTGTGACCT 1200

AGTCCCCCA TCAGGCCACA CTGCTGCCAC CTCTCACAG CCCCACCCA GCTTCCCTCT 1260

GCTGTGCCAC GGCTGTGCT TCGGTTATTT AAATAAAAAG AAAGTGAAC TGGAAAAAA 1320

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AAAAAAAAA AAAAAAAAAAG GGGGNCNC 1350

5 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

15 TCCCAGAGGC CGGGGGGTTC CAGCTCTGCC TGTAGCAGAG CCCTGAGGAG GAGGAGGAAG 60
AGGATGTGCT GAAATACGTC CGGGAGATCT TTTTCAGCTA GGGCATAAAC TGTGCACTGA 120
ACTGTCTGCC GAGAGCAGCT GGAGGACAGC TGAGCTTCCA CTGGTGCTGC TGGGCCGMCC 180
20 GCCGTGTTGGA ATGGGGCTCT CTGTGCTCCT ACCTTTGTGC CTCTCTGGGC CTGGCAGATT 240
CACCTCAGGC CAGAAGCCCC TGGACACTCC GGGCCTTGGG GTGCCGTTCT GAGTGTGCGG 300
25 AAGGCAGGAC TCAAAATGAG ATCCCATTTG ACTCCCTCTG TATGTACTGT GCCCTCTCCT 360
GGCTCTTGAG GCTCTGGAGT CCCAATTGTC TGTGTTAGTC AGTGACCAGG TTCCAGGGAA 420
AATRATGTCA TGTGGTGGTC CAACTTACTG GAACCAAAGA GACAGTACTT TGCAAAGAAA 480
30 AGGATCACTG CCAGGTGCAC TGAATTGCT ACAGTTTAGT CCGCATGATC TCTCCTGAAG 540
GAGGAAGCCT GTTTCAAAAA TAGTTTCCAT CATGAGTCTA TCAATGAGCT CCCACCTCTC 600
35 CAGCCAGCCT AGAAAGCAAA CGAGCTGCCC ACAGTTCTCT GCCCTGTCTG GGAGGTTGAG 660
GCCACAGTGT ATAGACTGGT AAGCCAGACA GGCCTCCTCC CGCAAGCTGC TACCTTGCTT 720
TCACCTGTAC CTTGGTCCCC GGGCAGCTAG CTATAAAGCA AGAGGGACAG GAGCCCAGAA 780
40 GAGACACTGA GGACAAGAGA TCACACCAGA GTACATGTCT CTGCCCTCTGT TTTCACTGTG 840
GCTTTGGACA GGAATATATG AATAAATCAC TGCCATACAG GTTTTCCAAT ACACAAGTGC 900
45 TAGAAAATAC ACACAATTCC CCAATGCGTA AGTTGTGCTA ATGTCTTTCC AAGTTCTGGG 960
TTGGGAAGTG GAGGGTGGCA GCGTTTGTMT GTGCGCAACC GTCCAGTCCT GTTCACAGCG 1020
AGGATTTGGA GTCTCCAGG GTCTCATCAT GGGAGTGATT TGTACGCGGA CGCCTCTGCC 1080
50 CTGTCTGGCT TCAGGTCCAG GGAAGCTTTG AAGCAGTCAA GCCTTGTCIT TGTACCCCAT 1140
GTGTCCTGTC TTTGTTGAGT CACTCAGAGA TCACTCCTGG ACCTCTGGGG TTGGAGTTCC 1200
55 AGTGATGGCT TATGGCGGCC CACTCACTAT GGTGGGCTGA GTGGAAGCTC CTTAACCATG 1260
TCCCCAGAGA CACTGAGGTG CTCGCTCTTT TAATGTCTC GTTTGTGCC GTAAGTTCTT 1320
TGCTAGGTTT CATTTTGGCA TTTGGCAAAT CAGCCTGGAA GTCTGGCCCC ATGACAGCAA 1380
60

TCAC'TCCCTC CCCACCCTCC TGAAGCTAGA GGAAGATTTC CTCAGATCCA TTAATTAAAG 1440
CAGGAATTGG TGTGACAATG AGCTGCATGG TTTAGGGAGT CTTGGGAGC CTTGGAAGTC 1500
5 CTGAAGGACA AACAATCTTG TACTAAGAA 1529

10 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

20 GTGCGAGGTC CCCGCCAGCC CCCAGCGGCC TTCCCGGCCC GGGGCGCTCC CAGAGCAAAC 60
GAGGCCCTCT AGAGCTCCAC CTAGTTCACA GGATAAAATC CCACAGCAGA ACTCGGAGTC 120
AGCAATGGCT AAGCCCCAGG TGGTGTAGC TCCTGTATTA ATGTCTAAGC TGTCTGTGAA 180
25 TGCCCTGAA TTTTACCCTT CAGGTTATTC TTCCAGTTAC ACAGAATCCT ATGAGGATGG 240
TTGTGAGGAT TATCCTACTC TATCAGAATA TGTTCAGGAT TTTTGAATC ATCTTACAGA 300
30 GCAGCCTGGC AGTTTGAAG CTGAAATTGA ACAGTTTGCA GAGACCCTGA ATGGTTGTGT 360
TACAACAGAT GATGCTTTGC AAGAACTTGT GGAATCATC TATCAACAGG CCACATCTAT 420
CCCCAAATTC TCTTATATGG GAGCTCGCCT GTGTAATTAC CTGTCCCATC ATCTGACAAT 480
35 TAGCCACAG AGTGGCAACT TCCGCCAATT GCTACTTCAA AGATGTGGA CTGAATATGA 540
AGTTAAAGAT CAAGCTGCAA AAGGGGATGA AGTTACTCGA AAACGATTTT ATGCATTTGT 600
40 ACTCTTTCTG GGAGAACTTT ATCTTAACCT GGAGATCAAG GGAACAAATG GACAGGTTAC 660
AAGAGCAGAT ATTCTTCAGG TTGGTCTTCG AGAATTGCTG AATGCCCTGT TTTCTAATCC 720
TATGGATGAC AATTTAATTT GTGCAGTAAA ATTGTTAAAG TTGACAGGAT CAGTTTGGGA 780
45 AGATGCTTGG AAGGAAAAAG GAAAGATGGA TATGGAAGAA ATTATTCAGA GAATTGAAAA 840
CGTTGTCTTA GATGCAAACT GCAGTAGAGA GTTAAACAG ATGCTCTTGA AGCTTGTAGA 900
50 ACTCCGGTCA AGTAACTGGG GCAGAGTCCA TGCAACTTCA ACATATAGAG AAGCAACACC 960
AGAAAAATGAT CCTAACTACT TTATGAATGA ACCAACATTT TATACATCTG ATGGTGTTC 1020
TTTCACTGCA GCTGATCCAG ATTACCAAGA GAAATACCAA GAATTACTTG AAAGAGAGGA 1080
55 CTTTCTTCCA GATTATGAAG AAAATGGAAC AGATTTATCC GGGGCTGGTG ATCCATACTT 1140
GGATGATATT GATGATGAGA TGGACCCAGA GATAGAAGAA GCTTATGAAA AGTTTGTGTT 1200
60 GGAATCAGAG CGTAAGCGAA AACAGTAAAG TTAAATTICA GCATATCAGT TTTATAAAGC 1260

AGTTTAGGTA TGGTGATTTA GCAGAACACA AGAGAGCAAG AAAATGTGTC ACATCTATAC 1320
CAAATTRAGG ATGTTGAGTT ATGTTACTAA TGTATGCAAC TTTAATTTTG TTAAACACTA 1380
5 TCTGCCAAAA TAAACTTTAT TCCCTATAAC TTAAATGTG TATATATATA TAATAGTTTA 1440
TTATGTACAG TTAATCTAC TGTTTGGCT GCAATAAAT CGATTTTGAA ATAAAWRAAA 1500
10 AAAAAAAAAA AAGGGNGGCC GCTCTAGAG ANCCAAG 1537

15 (2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

25 TGCAGGATTT GGCCAGGACC CSCCGGGTG GCGTTGCTA TCGCTTCGCA GAACCTACTC 60
AGGCAGCCAG CTGAGAAGAG TTGAGGAAA GTGCTGCTGC TGGGTCTGCA GACCGGATGG 120
ATAACGTGCA GCCGAAAATA AAACATCGCC CCTTCTGCTT CAGTGTGAAA GGCCACGTGA 180
30 AGATGCTGCG GCTGGATATT ATCAACTCAC TGGTAACAAC AGTATTCATG CTCATCGTAT 240
CTGTGTTGGC ACTGATACCA GAAACCACAA CATTGACAGT TGGTGGAGGG GTGTTTGCAC 300
35 TTGTGACAGC AGTATGCTGT CTGCGGACG GGGCCCTTAT TTACCGGAAG CTCTCTGTCA 360
ATCCACGGG TCCTTACCAG AAAAAGCCTG TGCATGAAAA AAAAGAAGTT TTGTAATTTT 420
ATATTACTTT TTAGTTTGAT ACTAAGTATT AAACATATTT CTGKATTATT CCAAAAAAAAA 480
40 AAAAAAAAAA AAAAAAATT TGGTGG 506

45

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1348 base pairs

50 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 GTCCTTCTTT TNCTGTTTGT AGTTGGTGAG TGAGTGAATA GGGTAACATG GGCCTTCAGG 60
ATGACCCCTT GGAAGTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG 120
60 GCCCTGTGA GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGY TGGGAAGAAC 180

	TCTGCTCGAG GGCAGGGTGC CCTGGAACAC TGGTAGTTCT GGGGCTGGGA GGGAGAGGGG	240
	CTCCGGCTTT CTCTGAAATG AACACTGCTC TTCAGCAGTT CAAGTACTTG TTCTCAAAAC	300
5	ATTTTCTAAT TGATTGGTAG GTTTCATAA GCATTGTTTC TTTAAGGCAT GGAAAGGGAA	360
	GAATGCTCAA GCAAGTCATG TTTGTTTCA GTGGGATGGG CCCGCGTTCT CACTGCTGGG	420
10	GGCTTCCCTT TGCATGTGGC ACCTTTGTGC AGGGCCACCA GGCAGACTCT TCCCACCTTC	480
	TCCCCTGAA GCACCAAGGG GCTTGAACCG TAATTTGGCT AATCAGAGGC ATTTTTTTTG	540
	TCCTAGTATC TTTCACACTT GTCCAACCGT CTTATTTTTT TAAAGTTCT GTTGCTTGTA	600
15	TTAACACGAA ACTAGAGAGA AATAGTTTCT GAAGCCAGTT TATTGTGAAG ATCCCCAAGG	660
	GGAGGTTTCG TAGAGAAAAA TAGTAAGCTG GTTTAGAAAC TGACGAGGGC AAACAGCCAG	720
20	GACGCATTGG AGAGGAATTT GCCAAAGATC TACCCTGAGA TAACGCCTGT CCAGTGTCTT	780
	CACCACGTGA ATAACCAGCG CTCCAAAGTG TTTTCTGCT TTGAAAAAA AAATTCACA	840
	AGCTTTTAAA GGTGCATTTA AGAATCCATG TGACTTTAGA ATGGAAGTGC CGGCCCTGGC	900
25	AACTGTCAGG TGTGCTAGAA GGTTCGATGC CTCTGGAATG CATGTGATAC TCATCTCCAT	960
	TTTGTTTCCT TGATTGCATT TTTGTTCTTT TAGCAGATCT GTCCCTGTGG GTGGTGTCTA	1020
30	AGAAGTCGGA CACCTTGGTT TTTGTGTTAG ATTGAGCTGG GCAGCTGCAA TCAGCTTCTT	1080
	TATATGCAAA TTAGGCACGA CCCATCTGTG GTTCCCTGGT TGGTGGCTAA TGAAGTGAGG	1140
	GGAGGGAGGG ATGTCACCCC AAAAGTAGGC CCTCCCATTG GCTTTGGCCA GGCCAGACAC	1200
35	TTACATCGT TTACATGGTT CTGTGTAATT TTAAAGTTTA TGTGTATAAA GCGAAGCTGT	1260
	TTCTGTGAAA CTGTATATTT TGTAAATAAA TATATTGCTA CTTTGAGAWR AAAAAAAAAA	1320
40	AAAAACTCGA GGGGGGCCCC GTACCCAA	1348

45 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1766 base pairs.
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

55	GTGCCGAATC GGCAGAGCGG CACGAGCGGC CACGAGAGCA GGCGAGTAA AGGGACTTGA	60
	GCGAGCCAGT TGCCGATTA TTCTATTTCC CCTCCCTCTC TCCGCCCCG TATCTCTTTT	120
60	CACCCCTCTC CCACCCCTCG TCGCGTASCA TGGCGGAGCG TCGGCGGCCA CTCAGTCCCA	180

	TTCCATCTCC TCGTCGTCCCT TCGGAGCCGA GCCGTCCGCG CCCGGCGGCG GCGGGAGCCC	240
	AGGAGCCTGC CCCGCCCTGG GGACGAAGAG CTGCAGCTCC TCCTGTGCGG TGCACGATCT	300
5	GATTTTCTGG AGAGATGTGA AGAAGACTGG GTTTGTCTTT GGCACCACGC TGATCATGCT	360
	GCTTTCCCTG GCAGCTTTCA GTGTCACTAG TGTGGTTTCT TACCTCATCC TGGCTCTTCT	420
10	CTCTGTCACC ATCAGCTTCA GGATCTACAA GTCCGTGATC CAAGCTGTAC AGAAGTCAGA	480
	AGAAGGCCAT CCATTCAAAG CCTACCTGGA CGTAGACATT ACTCTGTCTT CAGAAGCTTT	540
	CCATAATTAC ATGAATGCTG CCATGGTGCA CATCAACAGG GCCCTGAAAC TCATTATTCG	600
15	TCTCTTTCTG GTAGAAGATC TGGTTGACTC CTTGAAGCTG GCTGTCTTCA TGTGGCTGAT	660
	GACCTATGTT GGTGCTGTTT TTAACGGAAT CACCCTTCTA ATTCTTGCTG AACTGCTCAT	720
20	TTTCAGTGTC CCGATTGTCT ATGAGAAGTA CAAGACCCAG ATTGATCACT ATGTTGGCAT	780
	CGCCCGAGAT CAGACCAAGT CAATTGTGA AAAGATCCAA GCAAAACTCC CTGGAATCGC	840
	CAAAAAAAG GCAGAATAAG TACATCGAAA CCAGAAATGC AACAGTTACT AAAACACCAT	900
25	TTAATAGTTA TAACGTCGTT ACTTGTAATA TGAAGGAAAA TACTCAGTGT CAGCTTGAGC	960
	CTGCATTCCA AGCTTTTTTT TTAATTTGGT GTTTTCTCCC ATCCTTTCCC TTTAACCCTC	1020
30	AGTATCAAGC ACAAAAAATTG ATGGACTGAT AAAAGAACTA TCTTAGAACT CAGAAGAAGA	1080
	AAGAATCAAA TTCATAGGAT AAGTCAATAC CTTAATGGTG GTAGAGCCTT TACCTGTAGC	1140
	TTGAAAGGGG AAAGATTGGA GGTAAAGAG AAAATGAAAG AACACCTCTG GGTCTTCTG	1200
35	TCCAGTTTTC AGCACTAGTC TTAAGTCACT ATCCATTATA GTTTTGCCCT TAAGAAGTCA	1260
	TGATTAACTT ATGAAAAAAT TATTTGGGGA CAGGAGTGTG ATACCTTCTT TGGTTTPTTT	1320
40	TTGCAGCCCT CAAATCCTAT CTTCTGCCC CACAATGTGA GCAGCTACCC CTGATACTCC	1380
	TTTTCTTTAA TGATTTAACT ATCAACTTGA TAAATAACTT ATAGGTGATA GTGATAATTC	1440
	CTGATTCCAA GAATGCCATC TGATAAAAAA GAATAGAAAT GGAAAGTGGG ACTGAGAGGG	1500
45	AGTCAGCAGG CATGCTGCGG TGGCGGTCAC TCCCTCTGCC ACTATCCCCA GGAAGGAAA	1560
	RGCTCCGCCA TTTGGGAAAG TGGTTTCTAC GTCAGTGAC ACCGGTTCTG AGCAITAGTT	1620
50	TGAGAACTCG TTCCCGAATG TGCTTTCTCT CCTCTCCCCT GCCCACCTCA AGTTTAATAA	1680
	ATAAGGTGTG ACTTTTCTTA CTATAAAATA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA	1740
	CCCAAATCGC CGGATATGAT CGTAAA	1766
55		

(2) INFORMATION FOR SEQ ID NO: 249:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

	AGTGTCTCTG GAGCAGGCCG AGTAAAGGA CTTGAGCGAG CCAGTTGCCG GATTATTCTA	60
10	TTTCCCCCTC CTCTCTCCCG CCCCGTATCT CTTTTCACCC TTCTCCCACC CTCGCTCGCG	120
	TASCATGGCG GAGCGTCGGC GGCCACTCAG TCCCATTCCT TCTCCTCGTC GTCCTTCGGA	180
	GCCGAGCCGT CCGCGCCCGG CGGCGGCGGG AGCCCAGGAG CCTGCCCCGC CCTGGGGACG	240
15	AAGAGCTGCA GCTCCTCCTG TGGGTGACAC GATCTGATTT TCTGGAGAGA TGTGAAGAAG	300
	ACTGGGTTTG TCTTTGGCAC CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTC	360
20	ATCAGTGTGG TTTCTTACCT CATCCTGGCT CTTCTCTCTG TCACCATCAG CTTCAGGATC	420
	TACAAGTCCG TCATCCAAGC TGTACAGAAG TCAGAAGAAG GCCATCCATT CAAAGCCTAC	480
	CTGGACGTAG ACATTACTCT GTCCTCAGAA GCTTTCCATA ATTACATGAA TGCTGCCATG	540
25	GTGCACATCA ACAGGGCCCT GAAACTCATT ATTCGTCTCT TTCTGGTAGA AGATCTGGTT	600
	GACTCCTTGA AGCTGGCTGT CTTCAATGTG CTGATGACCT ATGTTGGTGC TGTTTTTAAC	660
30	GGAATCACCC TTCTAATTTT TGCTGAACTG CTCATTTTCA GTGTCCCGAT TGTCTATGAG	720
	AAGTACAAGA CCCAGATTGA TCACTATGTT GGCATCGCCC GAGATCAGAC CAAGTCAATT	780
	GTTGAAAAGA TCCAAGCAAA ACTCCCTGGA ATCGCCAAAA AAAAGGCAGA ATAAGTACAT	840
35	GGAAACCAGA AATGCAACAG TTAATAAAC ACCATTTAAT AGTTATAACG TCGTTACTTG	900
	TACTATGAAG GAAAATACTC AGTGTACGCT TGAGCCTGCA TTCCAAGCTT TTTTTTTAAT	960
40	TTGGTGTITT CTCCCATCCT TTCCCTTTAA CCCTCAGTAT CAAGCACAAA AATTGATGGA	1020
	CTGATAAAAG AACTATCTTA GAACTCAGAA GAAGAAAGAA TCAAATTCAT AGGATAAGTC	1080
	AATACCTTAA TGGTGGTAGA GCCTTTACCT GTAGCTTGAA AGGGGAAAGA TTGGAGGTAA	1140
45	GAGAGAAAAT GAAAGAACAC CTCTGGGTCC TTCTGTCCAG TTTTCAGCAC TAGTCTTACT	1200
	CAGCTATCCA TTATAGTTTT GCCCTTAAGA AGTCATGATT AACTTATGAA AAAATTATTT	1260
50	GGGGACAGGA GTGTGATACC TTCCTTGGTT TTTTPTTGCA GCCCTCAAAT CCTATCTTCC	1320
	TGCCCCACAA TGTGAGCAGC TACCCCTGAT ACTCCTTTTC TTTAATGATT TAACTATCAA	1380
	CTTGATAAAT AACTTATAGG TGATAGTGAT AATTCCTGAT TCCAAGAATG CCATCTGATA	1440
55	AAAAAGAATA GAAATGGAAA GTGGGACTGA GAGGGAGTCA GCAGGCATGC TCGGCTGGCG	1500
	GTCACITCCCT CTGCCACTAT CCCCAGGGAA GGAAARGCTC CGCCATTTGG GAAAGTGGTT	1560
60	TCTACGTCAC TGGACACCGG TTCTGAGCAT TAGTTTGAGA ACTCGTTCCT GAATGTGCTT	1620

5 TCCTCCCTCT CCCCTGCCCA CCTCAAGTTT AATAAATAAG GTTGACTTTT TCTTACTATA 1680
AAATAAATGT CTGTAACGCG TGTGCACTGC TGTAAACTTG TTAGAGAAAA AAATAACCTG 1740
CATGTGGGCT CCTCAGTTAT TGAGTTTTTG TGATCCTATC TCAGTCTGGG GGGGAACATT 1800
CTCAAGAGGT GAAATACAGA AAGCCTTTTT TTCTTGATCT TTCCCGAGA TTCAAATCTC 1860
10 CGATTCCCAT TTGGGGGCAA GTTTTTTCT TCACCTTCAA TATGAGAATT CAGCGAATT 1920
GAAAGAAAA TCATCTGTGA GTTCCTTCAG GTTCTCACTC ATAGTCATGA TCCTTCAGAG 1980
GGAATATGCA CTGGCGAGTT TAAAGTAAGG GCTATGATAT TTGATGGTCC CAAAGTACGG 2040
15 CAGCTGCAAA AAGTAGTGA AGGAAATTGT CTACGTGTCT TGGAAAAATT AGTTAGGAAT 2100
TTGGATGGGT AAAAGGTACC CTGCGCTTAC TCCATCTTAT TTCTTAGCC CCCTTTGAGT 2160
20 GTTTTAACTG GTTTCATGTC CTAGTAGGAA GTGCATTCTC CATCCTCATC CTCTGCCCTC 2220
CCAGGAAGTC AGTGATGTC TTTTGGGCT TCCCCTCCAA AGGACCTTCT GCAGTGAAG 2280
TGCCACATCC AGTCTTTTC TTTGTGCT GCTGTGTTA GATAATGAA GAGATCTTTG 2340
25 TGCCACACAG GATTTTTTTT TTTTAAAGA AAAACCTATA GATGAAAAAT TACTAATGAA 2400
ACTGTGTGTA CGTGTCTGTG CGTGCAACAT AAAAATACAG TAGCACCTAA GGAGCTTGAA 2460
30 TCTTGGTTCC TGTAATAATT CAAATGATG TGGTATTAAT AAAAAAAAAA AAAACAMAAA 2520
AAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGATCCAAGC TTACGTACGC GTGCATGCCA 2580
CGTCCATAGC TCTTCTATA GGGGTCCCC AAATTCATT CANGGGCCG TCGGTTTTAN 2640
35 AAAGGTCGTG ANTGGGGGAA ANCC 2664

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(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

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CGTGGGAGTG AGGTACCAGA TTCAGCCCAT TTGGCCCCGA CGCCTCTKTT CTCGGAATCC 60
GGGTGCTGCG GATGAGGTC CCGGTTCTTA ACGGTGGGAT CCGTGTCTC GGGATGAGAT 120
TTGGCGTTTC CTCGGGGCTT TGGTGGGATC GGTGTCTCA GGATGAGATT TAGGGTTTCC 180
TCGGGGCTTT CGGATCTTC ACCTAATATC CGGACTGCAA GATGGAGGAA GCGGGGAACC 240
TAGGAGGCCT GATTAARATG GTCCATCTAC TGGTCTTGTC AGGTGCCTGG GGCATGCAAA 300

TGTGGGTGAC CTTCGTCTCA GGCTTCCTGC TTTTCCGAAG CCTTCCCCGA CATACCTTCG 360
GACTAGTGCA GAGCAAATC TTCCCCTTCT ACTTCCACAT CTCCATGGGC TGTGCCTTCA 420
5 TCAACCTCTG CATCTTGGCT TCACAGCATG CTTGGGCTCA GCTCACATTC TGGGAGGCCA 480
GCCAGCTTTA CTGCTGTTC CTGAGCCTTA CGCTGGCCAC TGTCAACGCC CGCTGGCTGG 540
AACCCCGCAC CACAGCTGCC ATGTGGGCCC TGCAAACCGT GGAGAAGGAG CGAGGCCTGG 600
10 GTGGGGAGGT ACCAGGCAGC CACCAGGGTC CCGATCCCTA CCGCCAGCTG CGAGAGAAGG 660
ACCCCAAGTA CAGTGCTCTC CGCCAGAATT TCTTCCGCTA CCATGGGCTG TCCTCTCTTT 720
15 GCAATCTGGG CTGCGTCTG AGCAATGGGC TCTGTCTCGC TGGCCTTGCC CTGGAAATAA 780
GGAGCTCTA GCATGGGCCC TGCATGCTAA TAAATGCTTC TTCAGAAAAA AAAAAAAAAA 840
AAACTCGAGG GGGGCCCGGT ACCCA 865
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(2) INFORMATION FOR SEQ ID NO: 251:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2082 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

TGGGGGGGNN AATGGGTGTC TGGCTCANGG ATTGCCNAAT CTGGAAATTC TCCATAACTT 60
35 GCTAGCTTGT TTTTITTTTT TTTTITTACA CCCCCCGCC CCACCCCGG ACTTGCACAA 120
TGTTCAATGA TCTCAGCAGA GTTCTTCATG TGAAACGTTG ATCACCTTGG AAGCCTGCAT 180
40 CATTCACATA TTTTITCTTC TTCTTCCCCT TCAGTTCATG AACTGGTGT CATTTTCTGT 240
GTGTGTGTGT GTTTATTTTT GTTTGGATTT TTTTITTTAA TTTTACTTTT AGAGCTTGCT 300
GTGTTGCCCA CCTTTTTC CACCTCCACC CTCACTCCTT CTCAACCCAT CTCTTCCGAG 360
45 ATGAAAGAAA AAAAAAGCA AAGTTTTTTT TTCTTCTCCT GAGTTCCTCA TGTGAGATG 420
AGCTTGCAAA GGAAAAAAA ATGTGAAATG TTATAGACTT GCAGCGTGCC GAGTTCCATC 480
50 GGGTTTTTTT TTTAGCATIG TTATGCTAAA ATAGAGAAAA AAATGCTCAT GAACCTTCCA 540
CAATCAAGCC TGCATCAACC TTCTGGGTGT GACTTGTGAG TTTTGGCCTT GTGATGCCAA 600
ATCTGAGAGT TTAGTCTGCC ATTAAAAAAA CTCATTCTCA TCTCATGCAT TATTATGCTT 660
55 GCTACTTTGT CTTAGCAACA ATGAAGTATA ACTGTTTCAA AGACTTTATG GAAAAGAGAC 720
ATTATATTAA TAAAAAAA AAGCCTGCAT GCTGGACATG TATGGTATAA TTATTTTTTC 780
60 CTTTTTTTTT CCTTTTGGCT TGGAAATGGA CGTTCGAAGA CTTATAGCAT GGCATTCATA 840

CTTTGTGTTT ATTGCCTCAT GACTTTTTTG AGTTTAGAAC AAAACAGTGC AACCGTAGAG 900
 CCTTCTTCCC ATGAAATTTT GCATCTGCTC CAAAACCTGCT TTGAGTTACT CAGAACTTCA 960
 5 ACCTCCCAAT GCACTGAAGG CATTCCTTGT GCAAAGATAC CAGAATGGGT TACACATTTA 1020
 ACCTGGCAAA CATTGAAGAA CTCCTRATGT TTTCTTTTTA ATAAGATGA CGCCCCACTT 1080
 10 TGGGGACTAA AATTGTGCTA TTGCCGAGAA GCAGTCTAAA ATTTATTTTT TAAAAAGAGA 1140
 AACTGCCCCA TTATTTTTGG TTTGTTTTAT TTTTATTTTA TATTTTTTGG CTTTGGTCA 1200
 TTGTCAAATG TGAATGCTC TGGGTTTCTA GTATATAATT TAATTTCTAGT TTTTATAATC 1260
 15 TGTTAGCCCA GTTAAATGT ATGCTACAGA TAAAGGAATG TTATAGATAA ATTTGAAAGA 1320
 GTTAGGCTCG TTTAGCTGTA GATTTTTTAA ACGATTGATG CACTAAATTG TTTACTATTG 1380
 20 TGATGTTAAG GGGGGTAGAG TTTGCAAGGG GACTGTTTAA AAAAAGTAGC TTATACAGCA 1440
 TGTGCTTGCA ACTTAAATAT AAGTTGGGTA TGTGTAGTCT TTGCTATACC ACTGACTGTA 1500
 TTGAAAACCA AAGTATTAAG AGGGGAAACG CCCCTGTTTA TATCTGTAGG GGTATTTTAC 1560
 25 ATTCAAAAAT GTATGTTTTT TTTTCTTTTC AAAATTAAAG TATTTGGGAC TGAATTGCAC 1620
 TAAGATATAA CCTGCAAGCA TATAATACAA AAAAAAATG CAAAACGTG TAGAACGCTA 1680
 30 ATAAATTTA TGCAGTTATA AAAATGGCAT TACTGCACAG TTTTAAGATG ATGCAGATTT 1740
 TTTTACAGTT GTATTGTGGT GCAGAAGTGG ATTTTCTGTA ACTTAAAAAA AAATCCACAG 1800
 TTTTAAAGGC AATAATCAGT AAATGTTATT TTCAGGGACT GACATCCTGT CTTTAAAAAG 1860
 35 AAATGAAAAG TAATCTTAC CACAATAAAT ATAAAAAAT CTGTGAGTT ACTTTTCITT 1920
 TACATATTTT GCTGTGCAAA ATTGTTTTAT ATCTTGAGTT ACTAACTAAC CACGCGTGTT 1980
 40 GTTCCTATGT GCTTTTCTTT CATTTTCAAT TCTGTTATA TCAAGAAAAG AATAATCTAC 2040
 AATAATAAAC GGCATTTTTT TTTGAAAAAA AAAAAAAAAA AA 2082

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(2) INFORMATION FOR SEQ ID NO: 252:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

CAGGCAGGCT GGCCCCGGG ACTTCTCTCT GGCCCTGCTC CCTCCGAGCG CTCCGCCGTT 60
 GCCCGCCTGG CCCCTACGGA GTCCTTAGCC AGGATGGAGG CTGTTGTGAA CTTGTACCAA 120
 60

GAGGTGATGA AGCACGCAGA TCCCCGGATC CAGGGCTACC CTCTGATGGG GTCCCCCTTG 180
 CTAATGACCT CCATTCTCCT GACCTACGTG TACTTCGTTC TCTCACTTGG GCCTCGCATC 240
 5 ATGGCTAATC GGAAGCCCTT CCAGCTCCGT GGCTTCATGA TTGTCTACAA CTTCTCACTG 300
 GTGGCACTCT CCGTCTACAT TGTCTATGAG TTCCTGATGT CGGGCTGGCT GAGCACCTAT 360
 10 ACCTGGCGCT GTGACCCTGT GGACTATTCC AACAGCCCTG AGGCACTTAG GATGGTTCGG 420
 GTGGCCTGGC TCTTCCTCTT CTCCAAGTTC ATTGAGCTGA TGGACACAGT GATCTTTATT 480
 CTCCGAAAGA AAGACGGGCA GGTGACCTTC CTACATGTCT TCCATCACTC TGTGCTTCCC 540
 15 TGGAGCTGGT GGTGGGGGGT AAAGATTGCC CCGGGAGGAA TGGGCTCTTT CCATGCCATG 600
 ATAAACTCTT CCGTGCATGT CATAATGTAC CTGTACTACG GATTATCTGC CTTTGGCCCT 660
 GTGGCACAAC CCTACCTTTG GTGAAAAAG CACATGACAG CCATTCACTG GATCCAGTTT 720
 20 GTCTGGTCT CACTGCACAT CTCCCAGTAC TACTTTATGT CCAGCTGTAA CTACCAGTAC 780
 CCAGTCATTA TTCACCTCAT CTGGATGTAT GGCACCATCT TCTTCATGCT GTTCTCCAAC 840
 25 TTCTGGTATC ACTCTTATAC CAAGGGCAAG CCGCTGCCCC GTGCACTTCA GCAAAATGGA 900
 GCTCCAGGTA TTGCCAAGGT CAAGGCCAAC TGAGAAGCAT GGCCTAGATA GGCGCCAC 960
 TAAGTGCCTC AGGACTGCAC CTTAGGGCAG TGTCCGTCAG TGCCCTCTCC ACCTACACCT 1020
 30 GTGACCAAGG CTTATGTGGT CAGGACTGAG CAGGGGACTG GCCCTCCCT CCCACAGCT 1080
 GCTCTACAGG GACCACGGCT TTGGTTCTTC ACCCACTTCC CCCGGGCAGC TCCAGGGATG 1140
 35 TGGCCTCATT GCTGTCTGCC ACTCCAGAGC TGGGGGCTAA AAGGGCTGTA CAGTTATTTC 1200
 CCCCTCCCTG CCTTAAACT TGGGAGAGGA GCACTCAGGG CTGGCCCCAC AAAGGGTCTC 1260
 GTGGCCTTTT TCCTCACACA GAAGAGGTCA GCAATAATGT CACTGTGGAC CCAGTCTCAC 1320
 40 TCCTCCACCC CACACACTGA AGCAGTAGCT TCTGGGCCAA AGGTCAGGGT GGGCGGGGGC 1380
 CTGGGAATAC AGCCTGTGGA GGCTGCTTAC TCAACTTGTG TCTTAATTAA AAGTGACAGA 1440
 45 GGAAACCAAA AAAAAAAAAA AAAAATCGA GGGGGGCCCG TA 1482

50 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

60 GGCACGAGCG CCGTTGCCCG CCTGGCCCTT ACGGAGTCCT TAGCCAGGAT GGAGGCTGTT 60

GTGAACTTGT ACCAAGAGGT GATGAAGCAC GCAGATCCCC GGATCCAGGG CTACCCCTCTG 120
ATGGGGTCCC CCTTGCTAAT GACCTCCATT CTCCTGACCT ACGTGTACTT CGTTCTCTCA 180
5 CTGCGGCTC GCATCATGGC TAATCGGAAG CCCTTCCAGC TCCGTGGCTT CATGATTGTC 240
TACAACTTCT CACTGGTGGC ACTCTCCCTC TACATTGTCT ATGAGTTCTT GATGTCGGGC 300
10 TGGCTGAGCA CCTATACCTG GCGCTGTGAC CTCAGGACT GCACCTTAGG GCAGTGTCGG 360
TCAGTGCCTT CTCCAMCTAC ACCTGTGACC AAGGCTTATG TGGTCAGGAC TGAGCAGGGG 420
ACTGGCCCTC CCTCCCCAC AGCTGCTCTA CAGGGACCAC GGCTTTGGTT CCTCACCAC 480
15 TTCCCCGGG CAGCTCCAGG GATGTGCCCT CATGTCTGTC TGCCACTCCA GAGCTGGGGG 540
CTAAAAGGGC TGTACAGTTA TTTCCCCCTC CTGCGCTTAA AACTTGGGAG AGGAGCACTC 600
20 AGGGCTGGCC CCACAAAGGG TCTCGTGGCC TTTTTCCTCA CACAGAAGAG GTCAGCAATA 660
ATGTCACTGT GGACCCAGTC TCACTCCTCC ACCCCACACA CTGAAGCAGT AGCTTCTGGG 720
CCAAAGGTCA GGGTGGGCGG GGGCCTGGGA ATACAGCCTG TGGAGGCTGC TTAICTCAACT 780
25 TGTGTCTTAA TTAAGTGA CAGAGGAAAC CACGAAAAA AAAAAAAAAA AAAA 834

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(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

TTGAACTTTT AAAATTTTAG ATCAGCAAAC TCTAAGATCC TAGAATGGAA GCTGTTCTC 60
ATTCTCCAT GCTCACCCTC CCAGGTCAGC GAGATGGTGA AGAAGCTGCA CGCGGCAACA 120
45 CCACCAACGT TCGGAGTGGG CCTCATCAAT GAGCTTGTGG AGAACTTTGG CAGATGTCCC 180
AAGTGGTCTG GTCGGCAAGC CTTTGTCTTT GTCTGCCAGA CTGTCAATTGA GGATGACTGC 240
CTTCCCATGG ACCAGTTTGC TGTGCATCTC ATGCCGCATC TGCTAACCTT AGCAAATGAC 300
50 AGGGTTCCCTA ACGTGCAGT GCTGCTTGCA AAGACATTAA GACAACTCT ACTAGAAAAA 360
GACTATTTCT TGGCCTCTGC CAGCTGCCAC CAGGAGGCTG TGGAGCAGAC CATCATGGCT 420
55 CTTTCAGATGG ACCGTGACAG CGATGTCAAG TATTTTGCAA GCATCCACCC TGCCAGTACC 480
AAAATCTCCG AAGATGCCAT GAGCACAGCG TCCTCAACCT ACTAGAAGGC TTGAATCTCG 540
GTGTCTTTCC TGCTTCCATG AGAGCCGAGG TTCAGTGGG ATTGCCACG CATGTGACCT 600

60

GGGATAGCTT TCGGGGAGG AGAGACCTTC CTCTCCTGCG GACTTCATTG CAGGTGCAAG 660
TTGCCTACAC CCAATACCAG GGATTTCAG AGTCAAGAGA AAGTACAGTA AACACTATTA 720
5 TCTTATCTTG ACTTTAAGGG GAAATAATTT CTCAGAGGAT TATAATTGTC ACCGAAGCCT 780
TAAATCCTTC TGTCTTCTG ACTGAATGAA ACTTGAATTG GCAGAGCATT TTCCTTATGG 840
AAGGGATGAG ATTCCCAGAG ACCTGCATTG CTTTCTCCTG GTTTTATTTA ACAATCGACA 900
10 AATGAAATTC TTACAGCCTG AAGGCAGACG TGTGCCCAGA TGTGAAAGAG ACCTTCAGTA 960
TCAGCCCTAA CTCTTCTCTC CCAGGAAGGA CTGTCTGGG TCTGTGGCCA GCTGTCCAGC 1020
CCAGCCCTGT GTGTGAATCG TTTGTGACGT GTGCAAATGG GAAAGGAGGG GTTTTACAT 1080
CTCTAAAGG ACCTGATGCC AACACAAGTA GGATTGACTT AAATCTTAA GCGCAGCATA 1140
TTGCTGTACA CATTTACAGA ATGGTTGCTG AGTGTCTGTG TCTGATTTTT TCATGCTGGT 1200
20 CATGACCTGA AGGAAATTTA TTAGACGTAT AATGTATGTC TGGTGTTTTT AACTTGATCA 1260
TGATCAGCTC TGAGGTGCAA CTTCTTCACA TACTGTACAT ACCTGTGACC ACTCTGGGA 1320
GTGCTGCAGT CTTTAATCAT GCTGTTTAAA CTGTGTGGC ACAAGTTCTC TTGTCCAAAT 1380
AAAATTTATT AATAAGATCT ATAGAGAGAG ATATATACAC TTTTGATTGT TTTCTAGATG 1440
TCTACCAATA AATGCAATTT GTGACCTGTA TTAATAAAAA NTAAAAAAC TCGAGGGGGG 1500
30 CCCGGTAC 1508

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(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

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GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
GCACCTACCT GTGTTGGTGA GGTGTGTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
50 AGGCTTCCTG CTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC AACTATGAT 180
AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
TGGATTTTCT TCCAAAATGA AAGTTGTGTC TTCTAGACTT TTAGAGAAAT ATCCCCAAGC 300
55 TATCTACACA CTCTGCTCTT CCTGTGCCTT AAATATGTGG TTGGCAAAT CAGTACCTGT 360
TATGGGAGTA TCTGTTGCAT TAGGAACAAT TGAGGAAGTT TGTTCTTTT TCCATCGATC 420
60 ACCACAAC TG CTTTATAGAAC TTGACAACGT AATTTCTGTT CTTTTCAGA ACAGTAAAGA 480

	AAGGGGTAAA GAACTGAAGG AAATCTGCCA TTCTCAGTGG ACAGGCAGGC ATGATGCTTT	540
	TGAAATTTTA GTGGAAGTCC TGCAAGCACT TGTTTTATGT TTAGATGGTA TAAATAGTGA	600
5	CACAAATATT AGATGGAATA ACTATATAGC TGGCCGAGCA TTTGTACTCT GCAGTGCAGT	660
	GTCAGATTTT GATTTTCATTG TTAATATTGT TGTCTTAAA AATGTCCTAT CTTTACAAG	720
10	AGCCTTTGGG AAAAACCTCC AGGGGCAAAC CTCTGATGTC TTCTTTGCGG CCGGTAGCTT	780
	GACTGCAGTA CTGCATTAC TCAACGAAGT GATTGGAAAA TATTGAAGTT TATCATGAAT	840
	TTTGGTTTGA GGAAGCCACA AATTTGGCAA CCAAACTTGA TATTCAAATG AAATCCCTG	900
15	GGAAATTCG CAGAGCTCAC CAGGGTAACT TGAATCTCA GCTAACCTCT GAGAGTTACT	960
	ATAAGAAAC CCTAAGTGT CCAACAGTGG AGCACATTAT TCAGGAACCT AAAGATATAT	1020
20	TCTCAGAACA GCACCTCAAA GCTCTTAAAT GCTTATCTCT GTTACCCTCA GTCATGGGAC	1080
	AACTCAAATT CAATACGTCG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA	1140
	ATCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA	1200
25	AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT	1260
	TTCTTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA	1320
30	ATGAGCGGTA TGAAATGGA CGAAAGCGTC TTAAGCATA TTTGAGGAAC ACTTTGACAG	1380
	ACCAAAGTTC AAGTAACTTG GCTTTGCTTA ACATAAATTT TGATATAAAA CACGACCTGG	1440
	ATTTAATGGT GGACACATAT ATTAACTCT ATACAAGTAA GTCAGAGCTT CCTACAGATA	1500
35	ATTCCGAAAC TGTGGAAAT ACCTAAGAGA CTTTAAAAA TAGGCTTTCT TATATTGAT	1560
	ATTGGAAGA AAAAGCCGTA AGTGTATGTA GACCACTTAA TCACTAAATA TCTTTGCCTA	1620
40	TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG CCCCTGTTG	1680
	AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA AGTGCCATGT	1740
	TTCTTTTGC GTGATCTCTG TTGATGGCAC TCTGGAATTG TTTCAATTAA GTCATTTTAG	1800
45	ACATAGCATT TATTATCACT GTGGATCTCT ACTGTGTTGG TGTATGAAT TCTTTGAAGA	1860
	AATATATTTT GAAGAGGTGT GGGAGGAAG AATACATTTT ATAAATGTT GTAGTGAAGC	1920
50	CCACAATTGA CCTTTGACTA ATAGGAGTTT TAAGTATGTT AAAATCTAT ACTGGACAGT	1980
	TACAAGAAAT TACCGGAGAA AAGCTTGTGA GCTCACCAA CAAGGATTTT AGTGTAGATT	2040
	TTGTCTTTCT TGAACCTAAA GAAACAAATG ACAAAGTTTG AATGGAAAAG CCTGCTGTTG	2100
55	TTCCACATCT CGTTGCTGTT TACATTCCTT TGTGGAGCCT ACATCTTCTT AAGCTTTTTA	2160
	GCAGGTATAT GTTGAACACT TCTGTTTCAT GGTGAGACA GAATCAGAGG CCATGGATAC	2220
60	TGACAACTGA TTTGTCTGTT TTTTCTCTCT GTCTTTTCC ATGACTCTTA TATACTGCCT	2280

5 CATCTTGATT TATAAGCAAA ACCTGGAAAA CCTACAAAAT AAGTGTGTG GTTTATCTAG 2340
AAAAATATGG AAAATATTGC TGTATTTTTT GGTGAAGAAA ATCAATTTTG TATAGTTTAT 2400
TTCAATCTAA ATAAAATGTG AATTTTGTTF AAAGCTTAGG CACATTATTT TTTGTGGGGT 2460
CAAAACATTC TTGTGTAAAT TCTCTTAAAC ATTTGATAAA CAGCTTCACA ATTC 2514
10

(2) INFORMATION FOR SEQ ID NO: 256:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CTGCCTTATG AAGCCGATGC AGAAATTTTG GCTGTGAAAT TTCACACTAT GATAACTGAG 60
25 AAGTGGGGAT TAAATATGGA GTATTGTCGT GGCCAGGCTT ACATTGTCTC TAGTGGATT 120
TCTTCCAAAA TGAAAGTTGT TGCTTCTAGA CTTTATAGAGA AATATCCCCA AGCTATCTAC 180
ACACTCTGCT CTTCTGTGTC CTAAATATG TGGTTGGCAA AATCAGTACC TGTATGGGA 240
30 GTATCTGTTG CATTAGGAAC AATTGAGGAA GTTGTCTCTT TTTTCCATCG ATCACCACAA 300
CTGCTTTTAG AACTTGACAA CGTAATTYCT GTTCTTTTTC AGAACAGTAA AGAAAGGGGT 360
35 AAAGAACTGA AGGAAATCTG CCATTCTCAG TGGACAGGCA GGCATGATGC TTTTGAAATT 420
TTAGTGAAC TCCTGCAAGC ACTTGTTTTA TGTTTAGATG GTATAAATAG TGACACAAAT 480
ATTAGATGGA ATAACTATAT AGCTGGCCGA GCATTTGTAC TCTGCAGTGC AGTGTGAGAT 540
40 TTTGATTTC TGTACTAT TGTGTTCTT AAAAATGTCC TATCTTTTAC AAGAGCCTTT 600
GGGAAAAACC TCCAGGGGCA AACCTCTGAT GTCTTCTTTG CGGCCGGTAG CTTGACTGCA 660
45 GTACTGCATT CACTCAACGA AGTGANTGGA AAATATGAA GTTATCATG AATTTTGGTT 720
TGAGGAAGCC ACAAATTTGG CAACCAAACT TGATATTCAA ATGAACTCC CTGGGAAATT 780
CCGCAGAGCT CACCAGGGTA ACTTGGAATC TCAGCTAACC TCTGAGAGTT ACTATAAAGA 840
50 AACCCTAAGT GTCCCAACAG TGGAGCACAT TATTCAGGAA CTAAAGATA TATTCTCAGA 900
ACAGCACCTC AAAGCTCTTA AATGCTTATC TCTGGTACCC TCAGTCATGG GACAACTCAA 960
55 ATTCAATACG TCGGAGGAAC ACCATGCTGA CATGTATAGA AGTGACTTAC CCAATCCTGA 1020
CACGCTGTCA GCTGAGCTTC ATGTTGGAG AATCAAATGG AAACACAGGG GGAAAGATAT 1080
AGAGCTCCG TCCACCATCT ATGAAGCCCT CCACCTGCCT GACATCAAGT TTTTTCCTAA 1140
60

	TGIGTATGCA TTGCTGAAGG TCCTGTGTAT TCTTCCTGTG ATGAAGGTTG AGAATGAGCG	1200
	GTATGAAAAT GGACGAAAGC GTCTTAAAGC ATATTTGAGG AACACTTTGA CAGACCAAAG	1260
5	GTCAAGTAAC TTGGCTTTGC TTAACATAAA TTTTGATATA AAACACGACC TGGATTTAAT	1320
	GGTGGACACA TATATTAAAC TCTATACAAG TAAGTCAGAG CTTCTTACAG ATAATTCGGA	1380
10	AACGTGGAA AATACCTAAG AGACTTTTAA AAATAGGCTT TCTTATATTT GATATTGGGA	1440
	AGAAAAAGCC GTAAGTGTAT GTAGACCACT TAATCACTAA ATATCTTTGC CTATAGGACT	1500
	CCATTGAATA CATTAGCCAT TGATAATCTA CCTGTTTAAA TGGCCCCGTG TTGAACTCTC	1560
15	AAGCTTTGAA GACCTACCTG TTCTTCCAGA AGAGAACGTT GAAAGTGCCA TGTTCCTTTT	1620
	TGCGTGATCT CTGTTGATGG CACTCTGGAA TTGTTTCAGT TAAGTCATTT TAGACATAGC	1680
20	ATTTATTATC ACTGTGGATC TCTACTTGTT GGGTGTATG AATTCCTTGA AGAAATATAT	1740
	TTTGAAGAGG TGTGGGAGGA AGGAATACAT TTTATAAAAT GTTGTAGTGA AGCCCCAAT	1800
	TGACCTTTGA CTAATAGGAG TTTTAAGTAT GTTAAAAATC TATACTGGAC AGTTACAAGA	1860
25	AATTACCGGA GAAAAGCTTG TGAGCTCACC AAACAAGGAT TTCAGTGTAG ATTTTGTCTT	1920
	TCTTGAACCT AAAGAAACAA ATGACAAAGT TTGAATGGAA AAGCCTGCTG TTGTTCCACA	1980
30	TCTCGTGTCT GTTTACATTC CTTTGTGGAG CCTACATCTT CCTAAGCTTT TTAGCAGGTA	2040
	TATGTTGAAC ACTTCTGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC	2100
	TGATTTGTCT GTTTTTTTTC TCTGTCTTTT TCCATGACTC TTATATACTG CCTCATCTTG	2160
35	ATTTATAAGC AAAACCTGGA AAACCTACAA AATAAGTGTT GTGGTTTATC TAGAAAAATA	2220
	TGGAAATAT TGCTGTTATT TTTGGTGAAG AAAATCAATT TTGTATAGTT TATTTCAATC	2280
40	TAAATAAAAT GTGAATTTTG TTTAAAGCTT AGGCACATTA TTTTGTGTTG GGTCAAAACA	2340
	TTCTTGTGTA AATTCTC	2357

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(2) INFORMATION FOR SEQ ID NO: 257:

	(i) SEQUENCE CHARACTERISTICS:
50	(A) LENGTH: 689 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:
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	ACTTTCTGGT GCAAAAAGAT GTTCAAGCCT TATTTTATAC TTGCCTGCCC CTTTCTCTTT	60
	CATTATTGG AGTGAGCTGC AGCTCTAAGA AGACCTGTTC TTTTGAATGG AGAGTAGCAT	120
60	CAGGAACCAG GATGTGGGTG CGAGGCGTGC TCCTGGCTGT TGCAGATTGC TGCACCCGGG	180

AGCTCTTAGT GGACAGAGCT AGAGGATATG TGCACGTACT TCCATCTCTC TCTCTGTCTC 240
CGATTTTAGC CCAGCACCAC AGGGTACGTT CCAGTTTTC TCTCTTTCCA TAGCTGTAAG 300
5 GCCCTTTCTG GGAATGGTTC TCATTCTCCT TAATCTATTA TTGGGTCAGT TTTCCTGCAT 360
GTCCCCAGCC TCCCATCACT GCCACCCACT CCCCACAGAG ATGCCCTGCT CATCCGACTG 420
10 GGGCTTTGAC TCCCACACTG TGTACCCCTC TTGTGTGGAC GCCCTGCTGC CAAAACCTTC 480
AGCAAACAGC TTTCCAAATG GAAGTTGTCA CTGTCARGGS CTTTACAATC AGCAACAGCA 540
AAATCTACAT GCTGCTGAGG GTCCTGCCTC ATTAAGATGC AATAAATATG TAAGTACATA 600
15 AAAACAGCAA TAGAAGAAAC GTAATGCTTT ATTCTCAAAT ATGNATGTCT ACATAGAAAA 660
GCCAAAATTA TTAAGAATAG TAAGGAATT 689

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(2) INFORMATION FOR SEQ ID NO: 258:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TCGACCCACG CGTCCGCCGA TGTGATGATT CCTGCGTATT CCAAGAACCG GGCCTATGCC 60
35 ATCTTCTTCA TAGTCTTCAC TGTGATAGGG GACGCCCCCG GCGCTGTGCT ATCCTGTGCC 120
GGCCACCCTT GCGTGGTMTT TGCTGCTGTA CTGGTGGCGC CCCTGACCGT GGCTGTCTCC 180
TCTTGAAGGA AGCCTGTTTC TGATGAACCT GCTGACAGCC ATCATCTACA GTCAGTTCCG 240
40 GGGCTACCTG ATGAAATCTC TCCAGACCTC GCTGTTTCGG AGGCGGGTGG GAACCCGGCT 300
GCCTTGAAG TCCTATCCTC CATGGTGGG GAGGAGGAG CCTTCCCTCA GGCAGTTGGG 360
45 GTGAAGCCCC AGAAGTTGCT GCAGGTGCTT CAGAAGGTCC AGCTGGACAG CTCCCACAGA 420
CAGGCCATGA TGGAGAAGGT GCGTTCCTAT GGCAGTGTTG TGCTCTCAGC TGAGGAGTTT 480
CAGAAGCTCT TCAACGAGCT TGACAGAAGT GTGGTTAAAG AGCACCCGCC GAGGCCCGAG 540
50 TACCAGTCTC CGTTTCTGCA GAGCGNCCCA GTTCCTCTTC GGCCACTNAC TACTTTGACT 600
ACCTGGGGAA CCTCATCGCC CTGGCAAACC TGGTGTCCAT TTGCGTGTTC CTGGTGCTGG 660
55 ATGCAGATGT TGCTGCCTGC TGAGCGTGAT GACTTCATCC TGGGGGGTCT CAACTGCGTC 720
TTCATTGTGT ACTACCTGTT GGAGATGCTG GCTCAAGGTC TTTTGCCCTG GGGCCTGCGA 780
60 RGTACYYKT CCTAACCCCA RCAAMGTGTT TTGAACGGGC TCCTCAMCGT TTGTCTGGC 840

	TGGWWKKGSM GATCTCAACT CTGGCTGTGT ACCGATTGCC ACACCCAGGC TGGAGGCCGG	900
	ANATGGTGGG CCTGCTGTCTG CTGTGGGACA TGACCCGCAT ACTGAACATG CTCATCGTGT	960
5	TCCGCTTCCT CGGTATCATC CCCAGCATGA AGCCGATGGC CGTGGTGGCC AGTACCGTCC	1020
	TGGGCCCTGGT GCAAAACATG CGTGCGTTTG GCGGGATCCT GGTGGTGGTC TACTACGTAT	1080
10	TTGCCATCAT TGGGATCAAC TTGTTTAGAG GCGTCATTGT GGCTCTTCCT GGAAACAGCA	1140
	GCCTGGCCCC TGCCAATAGG TCGGCGCCCT GTGGGAGCTT CGAGCAGCTG GAGTACTGGG	1200
	CCAACAACCTT CGATGACTTT GCGGCTGCCC TGGTCACTCT GTGGAACCTG ATGGTGGTGA	1260
15	ACAACTGGCA GGTGTTTCTG GATGCATATC GGCCTACTA AGGCCCGTGG TCCAAGATCT	1320
	ATTTTGTATT GTGGTGGCTG GTGTCTCTG TCATCTGGGT CAACCTGTTT CTGGCCCTGA	1380
20	TTCTGGAGAA CTTCTTCAC AAGTGGGACC CCCGCAGCCA CCTGCAGCCC CTGTCTGGGA	1440
	CCCCAGAGGC CACCTACCAG ATGACTGTGG AGCTCCTGTT CAGGGATATT CTGGAGGAGC	1500
	CCGGGGAGGA TGAGCTCACA GAGAGGCTGA GCCAGCACCC GCACCTGTGG CTGTGCAGGT	1560
25	GACGTCCGGG TCTGCCATCC CAGCAGGGG GGCAGGAGAG AGAGGCTGGC ATAACACAGG	1620
	TGCCCATCAT GGAAGAGGCG GCCATGCTGT GCCCAGCCAG GCAGGAAGAG ACCTTTCTCTC	1680
30	TGACGGACCA CTAAGCTGGG GACAGGAACC AAGTCCTTTG CGTGTGGCCC AACAACCATT	1740
	TACAGAACAG CTGCTGGTGC TTCAGGGAGG CGCCGTGCCC TCCGCTTTCT TTTATAGCTG	1800
	CTTCAGTGAG AATTCCCTTG TCGACTCCAC AGGGACCTTT CAGACAAAAA TGCAAGAAGC	1860
35	AGCGGCCTCC CTGTCCCTT GCAGCTCCG TGGTGCCPTT GCTGCCGGCA GCCCTTGGGG	1920
	ACCACAGGCC TGACCAGGGC CTGCACAGGT TAACCGTCAG ACTTCCGGGG CATTCAGCTG	1980
40	GGAATGATAC TAATACCTCC GATTTTAGCC CAGCACCACA GGTACGTTT CAGTTTMTAT	2040
	TTCTTTCCAT AGCTGTAAGG CCCTTTCTGG GAATGGTTAT CATTCTCCTT AATCTATTAT	2100
	TGGGTCAGTT TTCTGCATG TCCCAGCCT CCCATCACTG CCACCCACTC CCCACAGAGA	2160
45	TGCCCTGCTC ATCCGACTGG GGCTTTGACT CCCACACTGT GTACCCCTCT TGTGTGGAGC	2220
	CCCTGCTGCC AAAACCTTCA GCAAACAGCT TTCCAAATGG AAGTTGTCAC TGTCAGGGCC	2280
50	TTTACAATCA GCAACAGCAA AATCTACATG CTGCTGAGGG TCCTGCCTCA TTAAGATGCA	2340
	ATAAATATGT AAGTACATAA AAAAAAAAAA AAAAAA	2377

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(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

5
TCTGNTCGCC GTCGCCCCGC CCCTGGCCTT TGCCCGGTCG GGCGGGACTT CCTGTGTGCT 60
ATTTCCAAGG ACTCCAAGC GAGGCCGGG ACTGAAGGTG TGGGTGTCGA GCCCTCTGGC 120
10 AGAGGGTTAA CCTGGGTCAA ATGCACGGAT TCTCACCTCG TACAGTTACG CTCTCCCGCG 180
GCACGTCCGC GAGGMYTTGA AGTCCTGAGC GCTCAAGTTT GTCCGTAGTC GAGAGAAGGC 240
CATGGAGGTG CCGCCACCGG CACCGCGGAG CTTTCTCTGT AGAGCATTGT GCCTATTTCC 300
15 CCGAGTCTTT GCTGCCGAAG CTGTGACTGC CGATTCGGAA GTCCCTGAGG AGCGTCAGAA 360
GCGGCTTCCC TACGTCCCAG AGCCCTATTA CCCGGAATCT GGATGGGACC GCCTCCGGGA 420
20 GCTGTTTGGC AAAGACACAG TGAACACTAG TCTGAATGTA TACCGAAATA AAGATGCCTT 480
AAGCCATTTT GTAATTGCAG GAGCTGTAC GGAAGTCTT TTTAGGATAA ACGTAGGCCT 540
GCGTGGCTGG TGGCTGGTGG CATAATTGGA GCCTTGCTGG GCACTCCTGT AGGAGGCCTG 600
25 CTGATGGCAT TTCAGAAGTA CTCTGGTGAG ACTGTTTCAGG AAAGAAAACA GAAGGATCGA 660
AAGGCACTCC ATGAGCTAAA ACTGGAAGAG TGGAAAGGCA GACTACAAGT TACTGAGCAC 720
30 CTCCCTGAGA AAATTGAAAG TAGTTTACAG GAAGATGAAC CTGAGAATGA TGCTAAGAAA 780
ATTGAAGCAC TGCTAAACCT TCCTAGAAAC CCTTCAGTAA TAGATAAACA AGACAAGGAC 840
TGAAAGTGCT CTGAACCTGA AACTCACTGG AGAGCTGAAG GGAGCTGCCA TGTCCGATGA 900
35 ATGCCAACAG ACAGGCCACT CTTTGGTCAG CTTGCTGACA AATTTAAGTG CTGGTACCTG 960
TGGTGGCAGT GGCTTGCTCT TGTCTTTTTC TTTTCTTTT AACTAAGAAT GGGGCTGTTG 1020
40 TACTCTCACT TACTTATCC TTAAATTTAA ATACATACTT ATGTTTGTAT TAATCTATCA 1080
ATATATGCAT ACATGAATAT ATCCACCCAC CTAGATTTTA AGCAGTAAAT AAAACATTTT 1140
45 GCAAAAGATT AAAGTTGAAT TTTACAGTTA AAAAAAAAAA AAAAAAAAAA AAA 1193

(2) INFORMATION FOR SEQ ID NO: 260:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

60
GAAAAACCCA AAGATGCAGA CAATCTCTTT GAACATGAAT TGGGGGCTCT CAATATGGCT 60

	GCATTACTAC GAAAAGAAGA AAGAGCAAGT CTTCTTAGTA ATCTTGGCCC ATGTTGTAAG	120
	GCGTGTGTCT TCAGACGGGA TTCTGCAATT CGAAAGCAGC TTGTTAAAAA TGAGAAGGGC	180
5	ACCATAAAAC AAGCTTACAC GAGTSCCTCA ATGGTAGACA ATGAATTACT TCGATTGAGT	240
	CTTCGGTTAT TTAAGCGGAA GACTACTTGC CATGCTCCAG GACATGAAAA GACTGAAGAT	300
10	AATAAACTTT CACAGTCCAG TATCCAACAG GAAGTGTGTG TGTCTTAAGA CCGAAGTTCA	360
	ATATGGTATT TTTGGTACTG TCTTCCTTCA GCAGTGCATA TTCTTTTGCA AAGTTCTTTG	420
	GTTTGACAAG CATTAGTGAC AAAGGCAGAA AAGATTTATC AGCCATGCTA AAAGAGTGAA	480
15	GAATTTTGAT CTTTAGAGAC ACTAGTTTGT GCCAACTTAA GATTTTACGT TAATTTTAC	540
	ATAGTATTGT ACACTCATGC AAAATAATGT GAAAACATCT AGATTTAGTA GTTTATTCTG	600
20	CGCCTTTTGT TAAACTGAA GATTTTGGAA AATGGTTGTC ACTGCTCTTC CAGCCTATGA	660
	ATATTTTGT GAAATGGAAC CATGGATTTA TGTCTGGATC ATCCATACAG AACCAACAAT	720
	TTTATTCAAA AACAAATGTGT TCATCAAAGT AATTGCTCAC ATTGTGCAGT ACTATGTTGT	780
25	ACAGACCACG TGAAAGGGAA TGCTGGTCTA GCTGGCGTGG TATGTTTATA GGCGAATTC	840
	AGCAGAAGGA AGCCAAAATA GTTTTTCCT TTTGAAAGTT TTTTAAAAAT TATTTTCATGG	900
30	GTCTTTTMT TAATTAATAT GTGTGCATTG TTACAATGTA TGTGGATGT CTTTGACCC	960
	TAAATGCTTT TTTTGTATC AGAGATGTG TACTATTTT ATTTTAAATA AATGTATCTT	1020
	CCCTTTCCTT GTTTTAGATT TACTTTGCTC TTCGTTAATC TTATTCCTGA TGATCTAGAA	1080
35	CATTAGTCAT CAACATTACA TGTTTCATGC TTCAGATATT TTAGTCTTG TGTCTTATT	1140
	GTTGGACAGC TTTAAACAGA GTTGATGGTA CTTCAAATAT AGCTCATTGA TACTTAAGGG	1200
40	CANCTTCCTT GGGATGTGGG CTTTTTGGAA GGAAAAAAT TNCCCCAAG GCAAATCCCA	1260
	GT	1262

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(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDELNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

55

GGCAAACCTT CCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
GGGTTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT	120
CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180

60

	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
5	ACCACTCAG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360
	CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT	420
10	GGATTCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC	480
	TCTTCGTCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTC ACCCCACAAT	540
	AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT	600
15	CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT	660
	CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG	720
20	TTCCAGGMIT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA	780
	TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCCTCA	840
	TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA	900
25	CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTC CTAATGTGGC	960
	TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA	1020
30	CTACATTGCA CAGGTTACGC CAGTATTACG GTGCCAGCAA CAGACCTACT CCACTTGGCT	1080
	ACCTTGCAAT TAAGAATCAT TAAAAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG	1140
35	GAGAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGC	1179

40 (2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

	GGCAAACITTT CCCCCAANGC TTCGAAACTTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
50	GGGTGCGNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT	120
	CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180
55	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
60	ACCACTCAG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360

CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT 420
 GGATTCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTCAAATCA AATTAGACTC 480
 5 TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTT ACCCCACAAT 540
 AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT 600
 CATTCGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT 660
 10 CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG 720
 TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA 780
 15 TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCCTCA 840
 TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA 900
 CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTC CTAATGTGGC 960
 20 TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA 1020
 CTACATTGCA CAGGTTTCAGC CAGTATTACG GTGCCAGCAA CAGACCTACT CCACTTGGCT 1080
 25 ACCCTGCAAT TAAGAATCAT TTAAAAATGT CCTGTGGGGA AGCCATTTCA GACAAGACAG 1140
 GAGAGAAAAA NAANGAAAAG AG 1162

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(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CGGGCTGGGT ATTTGCCTCG CACCATGGCG CCCAAGGGCA AAGTGGGCAC GAGAGGGAAG 60
 AAGCAGATAT TTGAAGAGAA CAGAGAGACT CTGAAGTTCT ACCTGCGGAT CATACTGGGG 120
 45 GCCAATGCCA TTTACTGCCT TGTGACGTTG GTCTTCTTTT ACTCATCTGC CTCATTTTGG 180
 GCCTGGTTGG CCTTGGGCTT TAGTCTGGCA GTGTATGGGG CCAGCTACCA CTCTATGAGC 240
 50 TCGATGGCAC GAGCAGCGTT CTTCTGAGGA TGGGCCCCTG ATGGATGGTG GCACGAGCTC 300
 AACATGGAGC AGGGCATGGC AGAGCACCTT AAGGATGTGA TCCTACTGAC AGCCATCGTG 360
 CAGGTGCTCA GCTGCTTCTC TCTCTATGTC TGGTCTTCTT GGCTTCTGGC TCCAGGCCGG 420
 55 GCCCTTTACC TCCTGTGGGT GAATGTGCTG GGCCCTGGT TCACTGCAGA CAGTGGCACC 480
 CCAGCACCAG AGCACAATGA GAAACGGCAG CGCCGACAGG AGCGGCGGCA GATGAAGCGG 540
 60 TTATAGCCAT TGACATTGTG GCCACAGGCC ACTGGCCCTG GGTGGCTCTG TCAGGGTGCA 600

5 CAGCCCCCTCA TGCCTGGAGC AATGAGGGTC TAGTCCAGGG GCCAAAAGCA GTCTGAGGTA 660
TTGGGTATAC TTATACTCTA TAGGGTCGTT GAATAAATGG CTTAGAATGT GAAAAAAAAA 720
AAAAAAAAA ATTTT 735

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(2) INFORMATION FOR SEQ ID NO: 264:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AAGTGCATGA GCTGCCGATG TGGTGCTTAG TGATTCCGGT TTCGGTCGCT CTCCCGTGTT 60
TCCCGGGCTG GGTATTTGCC TCGCACCATG GCGCCCAAGG GCAAAGTGGG CACGAGAGGG 120
25 AAGAAGCAGA TATTTGAAGA GAACAGAGAG ACTCTGAAGT TCTACCTGCG GATCATACTG 180
GGGGCCAATG CCATTTACTG CCTTGTGACG TTGGTCTTCT TTTACTCATC TGCCTCATTT 240
TGGGCTTGGT TGGCCTGGGC TTTAGTCTGG CAGTGTATGG GGCCAGCTAC CACTCTATGA 300
30 GCTCGATGGC ACGAGCAGCG TTCTCTGAGG ATGGGGCCCT GATGGATGGT GGCATGGACC 360
TCAACATGGA GCAGGGCATG GCAGAGTGAG TGTCCCCCAC CGCCAGCCCA GGCACCTTAA 420
35 GGATGTGATC CTA CTGACAG CCATCGTGCA GGTGCTCAGC TGCTTCTCTC TCTATGTCTG 480
GTCCCTTCTGG CTCTCTGGCTC CAGGCCGGGC CCTTTACCTC CTGTGGGTGA ATGTGCTGGG 540
CCCCCTGGTTC ACTGCAGACA GTGGCACCCC AGCACCAGAG CACAATGAGA AACGGCAGCG 600
40 CCGACAGGAG CGGCGGCAGA TGAAGCGGTT ATAGCCATTG ACGATTTKGC SACNRGCCAC 660
TGGCCCTGGG TGGCTCTGTC AGGGTGACA GCCCCTCATG CCTGGAGCAA TGAGGGTCTA 720
45 GTCCAGGGGC CAAAAGCAGT CTGAGGTATT GGGTATACTT ATACTCTATA GGGTCGTTGA 780
ATA 783

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(2) INFORMATION FOR SEQ ID NO: 265:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

	GGCACGAGGC GCGGGCAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT NCCCTTTCCC	60
	GTGCGGGAGC GCGGGGYCGG GGYCCAGGG ANCCCGGMC ACGGAGAGCG GGAAGAGGAT	120
5	GGATMGCCCG GCCCTCCCC CCGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAAGAAGT TCAGAAGCAA	240
10	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTGATCTC AGCAGTTTGT ACTTCAGAAC	300
	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
	CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC	420
15	AATTTTCAAA CAACCGGTAA CCAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA	480
	CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT	540
20	TAGTGATCA GATGTAAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGTCTTCA	600
	AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA	660
	CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGAAAAGA ACCCTGCTGT	720
25	TTGGCTTAAC ACATCTCAAC CCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG	780
	GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA	840
30	CATCTTGTG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA	900
	AGCCTAAGAA TATGATCAGG TAACTTTGCA CCGACTTTCC CCAAGAGAAA ATTCTAGAA	960
	ATTGAACAAA AATGTTTCCA CTGGCTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
35	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTGTAGATG TATTTTGTAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA	1140
40	TCAAGCAGGA CCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAACATTT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
	TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA	1320
45	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCCTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTAC AGACTGATTG GAATTCCTTC TGTGAAAAG CACACACAAT AAAGAACCCC	1440
50	TCGTTAGCCT TCCTCTGATT TACATTCAAC TCTGATCCCG GGGCCTTAGG TTTGACATGG	1500
	GAGGTGGGAG GAAGATAGCG CATATATTTG CAGTATGAAC TATTGCCTCT GGGACGTTGT	1560
	GAGGAATGTG GCTTTCACCA GAATTTCTAA GGATTTCTGG CTAAATATC ACCTAGCCTG	1620
55	TGGTAATTTT TTTTCCCT	1638
60		

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

10 CGTGCCTACT GCCATGCAGG TACCGGGTCC GGAATTCCCA GGGTCGACCC ACGCGTCCGC 60
TCAGTTGGCA AGGTACCTGG GAAATACTGT TGATCTCAGC AGTTTGTACT TCAGAACTGG 120
15 AAAGATGATG CCTAGTAAAT TACAGAAGAA CAAACAGAGA CTGCGAAACG ATCCTCTCAA 180
TCAAAATAAG GGTAACCAG ACTTGAATAC AACATTGCCA ATTAGACAAA CAGCATCAAT 240
TTTCAACAA CCGTAACCA AAGTCACAAA TCATCCTAGT AATAAAGTGA AATCAGACCC 300
20 ACAACGAATG AATGAACAGC CACGTCAGCT TTTCTGGGAG AAGAGGCTAC AAGGACTTAG 360
TGCATCAGAT GTAACAGAAC AAATTATAAA AACCATTGGAA CTACCCAAAG GTCTTCAAGG 420
25 AGTTGGTCCA GGTAGCAATG ATGAGACCCT TTTATCTGCT GTTGCCAGTG CTTTGACAC 480
AAGCTCTGCG CCAATCAGAG GGCAAGTCTC CGCTGCTGTG GAAAAGAACC CTGCTGTTTG 540
GCTTAACACA TCTCAACCCC TCTGCAAAGC TTTTATGTTC ACAGATGAAG ACATCAGGAA 600
30 ACAGGAAGAG CGAGTACAGC AAGTACGCAA GAAATTGGAA GAAGCACTGA TGGCAGACAT 660
CTTGTGCGGA GCTGCTGATA CAGAAGAGAT GGATATTGAA ATGGACAGTG GAGATGAAGC 720
35 CTAAGAATAT GATCAGGTAA CTTTCGACCG ACTTCCCCA AGAGAAAATT CCTAGAAATT 780
GAACAAAAT GTTCCACTG GCTTTTGCTT GTAAGAAAAA AAATGTACCC GAGCACATAG 840
AGCTTTTAA TAGCACTAAC CAATGCCTTT TTAGATGTAT TTTTGATGTA TATATCTATT 900
40 ATTCAAAAA TCATGTTTAT TTTGAGTCCT AGGACTTAAA ATTAGTCTTT TGTAATATCA 960
AGCAGGACCC TAAGATGAAG CTGAGCTTTT GATGCCAGGT GCAATCTACT GGAAATGTAG 1020
45 CACTTACGTA AAACATTTGT TTCCCCACA GTTTTAATAA GAACAGATCA GGAATTCTAA 1080
ATAAATTTC CAGTTAAAGA TTATTGTGAC TTCACTGTAT ATAAACATAT TTTTATACTT 1140
TATTGAAAGG GGACACCTGT ACATTCTTCC ATCCTCACTG TAAAGACAAA TAAATGATTA 1200
50 TATTCACAGA CTGATTGGAA TTCTTTCTGT TGAAAAGCAC ACACAATAAA GAACCCCTCG 1260
TTAGCCTTCC TCTGATTAC ATTCAACTCT GATCCCGGGG CCTTAGGTTT GACATGGGAG 1320
55 GTGGGAGGAA GATAGCGCAT ATATTGCAG TATGAACTAT TGCTCTGGG ACGTTGTGAG 1380
GAATTGTGCT TTCACCAGAA TTTCTAAGGA TTTCTGGCTT AAATATCACC TAGCCTGTGG 1440
TAATTTTTTT TCCCT 1455
60

(2) INFORMATION FOR SEQ ID NO: 267:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

15 CGCCTGCAGT ACCGGTCCGG AATTCCC GGG TCGACCCACG CGTCGCTGAC CCAGGAGAAG 60
CTGCCCTGTCT ACATCAGCCT GGGCTGCAGC GCGCTGCCGC CGCGGGGCCG GCAGCTGAAC 120
TATGTGCTCT TCAGGGCGGG CACCGTGTG CATTCATCTT TGTACCCCA GCATCTAGCA 180
20 GTGTTGGCAT GTAGTAGGCA CTCAAGAAAT GTGTGTTGAA TGAACGATGC CTGTGACAAG 240
CAAGCGGACT TTATTCTTTC CTGACCCTG CTCCTATGAC ACACCTCCTC CTGACTGCCA 300
CTGTCACTCC TTCAGAGCAG AACTCCTCTA GGAACCTGG ATGGGAACA GCCATGGCCA 360
25 AGGACATCCT GGGTGAAGCA GGGCTACACT TTGATGAACT GAACAAGCTG AGGGTGTGG 420
ACCCAGAGGT TACCCAGCAG ACCATAGAGC TGAAGGAAGA GTGCAAAGAC TTTGTGGACA 480
30 AAATTGCCCA GTTTCAGAAA ATAGTGGTG GTTTAATTGA GCTGTGTGAT CAACTGCAA 540
AAGAAGCAGA AAATGAAAAG ATGAAGGCCA TCGGTGCTCG GAACTTGCTC AAATCTATAG 600
CAAAGCAGAG AGAAGCTCAA CAGCAGCAAC TTCAAGCCCT AATAGCAGAA AAGAAAATGC 660
35 AGCTAGAAAG GTATCGGGTT GAATATGAAG CTTTGTGTAA AGTAGAAGCA GAACAAAATG 720
AATTTATTGA CCAATTATT TTTCAAAAAT GAACTGAAAA TTTGCTTTT ATAGTAGGAA 780
40 GGCAAAACAA AAAAAAGCCT CTCAAAACCA AAAAAACCTC TGTAGCATTC CAGCGGCTTG 840
ACCAATGACC TATGTCACAA GAGGTGGCGT GTAAGGAATG CAGCCCCCTG AAGACAGCAC 900
TACAAGTCTG GGGGAGCCAG TTTTAACATC AGTGACAGC TGCTGCTGGT GGCCCTGCAG 960
45 TGTACGTTCT CACCTCTTAT GCTTAGTTGG AACTAAGCAG TTTGTAACT TTCATCCTTT 1020
TTTTTGTAAT TTCACAAAGC TTTGGAAGGA GARGCAATAA ATTTTGTGTT TCNAAATGGC 1080
50 TTGATG 1086

55 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

5 GGCACGGGAG CAGCCGGGCT GGTCTGCTG CGAGCCGGCG GCCCGGAGTG GGGCGGCGGA 60
 GCAAACATGA ACGTTGGAGT TGCCACAGT GAAGTGAATC CAAATACCCG TGTCATGAAC 120
 AGCCGGGGTA TGTGGCTGAC ATATGCATTG GGAGTTGGCT TGCTTCATAT TGTCTTACTC 180
 10 AGCATTCCTT TCCTCAGTGT TCCTGTTGCT TGGACTTTAA CAAATATTAT ACATAATCTG 240
 GGGATGTACG TATTTTGTCA TGCAGTAAA GGAACACCTT TCGAAACTCC TGACCAGGGT 300
 15 AAAAGCAAGG CTCCTAACTC ATTGGGAACA ACTGGACTAT GGAGTACAGT TTACATCTTC 360
 ACGGAAGTTT TTCACAATT TCCTAATAAT TCTATATTTT CTGGCAAGTT TCTATACGAA 420
 GTATGATCCA ACTCACTTCA TCCTAAACAC AGCTTCTCTC CTGAGTGTAC TAATTCCCAA 480
 20 AATGCCACAA CTACATGGTG TTCGGATCTT TGGAAATTAAT AAGTATTGAA ATGTTTGTAA 540
 ACTGAAAAAA AATTTTACAG CTAAGTAATT TCTTATAAGG AAGGAGTGGT TAGTAACTG 600
 25 CACTGTTTCT CTGATAATGT GAAATGAGAA GTATTTACAT TGGAGGGCCA ATGGCTGGTC 660
 CTTCAAGTGC TGTTTTGAAG TGCAGATTTC CATTAAATGA TGCCTCTGTT TAATACACCT 720
 GGTACATTTC TGAAGAGGGG CTTTATAAGC AGGCTGGGCA GGCCAGCTT ATAAGTTAAA 780
 30 GGGCATCACA GTGAGGGTGT AGTAGATAAA TTCAAGGAAA TAAGAGATTT GTAAGAACT 840
 AGGACCAGCT TAACTTATAA TGAATGGGCA TTGTGTTAAG AAAAGAACAT TTCCAGTCAT 900
 35 TCAGCTGTGG TTATTTAAAG CAGACTTACA TGTAACCCGG AATCCTCTCT ATACAAGTTT 960
 ATTAAAGATT ATTTTATTA CCGTAAAAAA AAAAAAAAAA AAA 1003

40

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ATCAGCATCT ACAAGTAGCA TATTTTGGAT GGTGTTTGTG TGCTACTTCA AAGTAACTAG 60
 GAAAAAATAA TCCTCGCAAC ACAGGTACCT TGTCATGTCA GAATTGGGGG TGTTAGGTTG 120
 55 CCAGTTGTAT CAGTGTGTAT TCATTTTATT ACTTCTTACA GAGCAACAT GAACGTTGGA 180
 GTTGCCACCA GTGAAGTGAA TCCTAATACC CGTGTCTATGA ACAGCCGGGG TATGTGGCTG 240
 60 ACATATGCAT TGGGAGTTGG CTGCTTCAT ATTGCTTAC TCAGCATTC CTTCTTCAGT 300

GTTCCTGTTG CTTGGACTTT AACAAATATT ATACATAATC TGGGGATGTA CGTATTTTTG 360
 CATGCAGTGA AAGGAACACC TTTCGAAACT CCGACCAGG GTAAAGCAAG GCTCCTAACT 420
 5 CATTGGGAAC AACTGGACTA TGGAGTACAG TTTACATCTT CACGGAAGTT TTTCACAATT 480
 TCTCCAATAA TTCTATATTT TCTGGCAAGT TTCTATACGA AGTATGATCC AACTCACITC 540
 10 ATCCTAAACA CAGCTTCTCT CCGAGTGTGA CTAATCCCA AAATGCCACA ACTACATGGT 600
 GTTCGGATCT TTGGAATTAA TAAGTATTGA AATGTTTTGA AACTGAAAAA AAATTTTACA 660
 GCTACTGAAT TTCTTATAAG GAAGGAGTGG TTAGTAAACT GCACTGTTTC TSTGATAATG 720
 15 TGAAATGAGA AGTATTTACA TTGGAGGGCC AATGGCTGGT CCTTCAAGTG CTGTTTTGAA 780
 GTGCAGATTT CCATTAAATG ATGCCTCTGT TTAATACACC TGGTACATTT CTGAAGAGGG 840
 20 GCTTTATAAG CARGCTGGGC AGGCCAGCT TATAAGTTAA AGGGCATCAC AGTGAGGGTG 900
 TAGTAGATAA ATTCAAGGAA ATAAGAGATT TGTAAGAAAC TAGGACCAGC TTAACCTATA 960
 ATGAATGGGC ATTGTGTTAA GAAAAGAACA TTTCAGTCA TTCAGCTGTG GTTATTTAAA 1020
 25 GCAGACTTAC ATGTAAACCG GAATCCTCTC TATACAAGTT TATTAAAGAT TATTTTTATT 1080
 ACCRTACATA TTTCKCTTGT TTTATGTAAG YGGATGTATA TCCTCTTGTT TTATACAAGC 1140
 30 CAGTTCACAC TTATGAGGGT ACTTTTTTGG TTTTGCTGGG CTTAATATTG TGTATTGGTC 1200
 AATGAGGCCA TTTTACANT TATTAACGTT ACAG 1234

35

(2) INFORMATION FOR SEQ ID NO: 270:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

NGAGGTGCGT TCTGAGCCGT CTGTCCTGCG CCAAGATGCT TCAAAGTATT ATTAAAAACA 60
 TATGGATCCC CATGAAGCCC TACTACACCA AAGTTTACCA GGAGATTTGG ATAGGAATGG 120
 50 GGCTGATGGG CTTTCATCGTT TATAAAATCC GGGCTGCTGA TAAAAGAAGT AAGGCTTTGA 180
 AAGCTTCAGC GCCTGCTCCT GGTCACTCACT AACCAGATTT ACTTGGAGTA CATGTGAAAG 240
 55 AAAACGTCAG TCTGCCTGTA AATTTTCAGCA AGCCGTGTGA GATGGGGAGC GTGGAACGTC 300
 ACTGTACACT TGTATAAGTA CGTTTACTTT CATGGCATGA ATAAATGGAT CTGTGAGATG 360
 CACTGCTACC TGGTACTGCT TTCAGTGTGT TCCCCCTCAG CCCTCCGGCG TGTCAGGCAT 420
 60

	ACTCTGAGTA GATAATTTGT CATGCAGCGC ATGCAATCAG AATCTCACTG AGCCACCCAT	480
	CATTGTGAAA TAATTACCTC AGTTGTACAG GACTTGGTGA TCAGGATCCA GGCACCTCACT	540
5	TGTATTCTAC TGCTCAATAA ACGTTTATTA AACT	574
10	(2) INFORMATION FOR SEQ ID NO: 271:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1731 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:	
20	GCTGCAAGGT GCGCCTCGTG CCGCTGCAGA TCCAGCTCAC TACCCTGGGA AATCTTACAC	60
	CTTCAAGCAC TGTGTTTTTC TGCTGTGATA TGCAGGAAAG GTTCAGACCA GCCATCAAGT	120
25	ATTTTGGGGA TATTATTAGC GTGGGACAGA GATTGTTGCA AGGGGCCCGG ATTTTAGGAA	180
	TTCTTGTTAT TGTAACAGAA CAATACCCTA AAGGTCTTGG GAGCACGGTT CAAGAAATG	240
	ATTTAACAGG TGTAAGAACTG GTACTTCCAA AGACCAAGTT TTCAATGGTA TTACCAGAAG	300
30	TAGAAGCGGC ATTAGCAGAG ATTCCCGGAG TCAGGAGTGT TGTATTATTT GGAGTAGAAA	360
	CTCATGTGTG CATCCAACAA ACTGCCCTGG AGCTAGTTGG CCGAGGAGTC GAGGTTTACA	420
35	TTGTGTGCTGA TGCCACCTCA TCAAGAAGCA TGATGGACAG GATGTTTGCC CTCGAGCGTC	480
	TCGCTCRARC CNGGGATCAT AGTGACCACG AGTGNAGGCT GTTCTGCTTC AGCTGGTAGC	540
	TGATAAGGAC CATCCAAAAT TCAAGGAAAT TCAGAATCTA ATTAAGGCGA GTGCTCCAGA	600
40	GTGCGGTCTG CTTTCCAAAG TATAGGACAT TTGAAGAACT GGTATGCTAC TCACTGGTGA	660
	AGGACAGTCA GGTGAAGGAC TGTAAGCCCA CACAAGCTCT TCTTATCTCT ACTAGAATTA	720
45	AAATGTTAAG TCAAAAACGG CTCCTTTTTT GCGCCTCCTA GTGAAGCTTAA CCAGCTAGAC	780
	CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT CCGGTGCTGC TTACCTTCCT	840
	TTTTTGTTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA TGAAGATGCC TGTMTGTCT	900
50	CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT CTTGTGAAGT TTTCTTAAAT	960
	TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTTGG CTTTATATT ACTGTAAGAT	1020
55	GTATATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG ATTGATTGGA ATAAGATTAT	1080
	TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC CACTCCCCTC ACAATGTTGT	1140
	CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT GTTGAATAAT TACATATCTT	1200
60	TCTKGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA AATCTCTGTT AATATTCTCT	1260

CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG CCATATTATT GGTGGAGGGC 1320
 5 TGTMTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT ACCAACATCT TGAATATATA 1380
 TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG GTGGAATATC ATTTTAAAT 1440
 GTTCATGTTT TGTTCATAT TTTCTTCACC TACTCTCCAA ATATTGTAAT GCAAAAAGTC 1500
 10 TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCATGTT TCTCTTCGAT AAATTTATTT 1560
 TCATTAAATA CTTRTAGAG GGTTTTGAAA TGTMTTCAA ATATGTGAAA TGTGAACTG 1620
 15 CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG ATTGAAATTA TTTTGNCTC 1680
 CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT ATTTATTTAA G 1731

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(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1320 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

30 CTGCITAGGA AGAGAAGGTC AGAGTTGCG GGGCAGAGG CATTCTTGCC GCTGGCCCAG 60
 TCACTATGTA GTGGAGGGGC AGACACCCTC CCGCAAATTC TGGAAGGTTT TTAGTCTCGA 120
 35 CTAGGGCAGT AGCCCAGGAC TCCTAGTCGC CGGCTTCAGG TCACTGCCCG CTGAACGGAG 180
 CTGCCGTGCG CATGTTTGGC TGCTTGGTGG CGGGAGGCT GGTGCAACA GCTGCACAGC 240
 40 AAGTGGCAGA GGATAAATTT GTTTTGAAT TACCTGATTA TGAAAGTATC AACCATGTTG 300
 TGGTTTTTAT GCTGGGAACA ATCCCATTTT CTGAGGGAAT GGGAGGATCT GTCTACTTTT 360
 CTTATCCTGA TTCAAATGGA ATGCCAGTAT GGMAACTCCT AGGATTTGTC ACGAATGGGA 420
 45 AGCCAAGTGC CATCTTCAA ATTTAGGTC TTAAATCTGG AGAAGGAAGC CAACATCCTT 480
 TTGGAGCCAT GAATATTGTC CGAACTCCAT CTGTTGCTCA GATTGGAATT TCAGTGAAT 540
 TATTAGACAG TATGGCTCAG CAGACTCCTG TAGGTAATGC TGCTGTATCC TCAGTTGACT 600
 50 CATTCACTCA GTTCACACAA AAGATGTTGG ACAATTTCTA CAATTTTGCT TCATCATTTG 660
 CTGTCTCTCA GGCCAGATG ACACCAAGCC CATCTGAAAT GTTCATTCCG GCAAAATGTG 720
 55 TTCTGCAAAT GGTATGAGGC ATNTCTGTC TCCAATATTA AGGCTTTTTA TAACTGAATA 780
 TCTATTTTGT CTATGAATAT ATTCCTTTT TGACATTTAA ACATATTTCT TTATTGTGAA 840
 60 CATCAGCACT GCATGCCATT AAAGTATGTA CTATAGAGAT CTGATGAGAA ACAGTTCTTA 900